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(54) Title: METHODS OF DIAGNOSIS OF BLADDER CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF BLADDER CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in bladder cancer. Also described are such genes whose expression is further up-regulated or down-regulated in drug-resistant bladder cancer cells. Related methods and compositions that can be used for diagnosis, prognosis, or treatment of bladder cancer are disclosed. Also described herein are methods that can be used to identify modulators of bladder cancer.

CROSS-REFERENCES TO RELATED APPLICATIONS

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BACKGROUND OF THE INVENTION

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Within the United States, bladder cancer rates are higher among people who reside in northern versus southern states, and is higher for people who live in urban versus rural areas. Although this difference suggests that environmental as well as genetic factors may contribute to the development and progression of the disease, other studies confirm that certain genes play a role in bladder cancer.. For example, expression of the tumor suppressor gene p53 has been associated with an adverse prognosis for patients with invasive bladder cancer. A retrospective study of 243 patients treated by radical cystectomy found that the presence of nuclear p53 was an independent predictor for recurrence among patients with mid to late stage tumors. Esrig, et al (1994) N.E.J. Med. 331:1259-64.

Urinary bladder cancers represent a spectrum of diseases that can be grouped into three general categories: superficial, invasive, and metastatic. The prognosis for treatment is highly dependent on the stage at which the tumor is first diagnosed. A unique aspect of bladder cancer treatment is that repeated surgical biopsy is an integral part of routine patient management. This has permitted the conduct of molecular genetic studies of tumors from specific stages of the disease. The results of these studies suggest that bladder cancers develop and progress along at least two discrete pathways, which may account for differences in invasiveness and metastatic potential. Incorporating molecular genetic factors into the current paradigm for diagnosis and treatment will optimize the probability of cure and allow the quality of life for bladder cancer patients to be maintained.

Early detection and treatment can prevent reoccurrence and progression of the disease to an incurable stage. Thus, the identification of novel diagnostic markers and therapeutic targets will improve the current treatment of bladder cancer patients. While industry and academia have identified novel sequences, there has not been an equal effort exerted to identify the function of these novel sequences in disease states. The elucidation of a role for novel proteins and compounds in disease states for identification of diagnostic markers and therapeutic targets is essential for improving the current treatment of bladder cancer patients. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of bladder cancer. Additionally, provided herein are molecular targets for therapeutic intervention in bladder cancer and other related bladder diseases.. Further provided are

methods that can be used to screen candidate bioactive agents for the ability to modulate bladder cancer.

SUMMARY OF THE INVENTION

5 The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in bladder cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate bladder cancer, such as hormones or antibodies. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

10 In one aspect, the present invention provides a method of detecting a bladder cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.

15 In one embodiment, the present invention provides a method of determining the level of a bladder cancer associated transcript in a cell from a patient.

 In one embodiment, the present invention provides a method of detecting a bladder cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.

20 In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-13.

 In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

 In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

25 In one embodiment, the polynucleotide is immobilized on a solid surface.

 In one embodiment, the patient is undergoing a therapeutic regimen to treat bladder cancer. In another embodiment, the patient is suspected of having metastatic bladder cancer.

 In one embodiment, the patient is a human.

 In one embodiment, the bladder cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of bladder cancer, the method comprising the steps of: (i) providing
5 a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a bladder cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic bladder cancer. In a further
10 embodiment, the patient has a drug resistant form of bladder cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the bladder cancer-associated transcript to a level of the bladder cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

15 Additionally, provided herein is a method of evaluating the effect of a candidate bladder cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1A-
20 13.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-13.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded
25 by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-13.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-13.

In one embodiment, the antibody is conjugated to an effector component, e.g., a
30 fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting a bladder cancer cell in a biological sample from a patient, the method comprising contacting the biological
5 sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to bladder cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from
Tables 1A-13.

10 In another aspect, the present invention provides a method for identifying a compound that modulates a bladder cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a bladder cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13; and (ii) determining the functional effect of the
15 compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

20 In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of a bladder cancer-associated cell to treat bladder cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound
25 identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having bladder cancer or to a cell sample isolated therefrom; (ii) comparing the level of gene expression of a
30 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence

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as shown in Tables 1A-13 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of bladder cancer.

5 In one embodiment, the control is a mammal with bladder cancer or a cell sample therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

 In one embodiment, the test compound is administered in varying amounts or concentrations. In another embodiment, the test compound is administered for varying time
10 periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

 In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1A-13 are individually compared to their respective levels in a control cell sample or mammal. In a
15 preferred embodiment the plurality of polynucleotides is from three to ten.

 In another aspect, the present invention provides a method for treating a mammal having bladder cancer comprising administering a compound identified by the assay described herein.

 In another aspect, the present invention provides a pharmaceutical composition for
20 treating a mammal having bladder cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

 In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in a bladder cancer. In one embodiment, a gene is selected from Tables 1A-13. The method further includes
25 adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

 In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary
30 when present, and wherein the comparison can occur after addition or removal of the drug

candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate bladder cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the bladder cancer modulatory protein, or an animal lacking the bladder cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1A-13, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with bladder cancer is provided. The method comprises determining the expression of a gene of Tables 1A-13 in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with bladder cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in bladder cancer.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a bladder cancer modulating protein (bladder cancer modulatory protein) or a fragment thereof and an antibody which binds to said bladder cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining a bladder cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said bladder cancer modulatory protein or fragment thereof. The method further includes determining the binding of said bladder cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits bladder cancer.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a

composition comprising a bladder cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1A-13.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a bladder cancer modulating protein, preferably encoded by a nucleic acid of Tables 1A-13 or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a bladder cancer modulating protein, preferably selected from the nucleic acids of Tables 1A-13, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of a bladder cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1A-13.

In another aspect of the invention, a method of treating an individual for bladder cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of a bladder cancer modulating protein. In another embodiment, the method comprises administering to a patient having bladder cancer an antibody to a bladder cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for bladder disease (BD), e.g., cancer, including metastatic bladder cancer, as well as methods for screening for compositions which modulate bladder diseases. Also provided are methods and compositions for treating bladder disease. Various related conditions where these markers may be useful also, include, e.g., carcinoma in situ, various stages of papillary carcinomas; and such conditions in different stages, layers, structural portions, etc.

Recent advances in molecular medicine, generally, have increased the interest in tumor-specific cell surface antigens that could serve as diagnostic or prognostic markers, or as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in other, e.g., normal, adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated, as a physiological consequence of such expression would be limited. Examples of such antigens in cancers other than bladder cancer include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. Maloney, et al. (1997) Blood 90:2188-2195; and Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

Definitions

The term "bladder cancer protein" or "bladder cancer polynucleotide" or "bladder cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1A-13; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1A-13, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-13 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of over a region of at least

about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1A-13. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A
5 "bladder cancer polypeptide" and a "bladder cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" bladder cancer protein or nucleic acid refers to a bladder cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type bladder cancer
10 polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of splicing, including alternative splicing, or post-translation processing.

"Biological sample" as used herein is a sample of biological tissue or fluid, e.g., that contains nucleic acids or polypeptides of a bladder cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g.,
15 humans, or rodents, e.g., mice and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, urine, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most
20 preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, or mouse; rabbit; or a bird; reptile; or fish.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g.,
25 isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same
30 or have a specified percentage of amino acid residues or nucleotides that are the same (e.g.,

about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters
5 described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or additions, substitutions, naturally occurring variants, e.g., polymorphic or allelic, and man-
10 made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to
15 which test sequences are compared. When using a sequence comparison computer algorithm, test and reference sequences, subsequence coordinates, and sequence algorithm program parameters are typically designated. Default or alternative program parameters can be selected. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

20 A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from about 20-600, usually about 50-200, more usually about 100-150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are
25 well-known in the art. Optimal alignment of sequences for comparison can be conducted, by, e.g., the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l Acad. Sci. USA 85:2444-448, computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer
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Group, 575 Science Dr., Madison, WI), or manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Lippincott.

Preferred algorithms suitable for determining percent sequence identity and sequence
5 similarity include the BLAST and BLAST 2.0 algorithms. See Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402; and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information
10 (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for
15 initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to
20 calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN
25 program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of
30 both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between
5 two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

10 An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another
15 indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an
20 expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

25 The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a
30 preparation is substantially purified. In particular, an isolated nucleic acid is separated from

some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments typically denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95%
5 pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which
10 at least one amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and a non-naturally occurring amino acid polymer.

The term "amino acid" embraces naturally occurring or synthetic amino acids, amino acid analogs, and amino acid mimetics. Naturally occurring amino acids are those encoded
15 by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs include compounds that share a basic chemical structure with a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, or an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have
20 modified R groups (e.g., norleucine) or modified peptide backbones, but share some basic chemical structure with a naturally occurring amino acid. Amino acid mimetics include chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by their commonly known three letter symbols
25 or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to amino acid or nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to
30 those nucleic acids which encode identical or essentially identical amino acid sequences, or

where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Each nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions for one another include: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M). See, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman.

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. See, e.g., Alberts, et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The

Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains, which are portions of a polypeptide that often form a compact unit of the polypeptide, and are typically about 25-500 amino acids long. Typical domains are made of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are polymers, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds. In some cases, nucleic acid analogs are included that may have alternate backbones, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149); phosphorothioate (Mag, et al. (1991), Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048); phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-322); O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207. Other analog nucleic acids include those with positively charged backbones (Denpcy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101); non-ionic backbones (U.S. Patent Nos. 5,386,023; 5,637,684; 5,602,240; 5,216,141; and 4,469,863; Kiedrowshi, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426;

Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597-xxx; Chapters 2-3 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx); and non-ribose backbones (see U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6-7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also contemplated. See Jenkins and Turner (1995) Chem. Soc. Rev. 24:169-176. Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News. Modifications of the ribose-phosphate backbone may be made, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which include peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. The PNA backbone typically exhibits improved hybridization kinetics, exhibiting larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. And due to their non-ionic nature, hybridization of the polymers is relatively insensitive to salt concentration. In addition, PNAs are not as easily degraded by cellular enzymes, and can be more stable.

The nucleic acids may be single stranded or double stranded, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine, hypoxanthine,

isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures.

5 Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. Direct or indirect methods are contemplated. For example, useful labels include ^{32}P , fluorescent
10 dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the bladder cancer nucleic acids, proteins, and antibodies. Methods are well known for conjugating the antibody to the label,
15 including those methods described by Hunter, et al. (1962) Nature 144:945-946; David, et al. (1974) Biochemistry 13:1014-021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or
20 noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to a target, e.g., an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds; fluorescent compounds; an enzyme or substrate; tags such as epitope tags; a toxin; activatable moieties; a chemotherapeutic agent; a lipase; an antibiotic; a radioisotope emitting "hard", e.g., beta radiation; or an attracting moiety.

25 A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding
30 partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which streptavidin linked label may bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operable linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced

recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above.

5 The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a
10 coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

 A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid
15 sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is
20 active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

25 An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

5 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview
10 of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Techniques in Biochemistry and Molecular Biology; vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which
15 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g.,
20 about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least about two times background, preferably about 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC,
25 and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-

65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols. A Guide to Methods and Applications Academic Press NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least about twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a bladder cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the bladder cancer protein or nucleic acid, e.g., a functional, physical, or chemical effect, such as the ability to decrease bladder cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cell viability, cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of bladder cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a bladder cancer protein sequence, e.g., functional, enzymatic, physical and chemical effects.

Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the bladder cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation or metabolism. Determination of the functional effect of a compound on bladder cancer can also be performed using bladder cancer assays, such as, in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of bladder cancer cells. Functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for bladder cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of bladder cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of bladder cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of bladder cancer proteins, e.g., antagonists. Antisense nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate bladder cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of bladder cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g.,

expressing the bladder cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of bladder cancer can also be identified by incubating bladder cancer cells with the test compound and determining increases or decreases in the expression of 1 or more bladder cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more bladder cancer proteins, such as bladder cancer proteins encoded by the sequences set out in Tables 1A-13.

Samples or assays comprising bladder cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably about 50%, more preferably about 25-0%. Activation of a bladder cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably about 150%, more preferably about 200-500% (e.g., two to five fold higher relative to the control), more preferably about 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 of Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene.

Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an
5 immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG,
10 IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one
15 "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized
20 fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - CH_1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab
25 with part of the hinge region. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using

recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries. See, e.g., McCafferty, et al. (1990) Nature 348:552-554.

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques can be used. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; and Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of bladder cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue (e.g., normal bladder or other

tissue) may be distinguished from cancerous or metastatic cancerous tissue of the bladder, or bladder cancer tissue or metastatic bladder cancerous tissue can be compared with tissue samples of bladder and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different bladder cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in bladder cancer versus non-bladder cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate bladder cancer, and thus tumor growth or recurrence, in a particular patient; or does chemotherapy or radiation therapy induce expression of particular targets. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of bladder cancer in the tissue or origin of a primary tumor. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the bladder cancer expression profile. This may be done by making biochips comprising sets of important bladder cancer genes, which can then be used in these screens. These methods can also be applied on the protein basis; that is, protein expression levels of the bladder cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the bladder cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense or inhibitory nucleic acids, or the bladder cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in bladder disease or cancer relative to normal tissues and/or non-malignant bladder tissue, herein termed "bladder cancer sequences." As outlined below, bladder cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in bladder cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the bladder cancer sequences are from humans; however,

as will be appreciated by those in the art, bladder cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other bladder cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets, e.g., (dogs, cats, etc.). Bladder cancer sequences from other organisms may be obtained using the techniques outlined below.

Bladder cancer sequences can include both nucleic acid and amino acid sequences. Bladder cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications. Biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the bladder cancer sequences can be generated.

A bladder cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the bladder cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying bladder cancer-associated sequences, the bladder cancer screen typically includes comparing genes identified in different tissues, e.g., normal, non-malignant, or cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing bladder cancer samples with metastatic cancer samples from other cancers, such as lung, bladder, gastrointestinal cancers, ovarian, etc. Samples of different stages of bladder cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal bladder, but also including, and not limited to lung, heart, brain, liver, bladder, kidney,

muscle, colon, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the bladder cancer screen that are expressed in a significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable
5 that the target be disease specific, e.g., not be expressed on critical organs.

In a preferred embodiment, bladder cancer sequences are those that are up-regulated in bladder cancer; that is, the expression of these genes is higher in the bladder cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about
10 five-fold or higher being preferred. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and sequences of accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7 and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL)
15 and DNA Database of Japan (DDBJ).

In another preferred embodiment, bladder cancer sequences are those that are down-regulated in the bladder cancer; that is, the expression of these genes is lower in bladder cancer tissue as compared to non-cancerous tissue (see, e.g., Tables 1A-13). "Down-regulation" as used herein often means at least about a two-fold change, preferably at least
20 about a three fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in bladder cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas
25 of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with bladder cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation. See Anderson (June 11-12, 1998) Pharmaceutical Proteomics:
30 Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference,

Coronado, CA. Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, 5 saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic 10 database of the invention can be maintained on an electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent that similar databases can be assembled for 15 assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing bladder cancer, e.g., the identification of bladder cancer-associated sequences described herein, provide an abundance of information, which can be correlated 20 with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

25 An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing 30 information in a format that allows a collection of partial-length DNA sequences to be

catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge Univ. Press; Baxevanis and Ouellette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Oxford Univ. Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford Univ. Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g.,

with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for bladder cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention
5 in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at
10 least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem,
15 ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result
20 obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data
25 file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of
30 the query target and results are output via an I/O device. For example, a central processor

can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of bladder cancer-associated proteins

Bladder cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the bladder cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In

addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the bladder cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases

and receptor serine/threonine protein kinases contain a single transmembrane domain.

However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain

5 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors
10 include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved
15 motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example,
20 growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or
25 may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Bladder cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful
30 in imaging modalities. Antibodies may be used to label such readily accessible proteins in

situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods.

5 Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the bladder cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted
10 proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g. secretion into the blood stream), or exocrine (secretion, e.g., through a
15 duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Bladder cancer proteins that are secreted or released proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum,
20 or urine tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of bladder cancer nucleic acids

As described above, bladder cancer sequence is initially identified by substantial
25 nucleic acid and/or amino acid sequence homology or linkage to the bladder cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The bladder cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-13, can be fragments of larger genes, e.g., they are nucleic acid segments.

"Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the bladder cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see,

<http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a bladder cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire bladder cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant bladder cancer nucleic acid can be further-used as a probe to identify and isolate other bladder cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant bladder cancer nucleic acids and proteins.

The bladder cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the bladder cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense/inhibition applications. Alternatively, the bladder cancer nucleic acids that include coding regions of bladder cancer proteins can be put into expression vectors for the expression of bladder cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to bladder cancer nucleic acids (both the nucleic acid sequences outlined in the tables and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the bladder cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that

hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be a number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations
5 is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

10 A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole
15 genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a
20 particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical
25 equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of
30 the biotinylated probe to the streptavidin. By "covalent binding" and grammatical

equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See WO 00/55627.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being

particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of bladder cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a bladder cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of bladder cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative

PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification. See, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com.

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569; Landegren, et al. (1988) Science 241:1077-1080; and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Nat'l Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:1874-1878), dot PCR, and linker adapter PCR, etc.

Expression of bladder cancer proteins from nucleic acids

In a preferred embodiment, bladder cancer nucleic acids, e.g., encoding bladder cancer proteins, are used to make a variety of expression vectors to express bladder cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the bladder cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a

promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation; two sequences may be operably linked if they are physically linked on a single polynucleotide. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the bladder cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are useful in the present invention.

In addition, an expression vector may comprise additional elements. The expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and replication. For integrating expression vectors, the expression vector may contain at least one sequence homologous to the host cell genome, and preferably two homologous sequences

which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known (e.g., Fernandez and Hoeffler, *supra*).

5 In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

 The bladder cancer proteins of the present invention may be produced by culturing a host cell transformed with an expression vector under the appropriate conditions to induce or
10 cause expression of the bladder cancer protein. Conditions appropriate for bladder cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will typically require optimizing the growth and proliferation of the host cell, while the use of an
15 inducible promoter typically requires identifying the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and harvest time selection can be crucial for product yield.

 Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, insect, and
20 animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

 In a preferred embodiment, the bladder cancer proteins are expressed in mammalian
25 cells. Mammalian expression systems include retroviral and adenoviral systems. Retroviral vector systems are described in PCT/US97/01019 and PCT/US97/01048. Of particular use are promoters from mammalian viral genes, since viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the
30 CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription

termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

5 Methods of introducing exogenous nucleic acid into mammalian and other hosts are well known, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

10 In another embodiment, bladder cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. Synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. A bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. Often an efficient
15 ribosome binding site is desirable. The expression vector may include a signal peptide sequence that provides for secretion of the bladder cancer protein. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may include a selectable marker gene to allow for the selection of bacterial
20 strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs, e.g., ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline, or biosynthetic genes, e.g., those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus*
25 cremoris, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using, e.g., calcium chloride treatment, electroporation, and other methods.

 Bladder cancer proteins can also be produced in insect cells. See, e.g., Miller, et al. (1997) Baculovirus Expression Vectors: A Laboratory Manual Oxford Books; ISBN:
30 0716770172; and Makrides (1999) Prot. Expr. Purif. 17:183-202.

Bladder cancer protein may be produced in yeast cells. Yeast expression systems exist with expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*. See, e.g., Jones, et al. (eds. 5 1993) The Molecular and Cellular Biology of the Yeast Saccharomyces: Gene Expression CSH Press; ISBN: 0879693657.

The bladder cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the bladder cancer protein may be fused to a carrier protein to form an 10 immunogen. Alternatively, the bladder cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the bladder cancer protein is a bladder cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression or purification purposes.

The bladder cancer protein is typically purified or isolated after expression. Bladder 15 cancer proteins may be isolated or purified in a variety of ways, depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, reverse-phase HPLC chromatography, and chromatofocusing. The bladder cancer protein may be purified using a standard anti-bladder cancer protein antibody 20 affinity column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see, e.g., Scopes (1982) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the bladder cancer protein. In some instances no purification will be necessary, which may depend on the intended use.

25 Once expressed and purified, if necessary, the bladder cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of bladder cancer proteins

In one embodiment, the bladder cancer proteins are derivative or variant bladder cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative bladder cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at most residues within the bladder cancer peptide.

Certain embodiments of bladder cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the bladder cancer protein, using cassette or PCR, mutagenesis, or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant bladder cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are often characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the bladder cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. To optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed bladder cancer variants screened for the optimal combination of desired activities. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is performed using assays of bladder cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be

tolerated. Deletions range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combinations thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the bladder cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the bladder cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the bladder cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. Substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, e.g., the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic acid or aspartic acid; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

Covalent modifications of bladder cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a bladder cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a bladder cancer polypeptide. Derivatization with bifunctional agents is useful, e.g., for crosslinking bladder

cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-bladder cancer polypeptide antibodies or screening assays. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutaminy and asparaginy residues to the corresponding glutamic and aspartic residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine or tyrosine residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (pp. 79-86, Creighton (1984) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the bladder cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence bladder cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence bladder cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express bladder cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to bladder cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence bladder cancer polypeptide (for O-linked glycosylation sites). The bladder cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the bladder cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the bladder cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide.

Such methods are described in the art, e.g., in WO 87/05330, and pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the bladder cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art. See, e.g., Hakimuddin, et al. (1987) Arch. Biochem. Biophys. 259:52-57; and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases. See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of bladder cancer comprises linking the bladder cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337.

Bladder cancer polypeptides of the present invention may also be modified to form chimeric molecules comprising a bladder cancer polypeptide fused to a heterologous polypeptide or amino acid sequence. In one embodiment, a chimeric molecule comprises a fusion of a bladder cancer polypeptide with an epitope tag. The epitope tag is generally placed at the amino- or carboxyl-terminus of the bladder cancer polypeptide. The presence of such epitope-tagged forms of a bladder cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the bladder cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a bladder cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616);

and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other bladder cancer proteins of the bladder cancer family, and bladder cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related bladder cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the bladder cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known. See, e.g., Innis (1990) PCR Protocols, supra.

Antibodies to bladder cancer proteins

In a preferred embodiment, when the bladder cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the bladder cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller bladder cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known (see, e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a

nucleic acid of the tables or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor.

5 Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected as appropriate.

The antibodies may be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1A-13 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (pp. 59-103, Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two

epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Tables 1A-13 or a fragment thereof, the other one is for another antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create
5 multivalent reagents.

In a preferred embodiment, the antibodies to bladder cancer protein are capable of reducing or eliminating a biological function of a bladder cancer protein, as is described below. That is, the addition of anti-bladder cancer protein antibodies (either polyclonal or preferably monoclonal) to bladder cancer tissue (or cells containing bladder cancer) may
10 reduce or eliminate the bladder cancer. Generally, at least about 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred, and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the bladder cancer proteins are humanized antibodies (e.g., Xenerex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein
15 Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary
20 determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the
25 imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise
30 at least a portion of an immunoglobulin constant region (Fc), typically that of a human

immunoglobulin. See Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596. Humanization can be performed, e.g., following the method of Winter and co-workers (see Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or of human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Neuberger (1996) Nature Biotechnology 14:826 commenting on Fishwild, et al. (1996) Nature Biotechnology 14:845-51; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of bladder cancer with an antibody raised against bladder cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient), which may be used to target a label or toxin. Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As

appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

5 In a preferred embodiment the bladder cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted bladder cancer protein.

10 In another preferred embodiment, the bladder cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the bladder cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane bladder cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-
15 competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the bladder cancer protein. The antibody is also an antagonist of the bladder cancer protein. Further, the antibody prevents activation of the transmembrane bladder cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the bladder cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or
20 sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, bladder cancer is
25 treated by administering to a patient antibodies directed against the transmembrane bladder cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

 In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be a number of molecules, including labelling moieties such as
30 radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the

therapeutic moiety is a small molecule that modulates the activity of the bladder cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the bladder cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity
5 associated with bladder cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to bladder cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with bladder cancer. Cytotoxic agents are numerous and varied and include, but are not limited to,
10 cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against bladder cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to
15 the antibody. Targeting the therapeutic moiety to transmembrane bladder cancer proteins not only serves to increase the local concentration of therapeutic moiety in the bladder cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the bladder cancer protein against which the
20 antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the bladder cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a
25 nuclear localization signal.

The bladder cancer antibodies of the invention specifically bind to bladder cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_D of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also
30 important.

Detection of bladder cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the bladder cancer phenotype. Expression levels of genes in normal tissue (e.g., not experiencing bladder cancer) and in bladder cancer tissue (and in some cases, for varying severities of bladder cancer that relate to prognosis, as outlined below), or in non-malignant disease, are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus bladder cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR,

northern analysis and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from about 300-1000% being especially preferred.

- 5 Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the bladder cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass
- 10 spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to bladder cancer genes, e.g., those identified as being important in a bladder cancer or disease phenotype, can be evaluated in a bladder cancer diagnostic test.

- In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.
- 15 Similarly, these assays may be performed on an individual basis as well.

- In this embodiment, the bladder cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of bladder cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

- 20 In a preferred embodiment nucleic acids encoding the bladder cancer protein are detected. Although DNA or RNA encoding the bladder cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a bladder cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to,
- 25 oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method
- 30 permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid

probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example, a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a bladder cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, bladder cancer proteins, including intracellular, transmembrane or secreted proteins, find use as diagnostic or prognostic markers of bladder cancer, or to assist in selecting therapy based on expression profile and archival data. Detection of these proteins in putative bladder cancer tissue allows for detection or diagnosis of bladder cancer. In one embodiment, antibodies are used to detect bladder cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the bladder cancer protein is detected, e.g., by immunoblotting with antibodies raised against the bladder cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the bladder cancer protein find use in situ imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) "Antibodies in Cell Biology" Methods in Cell Biology (vol. 37)). In this method cells are contacted with from one to many antibodies to the bladder cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable

label. In another method the primary antibody to the bladder cancer protein(s) contains a detectable label, e.g. an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of bladder cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing bladder cancer from blood, serum, plasma, stool, urine, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of bladder cancer proteins. Antibodies can be used to detect a bladder cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous bladder cancer protein.

In a preferred embodiment, in situ hybridization of labeled bladder cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including bladder cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to bladder cancer, clinical, pathological, or other information, e.g., in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, bladder cancer probes may

be attached to biochips for the detection and quantification of bladder cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR methods may provide more sensitive and accurate quantification.

5 Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) Science 279:84-88; and Heid (1996) Genome Res. 6:986-94.

In a preferred embodiment, the bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified bladder cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the bladder cancer phenotype or an identified physiological function of a bladder cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in bladder cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the bladder cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing bladder cancer, with changes of at least about 10%, preferably about 50%, more preferably about 100-300%, and in some

embodiments about 300-1000% or greater. Thus, if a gene exhibits about 4-fold increase in bladder cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, about 10-fold decrease in bladder cancer tissue compared to normal tissue often provides a target value of about 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the bladder cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein..

In this embodiment, the bladder cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of bladder cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more bladder cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1A-13. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate bladder cancer, modulate bladder cancer proteins, bind to a bladder cancer protein, or interfere with the binding of a bladder cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the bladder cancer phenotype or the expression of a bladder cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter

expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a bladder cancer phenotype, e.g., to a normal tissue or non-malignant fingerprint. In another embodiment, a modulator induced a bladder cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than about 100 and less than about 2,500 daltons. Preferred small molecules are less than about 2000, or less than about 1500 or less than about 1000 or less than about 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl, or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a bladder cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a bladder cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See, e.g., Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88); peptoids (PCT Publication No WO 91/19735); encoded peptides (PCT Publication WO 93/20242); random bio-oligomers (PCT Publication WO 92/00091); benzodiazepines (U.S. Pat. No. 5,288,514); diversomers such as hydantoins, benzodiazepines, and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-6913); vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-6570); nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218); analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-2662); oligocarbamates (Cho, et al. (1993) Science 261:1303-1305); and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Strategene, Corp.); peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083); antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14:309-314, and PCT/US96/10287);

carbohydrate libraries (Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853); and small organic molecule libraries (see, e.g., benzodiazepines, Baum (p. 33, Jan 18, 1993) C&E News); isoprenoid (U.S. Patent No. 5,569,588); thiazolidinones and metathiazanones (U.S. Patent No. 5,549,974); pyrrolidines (U.S. Patent Nos. 5,525,735 and 5,519,134); morpholino compounds (U.S. Patent No. 5,506,337); benzodiazepines (U.S. Patent No. 5,288,514); and the like.

Devices for the preparation of combinatorial libraries are commercially available. See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; and 9050 Plus, Millipore, Bedford, MA.

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca, Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, NJ; Asinex, Moscow, Ru; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of bladder cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in

arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA; etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate nucleotide or amino acid substitutions. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the

length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of bladder cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag

or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the bladder cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a bladder cancer expression pattern leading to a normal expression pattern, or to modulate a single bladder cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated bladder cancer tissue reveals genes that are not expressed in normal tissue or bladder cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for bladder cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated bladder cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of bladder cancer cells, that have an associated bladder cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or

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retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some
5 period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., bladder cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress the bladder cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on
10 bladder cancer activity. By defining such a signature for the bladder cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual
15 genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "bladder cancer proteins" or a "bladder cancer modulatory protein". The bladder cancer modulatory protein may be a
20 fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables 1A-13. Preferably, the bladder cancer modulatory protein is a fragment. In a preferred embodiment, the bladder cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of Tables 1A-13. In another embodiment, the sequences are naturally occurring allelic variants of a protein
25 encoded by a nucleic acid of Tables 1A-13. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the bladder cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has

an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the bladder cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the bladder cancer protein is conjugated to
5 BSA.

Measurements of bladder cancer polypeptide activity, or of bladder cancer or the bladder cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the bladder cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that
10 affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of bladder cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g.,
15 northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian bladder cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a bladder cancer polypeptide is first contacted with a potential modulator and
20 incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the bladder cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the bladder cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or
25 hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the bladder cancer protein
30 promoter operably linked to a reporter gene such as luciferase, green fluorescent protein,

CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual
5 genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "bladder cancer proteins." The bladder cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown
10 herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate
15 differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products,
20 and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the bladder cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a bladder cancer protein and a candidate compound, and determining the binding of the compound to the bladder cancer protein. Preferred embodiments utilize the human bladder cancer protein,
25 although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative bladder cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the bladder cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated
30 sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be

made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, 5 teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving 10 areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the bladder cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the bladder cancer protein is added. Novel binding agents include specific 20 antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

25 The determination of the binding of the test modulating compound to the bladder cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the bladder cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. 30 Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also
5 useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (e.g., a bladder cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the
10 binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically
15 between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding
20 to the bladder cancer protein and thus is capable of binding to, and potentially modulating, the activity of the bladder cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate
25 that the test compound is bound to the bladder cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the bladder
30 cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the bladder cancer proteins. In this embodiment, the methods comprise combining a bladder cancer protein and a competitor in a first sample. A second sample comprises a test compound, a bladder cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the bladder cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the bladder cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native bladder cancer protein, but cannot bind to modified bladder cancer proteins. The structure of the bladder cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a bladder cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a bladder cancer protein. The methods

comprise adding a test compound, as defined above, to a cell comprising bladder cancer proteins. Many different cell types may be transfected to contain a recombinant nucleic acid that encodes a bladder cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

5 In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, and pharmacological agents including, e.g., chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In one example, the determinations are determined at different stages of the cell cycle process.

10 In this way, compounds that modulate bladder cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the bladder cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

 In one embodiment, a method of inhibiting bladder cancer cell division is provided.
15 The method comprises administration of a bladder cancer inhibitor. In another embodiment, a method of inhibiting bladder cancer is provided. The method comprises administration of a bladder cancer inhibitor. In a further embodiment, methods of treating cells or individuals with bladder cancer are provided. The method comprises administration of a bladder cancer inhibitor. In one embodiment, a bladder cancer inhibitor is an antibody as discussed above.
20 In another embodiment, the bladder cancer inhibitor is an antisense molecule.

 A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

 Normal cells require a solid substrate to attach and grow. When the cells are
25 transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify
30 modulators of bladder cancer sequences, which when expressed in host cells, inhibit

abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss, herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), supra, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^3H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^3H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a bladder cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. See, Freshney (1994), supra.

Growth factor or serum dependence

Transformed cells have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Nat'l Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879; Freshney (1994), supra). This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells. See, e.g., "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), supra. See also, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer, Plenum; and Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate bladder cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1984), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (2000), supra.

Tumor growth in vivo

Effects of bladder cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the bladder cancer gene is disrupted or in which a bladder cancer gene is inserted. Knock-out

transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous bladder cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous bladder cancer gene with a mutated version of the bladder cancer gene, or by mutating the endogenous bladder cancer gene, e.g., by exposure to carcinogens.

5 A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. By breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, 10 e.g., Capecchi, et al. (1989) Science 244:1288-1292. Chimeric targeted mice can be made. See Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

15 Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Nat'l Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 20 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a bladder cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have 25 statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of bladder cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a bladder cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a bladder cancer protein mRNA, or a subsequence thereof.

- 5 Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the bladder cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

15 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for bladder cancer molecules. A preferred antisense molecule is for a bladder cancer sequences in Tables 1A-13, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999)

Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of bladder cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes. See, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes.

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing them are well known. See, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of bladder cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of bladder cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating bladder cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-bladder cancer antibody that reduces or eliminates the biological activity of an endogenous bladder cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a bladder cancer protein. This may be accomplished in many ways. In a preferred embodiment, e.g., when the bladder cancer sequence is down-regulated in bladder cancer, such state may be reversed by increasing the amount of bladder cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous bladder cancer gene or administering a gene encoding the bladder cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the bladder cancer sequence is up-regulated in bladder cancer, the activity of the endogenous bladder cancer gene is decreased, e.g., by the administration of a bladder cancer antisense nucleic acid.

In one embodiment, the bladder cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to bladder cancer proteins. Similarly, the bladder cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify bladder cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a bladder cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The bladder cancer antibodies may be coupled to standard affinity chromatography columns and used to purify bladder cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the bladder cancer protein.

Methods of identifying variant bladder cancer-associated sequences

Without being bound by theory, expression of various bladder cancer sequences is correlated with bladder cancer. Accordingly, disorders based on mutant or variant bladder cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant bladder cancer genes, e.g., determining all or part of the sequence of at least one endogenous bladder cancer genes in a cell. This may be accomplished using many sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the bladder cancer genotype of an individual, e.g.,
5 determining all or part of the sequence of at least one bladder cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced bladder cancer gene to a known bladder cancer gene, e.g., a wild-type gene.

10 The sequence of all or part of the bladder cancer gene can then be compared to the sequence of a known bladder cancer gene to determine if differences exist. This can be done using many known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the bladder cancer gene of the patient and the known bladder cancer gene correlates with a disease state or a propensity for a disease
15 state, as outlined herein.

In a preferred embodiment, the bladder cancer genes are used as probes to determine the number of copies of the bladder cancer gene in the genome.

In another preferred embodiment, the bladder cancer genes are used as probes to determine the chromosomal localization of the bladder cancer genes. Information such as
20 chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the bladder cancer gene locus.

Administration of pharmaceutical and vaccine compositions

25 In one embodiment, a therapeutically effective dose of a bladder cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug
30 Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker,

ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharma. Assn.; and Pickar (1999) Dosage Calculations Thomson. As is known in the art, adjustments for bladder cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as
5 the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. USSN 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in bladder cancer and is hereby expressly incorporated by reference.

10 A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the bladder cancer proteins and modulators thereof of the
15 present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the bladder cancer proteins and modulators may be directly applied as a solution or spray.

20 The pharmaceutical compositions of the present invention comprise a bladder cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the
25 biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid,
30 methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like.

"Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that bladder cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a bladder cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary

widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics McGraw-Hill.

5 Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1-10 mg per patient per day. Dosages from about 0.1-100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally
10 administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman: The Pharmacological Basis of Therapeutics, supra.

 The compositions containing modulators of bladder cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications,
15 compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered
20 depending on the dosage and frequency as required and tolerated by the patient. The composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition
25 and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies
30 may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present bladder cancer protein-modulating compounds can be administered alone or in combination with additional bladder cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1A-13, such as antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of bladder cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo, or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell. See, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols in Molecular Biology Lippincott; and Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual (2d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, bladder cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, bladder cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the bladder cancer coding regions) can be administered in a gene therapy application. These bladder cancer genes can include antisense applications, either as gene therapy (e.g., for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Bladder cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (Vitiello, et al. (1995) J. Clin. Invest. 95:341-349); peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres

(Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681); peptide compositions contained in immune stimulating complexes (ISCOMS) (Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin. Exp. Immunol. 113:235-243); multiple antigen peptide systems (MAPs) (Tam (1988) Proc. Nat'l Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32); peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al. in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-547; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 7:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al. in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc., Needham, MA, may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides;

polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA
5 encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et al. (1990) Science 247:1465-1468 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery,
10 cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of
15 vaccinia virus, e.g., as a vector to express nucleotide sequences that encode bladder cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are
20 described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

25 Methods for the use of genes as DNA vaccines are well known, and include placing a bladder cancer gene or portion of a bladder cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a bladder cancer patient. The bladder cancer gene used for DNA vaccines can encode full-length bladder cancer proteins, but more preferably encodes portions of the bladder cancer proteins including peptides
30 derived from the bladder cancer protein. In one embodiment, a patient is immunized with a

DNA vaccine comprising a plurality of nucleotide sequences derived from a bladder cancer gene. For example, bladder cancer-associated genes or sequence encoding subfragments of a bladder cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the bladder cancer polypeptide encoded by the DNA vaccine.

Additional or alternative adjuvants are available.

In another preferred embodiment bladder cancer genes find use in generating animal models of bladder cancer. When the bladder cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the bladder cancer gene will also diminish or repress expression of the gene. Animal models of bladder cancer find use in screening for modulators of a bladder cancer-associated sequence or modulators of bladder cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the bladder cancer protein. When desired, tissue-specific expression or knockout of the bladder cancer protein may be necessary.

It is also possible that the bladder cancer protein is overexpressed in bladder cancer. As such, transgenic animals can be generated that overexpress the bladder cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of bladder cancer and are additionally useful in screening for modulators to treat bladder cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include one or more of the following: assay reagents, buffers, bladder cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense or inhibitory polynucleotides, ribozymes, dominant negative bladder cancer polypeptides or polynucleotides, small molecules inhibitors of bladder cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of bladder cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a bladder cancer-associated polypeptide or polynucleotide, control positive or negative samples, reaction tubes, and instructions for testing bladder cancer-associated activity. Optionally, the kit contains biologically active bladder cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynn, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

TABLE DESCRIPTIONS

Table 1A shows about 3413 that exhibit increased or decreased expression in bladder cancer samples. See USSN 60/302,814.

Table 2A shows about 485 genes overexpressed in bladder tumors relative to normal tissues as analyzed using the Affymetrix/Eos Hu03 GeneChip array. See USSN 60/343,705.

Table 3A shows about 414 genes upregulated in bladder cancer relative to normal body tissues and preferred for utility as small molecule, antibody, DNA vaccine targets for the therapy of bladder cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 4A shows about 129 genes upregulated in bladder cancer relative to normal body tissues and preferred for utility as diagnostics of bladder cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 5A shows about 149 genes upregulated in bladder cancer relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 6A shows about 199 genes upregulated in bladder cancer relative to normal bladder tissue. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 7A shows about 63 genes downregulated in bladder tumors relative to normal bladder. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip

array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5 Table 8A shows about 1440 genes upregulated in Ta or T1 bladder tumors from patients who later presented with muscle-invasive bladder tumors (stage T2-T4). Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

10 Table 9A shows about 1200 genes upregulated in Ta or T1 tumors of patients who later presented with either more Ta tumors or no tumors at all. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

15 Table 10A shows about 65 genes upregulated in non-invasive exophytic Ta bladder tumors relative to T2-T4 muscle-invasive tumors. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

20 Table 11A shows about 106 genes upregulated in muscle-invasive T2-T4 bladder tumors relative to non-invasive exophytic Ta bladder tumors. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

25 Table 12A shows the Pkey, ExAccn, UnigeneID, and Unigene Title for all of the sequences in Table 13. Seq ID No. is used to link Table 12A to table 13.

30 **Tables 1B-12B** show the accession numbers for those Pkey's lacking UnigeneID's for tables 1A -12A, respectively. For each probeset is listed a gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

35 **Tables 1C-12C** show genomic positioning for Pkey's lacking Unigene ID's and accession numbers for tables 1A -12A, respectively. For each predicted exon, is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

40 TABLE 1A:

45 Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: please refer to original application
R2: please refer to original application
Target Type: downregulate stage if target is downregulated in bladder tumors relative to normal bladder or

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early stage if target is an earl stage (Ta) bladder tumor marker or
late stage if target is a late stage (T2-T4) bladder tumor marker or
T2-T4 grade 3 papiloma marker or T2-T4 grade 3 solid tumor marker or Upregulate stage

	Pkey	ExAccon	UnigenelD	Unigene Title	R1	R2	Target Type
5	400440	X83957	Hs.83870	nebulin	0.17	2.05	downregulate stage
	400888				0.24	1.97	downregulate stage
	401566				0.19	4.06	downregulate stage
	401669				0.2	2.05	downregulate stage
10	401691				0.04	10.13	downregulate stage
	401905				0.3	1.87	downregulate stage
	402076				0.06	6.51	downregulate stage
	402110				0.43	2.35	downregulate stage
15	402271	NM_002197	Hs.154721	aconitase 1, soluble	0.21	2.16	downregulate stage
	403362				0.18	4.44	downregulate stage
	403687				0.32	1.91	downregulate stage
	403959				0.14	2.27	downregulate stage
	404015				0.2	2.48	downregulate stage
20	404059				0.36	1.84	downregulate stage
	404152				0.32	1.85	downregulate stage
	404498				0.14	2.18	downregulate stage
	404819				0.19	5.25	downregulate stage
	405001	U58196	Hs.296281	Interleukin enhancer binding factor 1	0.16	2.92	downregulate stage
	405349				0.18	3.8	downregulate stage
25	405390				0.3	2.54	downregulate stage
	405735				0.13	2.44	downregulate stage
	405968				0.26	1.85	downregulate stage
	406017				0.32	2.28	downregulate stage
30	406305	BE261320	Hs.297096	transcriptional adaptor 3 (ADA3, yeast h	0.42	1.93	downregulate stage
	406320				0.37	2.01	downregulate stage
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	0.3	2.84	downregulate stage
	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	0.14	7.4	downregulate stage
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	0.05	12.51	downregulate stage
	407013	U35637		gb:Human nebulin mRNA, partial cds	0.14	2.17	downregulate stage
35	407245	X90568	Hs.172004	titin	0.02	15.21	downregulate stage
	407330	AA582607		gb:nn51b05.s1 NCL_CGAP_Kid6 Homo sapiens	0.42	1.87	downregulate stage
	407571	AI446183	Hs.9572	ESTs	0.38	2.13	downregulate stage
	407682	AL035858	Hs.3807	FXFD domain-containing ion transport reg	0.34	2.56	downregulate stage
	407815	AW373860	Hs.301716	ESTs	0.31	2.44	downregulate stage
40	407834	AW084991	Hs.26100	ESTs	0.15	2.98	downregulate stage
	407891	AA486620	Hs.41135	endomucin-2	0.15	3.33	downregulate stage
	407906	AA369665	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	0.12	8.05	downregulate stage
	407938	AA905097	Hs.85050	phospholamban	0.08	8.77	downregulate stage
	407965	W21483	Hs.41707	heat shock 27kD protein 3	0.26	2.29	downregulate stage
45	408009	AF020498	Hs.41735	purinergic receptor P2X, ligand-gated io	0.49	1.91	downregulate stage
	408139	AA451966	Hs.43005	RAB9-like protein	0.41	1.88	downregulate stage
	408221	AA912183	Hs.47447	ESTs	0.04	24.1	downregulate stage
	408374	AW025430	Hs.155591	forkhead box F1	0.35	2.85	downregulate stage
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	0.09	9.04	downregulate stage
50	408508	AI806109	Hs.135736	KIAA1580 protein	0.45	2.2	downregulate stage
	408614	AL137898	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (f	0.13	5.48	downregulate stage
	408652	R43409	Hs.6829	ESTs	0.33	2.5	downregulate stage
	408753	AI337192	Hs.47438	SH3 domain binding glutamic acid-rich pr	0.05	6.94	downregulate stage
	408896	AI610447	Hs.48778	niban protein	0.39	2.01	downregulate stage
55	409277	T05558	Hs.156880	ESTs	0.18	2.75	downregulate stage
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	0.07	2.7	downregulate stage
	410036	R57171	Hs.57975	calsequestrin 2, cardiac muscle	0.09	5.23	downregulate stage
	410132	NM_003480	Hs.58882	Microfibril-associated glycoprotein-2	0.24	2.34	downregulate stage
	410168	AW834050	Hs.9973	tensin	0.39	2.17	downregulate stage
60	410243	D83402	Hs.269006	ESTs, Weakly similar to alternatively sp	0.11	2.82	downregulate stage
	410339	AI916499	Hs.298258	ESTs	0.15	2.16	downregulate stage
	410677	NM_003278	Hs.65424	telranectin (plasminogen-binding protein	0.32	2.65	downregulate stage
	410868	T06529	Hs.98518	Homo sapiens cDNA FLJ11490 fis, clone HE	0.2	2.74	downregulate stage
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	0.2	1.92	downregulate stage
65	411067	AI681006	Hs.301543	ESTs	0.11	3.41	downregulate stage
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	0.17	5.8	downregulate stage
	411644	H82064	Hs.301548	ESTs	0.06	13.8	downregulate stage
	411741	AW859650		gb:RC0-CT0358-071299-011-d03 CT0358 Homo	0.36	2.5	downregulate stage
	412047	AA934589	Hs.49696	ESTs	0.18	3.57	downregulate stage
70	412095	AI624707	Hs.5921	Homo sapiens cDNA; FLJ21592 fis, clone C	0.32	1.89	downregulate stage
	412389	AW947655		gb:RC0-MT0003-140300-031-b07 MT0003 Homo	0.38	2.6	downregulate stage
	412442	AI983730	Hs.26530	serum deprivation response (phosphatidyl	0.12	3.67	downregulate stage
	412519	AA196241	Hs.73980	troponin T1, skeletal, slow	0.24	1.86	downregulate stage
	412622	AW664708	Hs.171959	ESTs	0.06	5.45	downregulate stage
75	412649	NM_002206	Hs.74369	integrin, alpha 7	0.29	2.95	downregulate stage
	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	0.18	2.06	downregulate stage
	412758	Y07818	Hs.74566	dihydropyrimidinase-like 3	0.3	2.23	downregulate stage

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	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	0.11	2.71	downregulate stage
	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, S	0.44	2.03	downregulate stage
	413074	AI871368	Hs.8417	ESTs	0.47	1.91	downregulate stage
5	413272	AA127923	Hs.293256	ESTs	0.09	4.44	downregulate stage
	413276	Z24725	Hs.75260	mitogen inducible 2	0.23	2.48	downregulate stage
	413508	BE145364		gb:LQ-HT0198-151099-125-e05 HT0198 Homo	0.31	2.53	downregulate stage
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev1n)	0.33	2.17	downregulate stage
	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	0.33	2.63	downregulate stage
10	414063	H26904	Hs.75736	apolipoprotein D	0.42	1.85	downregulate stage
	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	0.16	2.22	downregulate stage
	414290	AI568801	Hs.71721	ESTs	0.02	10	downregulate stage
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	0.13	4.14	downregulate stage
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	0.33	2.14	downregulate stage
15	414712	N88858	Hs.77039	ribosomal protein S3A	0.4	2.5	downregulate stage
	414903	AA451700	Hs.85835	Homo sapiens cDNA: FLJ22841 fis, clone K	0.3	3.3	downregulate stage
	415165	AW887604	Hs.78065	complement component 7	0.04	3.41	downregulate stage
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	0.2	3.29	downregulate stage
	415447	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	0.15	6.55	downregulate stage
20	415672	N53097	Hs.193579	ESTs	0.28	3.55	downregulate stage
	415934	NM_000928	Hs.992	phospholipase A2, group 1B (pancreas)	0.34	2.64	downregulate stage
	416127	N49843	Hs.79022	GTP-binding protein overexpressed in sike	0.3	1.98	downregulate stage
	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	0.41	1.96	downregulate stage
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	0.02	49.3	downregulate stage
25	416854	H40164	Hs.80296	Purkinje cell protein 4	0.02	7.55	downregulate stage
	416941	BE000150	Hs.48778	niban protein	0.27	2.16	downregulate stage
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	0.29	2.43	downregulate stage
	417011	F08212	Hs.234898	ESTs	0.41	2.06	downregulate stage
	417298	AW665639	Hs.37958	ESTs	0.27	3.7	downregulate stage
30	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (lg),	0.39	2.08	downregulate stage
	417553	L09190	Hs.82276	trichohyalin	0.29	2.59	downregulate stage
	417987	AA210872	Hs.50133	ESTs	0.22	2.09	downregulate stage
	418297	R91254		gb:yp94e12.s1 Soares fetal liver spleen	0.28	1.9	downregulate stage
	418332	R34976	Hs.78293	ESTs	0.2	3.9	downregulate stage
35	418391	NM_003281	Hs.84673	tropoin 1, skeletal, slow	0.35	2.02	downregulate stage
	418409	AA219332	Hs.120869	ESTs, Weakly similar to AF092922 1 retin	0.21	3.8	downregulate stage
	418421	R58620	Hs.85050	phospholamban	0.2	2.08	downregulate stage
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.05	21.55	downregulate stage
	418533	NM_004533	Hs.85937	myosin-binding protein C, fast-type	0.42	1.95	downregulate stage
40	418787	AW296134	Hs.88999	ESTs	0.48	1.87	downregulate stage
	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	0.26	2.43	downregulate stage
	418947	W52990	Hs.22860	ESTs	0.13	7.18	downregulate stage
	419037	R39895	Hs.7864	ESTs	0.27	2	downregulate stage
	419441	AW023731	Hs.274368	Homo sapiens mRNA; cDNA DKFZp586I1524 (f	0.19	5.25	downregulate stage
45	419535	AW139550	Hs.115173	ESTs	0.31	2.59	downregulate stage
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	0.28	2.38	downregulate stage
	419685	W76083	Hs.173077	ESTs	0.4	2.21	downregulate stage
	419703	AI793257	Hs.128151	ESTs	0.09	3.52	downregulate stage
	419942	U25138	Hs.93841	potassium large conductance calcium-acti	0.28	2.96	downregulate stage
50	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	0.3	2.09	downregulate stage
	420195	N44348	Hs.300794	ESTs	0.22	2.79	downregulate stage
	420261	AW206093	Hs.748	fibroblast growth factor receptor 1 (fms	0.35	1.98	downregulate stage
	420674	NM_000055	Hs.1327	butyrylcholinesterase	0.29	3.5	downregulate stage
	421296	NM_002666	Hs.103253	perilipin	0.36	2.11	downregulate stage
55	421639	NM_012082	Hs.297921	Homo sapiens mRNA full length insert cDN	0.13	4.3	downregulate stage
	421763	AW163500	Hs.108090	cysteine and glycine-rich protein 1	0.26	3.49	downregulate stage
	421853	AL117472	Hs.108924	DKFZP586P1422 protein	0.14	5	downregulate stage
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	0.2	2.29	downregulate stage
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	0.27	2.58	downregulate stage
60	422320	AI745249	Hs.23650	ESTs, Weakly similar to AAB47496 NG5 [H.	0.24	2.95	downregulate stage
	422633	X56832	Hs.118804	enolase 3, (beta, muscle)	0.23	3.57	downregulate stage
	422639	AI929377	Hs.173724	creatine kinase, brain	0.39	1.97	downregulate stage
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	0.37	2.29	downregulate stage
	423587	AA328074	Hs.284256	hypothetical protein FLJ14033 similar to	0.37	2.47	downregulate stage
65	423889	AL035447	Hs.124594	hypothetical protein LOC57158	0.24	2.43	downregulate stage
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	0.27	2.28	downregulate stage
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	0.3	2.59	downregulate stage
	424479	AF064238	Hs.149098	smoothelin	0.26	3.29	downregulate stage
	424580	AA446539	Hs.35092	ESTs	0.15	2.57	downregulate stage
70	424846	AU077324	Hs.1832	neuropeptide Y	0.4	2.04	downregulate stage
	424938	AW102607	Hs.245233	ESTs	0.29	2.16	downregulate stage
	424982	U94777	Hs.154084	phosphorylase, glycogen; muscle (McArdle	0.42	1.89	downregulate stage
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	0.14	1.86	downregulate stage
	425645	N98529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	0.03	13.25	downregulate stage
75	425622	AW360847	Hs.16578	ESTs	0.3	2.19	downregulate stage
	425751	T19239	Hs.1940	crystallin, alpha B	0.47	1.92	downregulate stage
	425869	AA524547	Hs.160318	FXD domain-containing ion transport reg	0.45	1.85	downregulate stage
	425887	AL049443	Hs.161283	Homo sapiens mRNA; cDNA DKFZp586N2020 (f	0.19	2.85	downregulate stage

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	425932	M81650	Hs.1968	semenogelin I	0.02	16.3	downregulate stage
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	0.27	2.52	downregulate stage
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	0.1	10.3	downregulate stage
5	426752	X69490	Hs.172004	titin	0.03	31.3	downregulate stage
	426809	BE313114	Hs.29706	ESTs	0.34	2.95	downregulate stage
	427078	A1676062	Hs.111902	ESTs	0.22	2.11	downregulate stage
	427136	AL117415	Hs.173716	Homo sapiens mRNA; cDNA DKFZp434K0521 (f	0.37	2.33	downregulate stage
	427164	AB037721	Hs.173871	KIAA1300 protein	0.12	5.47	downregulate stage
10	427185	AA398930	Hs.186674	ESTs	0.22	4.65	downregulate stage
	427373	AB007972	Hs.177533	Homo sapiens mRNA; cDNA DKFZp596N0318 (f	0.22	3.18	downregulate stage
	427393	AB029018	Hs.177635	KIAA1095 protein	0.27	2.13	downregulate stage
	427665	AF134803	Hs.180141	cofilin 2 (muscle)	0.05	4	downregulate stage
	427676	AA394052	Hs.180266	tropomyosin 2 (beta)	0.45	1.87	downregulate stage
15	427888	AA417088	Hs.137598	ESTs	0.36	2.04	downregulate stage
	427980	AA418305		gb:zv96g05.s1 Soares_NhHMPu_S1 Homo sapi	0.32	2.39	downregulate stage
	428087	AA100573	Hs.182421	Troponin C2, fast	0.17	4.37	downregulate stage
	428138	AA773842	Hs.293799	ESTs	0.45	2.2	downregulate stage
	428221	U96781	Hs.183075	ESTs, Highly similar to Ca2+ ATPase of f	0.23	3.36	downregulate stage
20	428329	AA426091	Hs.98453	ESTs	0.21	2.09	downregulate stage
	428409	AW117207	Hs.98523	ESTs	0.1	7.63	downregulate stage
	428411	AW291464	Hs.10338	ESTs	0.32	1.98	downregulate stage
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam	0.08	2.99	downregulate stage
	428649	AL045716	Hs.188228	Homo sapiens cDNA FLJ11003 fis, clone PL	0.11	2.07	downregulate stage
25	428899	AA744610	Hs.194431	palladin	0.42	1.84	downregulate stage
	429350	AI754634	Hs.131987	ESTs	0.06	4.73	downregulate stage
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	0.18	2.31	downregulate stage
	429545	AI824164	Hs.77657	lymphocyte antigen 6 complex, locus E	0.31	2.07	downregulate stage
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	0.33	2.18	downregulate stage
30	429892	NM_003803	Hs.2504	myomesin 1 (skelemin) (185kD)	0.36	2.17	downregulate stage
	429930	AI580609	Hs.99569	ESTs	0.18	5.6	downregulate stage
	429956	AI374651	Hs.22542	ESTs	0.22	4.45	downregulate stage
	430013	AA463833	Hs.151275	ESTs	0.21	3.03	downregulate stage
	430271	T06199	Hs.237506	heat shock cognate 40	0.47	1.85	downregulate stage
35	430310	U60115	Hs.239069	four and a half LIM domains 1	0.18	3.44	downregulate stage
	430418	R58852	Hs.36029	heart and neural crest derivatives expre	0.38	2.26	downregulate stage
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	0.16	2.52	downregulate stage
	430712	AW044647	Hs.196284	ESTs	0.29	1.94	downregulate stage
	430778	D90337	Hs.247916	natriuretic peptide precursor C	0.14	4.48	downregulate stage
40	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.35	1.87	downregulate stage
	432247	AA531287	Hs.105805	ESTs	0.21	3.99	downregulate stage
	432689	AB018320	Hs.278626	Arg/Abi-interacting protein ArgBP2	0.11	1.98	downregulate stage
	432792	AA448114	Hs.278950	protocadherin beta 1	0.22	2.93	downregulate stage
	433142	AL120697	Hs.110640	ESTs	0.21	2.18	downregulate stage
	433633	AI880516	Hs.84630	ESTs	0.34	2.67	downregulate stage
45	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	0.35	2.27	downregulate stage
	433826	AA609938	Hs.144492	ESTs	0.24	1.91	downregulate stage
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	0.07	3.46	downregulate stage
	434160	BE551196	Hs.114275	ESTs	0.5	2	downregulate stage
50	434352	AF129505	Hs.86492	small muscle protein, X-linked	0.34	2.13	downregulate stage
	434361	AF129755	Hs.117772	ESTs	0.03	31.3	downregulate stage
	435731	AA699581	Hs.186811	ESTs	0.31	3.25	downregulate stage
	435869	AF255910	Hs.54650	vascular endothelial junction-associated	0.21	3.73	downregulate stage
	435978	AF272899	Hs.135118	Homo sapiens PR-domain zinc finger prote	0.35	2.25	downregulate stage
55	436359	Z83306		gb:H.sapiens mRNA for axonemal dynein he	0.24	3.28	downregulate stage
	436638	AI271945	Hs.134984	ESTs	0.36	1.87	downregulate stage
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	0.14	6.95	downregulate stage
	437176	AW176909	Hs.42346	calcinurin-binding protein calsardin-1	0.32	2.19	downregulate stage
	437233	D81448	Hs.153961	ARP1 (actin-related protein 1, yeast) ho	0.27	2.38	downregulate stage
60	438619	AB032773	Hs.6341	TU12B1-TY protein	0.19	2.69	downregulate stage
	438666	AW014493	Hs.126727	ESTs	0.16	1.98	downregulate stage
	439231	AW581935	Hs.141480	ESTs	0.1	3.9	downregulate stage
	439973	AI733308	Hs.124663	ESTs	0.16	6.2	downregulate stage
	440172	AA868584	Hs.126154	ESTs	0.24	2.34	downregulate stage
65	440274	R24595	Hs.7122	scrapie responsive protein 1	0.11	3.02	downregulate stage
	440687	AL080222	Hs.7358	hypothetical protein FLJ13110	0.19	2.95	downregulate stage
	440700	AW952281	Hs.296184	ESTs, Highly similar to GB01_HUMAN GUAN	0.13	2.69	downregulate stage
	440737	AI375167	Hs.132221	Homo sapiens cDNA FLJ12401 fis, clone MA	0.5	2	downregulate stage
	441805	AA285136	Hs.7974	neuronal specific transcription factor D	0.07	13.55	downregulate stage
70	441969	AI733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.38	1.86	downregulate stage
	442109	BE218975	Hs.212395	ESTs	0.24	2.86	downregulate stage
	442985	AI025584	Hs.55467	ESTs	0.19	2	downregulate stage
	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	0.09	3.66	downregulate stage
	443164	AI038503	Hs.55780	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.2	1.86	downregulate stage
75	443476	AW068594	Hs.133878	ESTs, Weakly similar to AF151889 1 CGI-1	0.11	2.79	downregulate stage
	443604	C03677	Hs.9615	myosin regulatory light chain 2, smooth	0.24	3.41	downregulate stage
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chai	0.28	3.6	downregulate stage
	443932	AW888222	Hs.9973	tensin	0.32	2.57	downregulate stage

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	444195	AB002351	Hs.10587	KIAA0353 protein	0.19	4.04	downregulate stage
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	0.38	2.04	downregulate stage
	444684	AW044070	Hs.147037	ESTs	0.36	2.25	downregulate stage
5	444793	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	0.29	2.19	downregulate stage
	444938	AW470690	Hs.148814	ESTs	0.43	2.3	downregulate stage
	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	0.13	2.64	downregulate stage
	445235	AI564022	Hs.138207	ESTs	0.13	2.4	downregulate stage
	445621	AJ733818	Hs.145549	ESTs	0.25	1.91	downregulate stage
10	445687	W80382	Hs.149297	ESTs	0.2	3.5	downregulate stage
	445850	AI262049	Hs.145560	ESTs	0.53	1.9	downregulate stage
	446406	AI553681	Hs.25248	ESTs	0.07	3.25	downregulate stage
	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	0.33	1.9	downregulate stage
	447595	AW379130	Hs.18953	phosphodiesterase 9A	0.28	1.85	downregulate stage
15	447918	AI129320	Hs.16930	ESTs	0.29	2.46	downregulate stage
	448076	AJ133123	Hs.20196	adenylate cyclase 9	0.2	2.27	downregulate stage
	448283	AJ340462	Hs.182979	ribosomal protein L12	0.53	1.9	downregulate stage
	448303	BE622468	Hs.11924	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.39	1.84	downregulate stage
	448425	AI500359	Hs.233401	ESTs	0.16	1.97	downregulate stage
20	448429	D17408	Hs.21223	calpocin 1, basic, smooth muscle	0.12	5.43	downregulate stage
	448555	AI536697	Hs.159863	ESTs	0.32	2.86	downregulate stage
	448901	AK001021	Hs.22505	hypothetical protein FLJ10159	0.17	2.66	downregulate stage
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	0.24	1.86	downregulate stage
	449226	AB002365	Hs.23311	KIAA0367 protein	0.1	4.96	downregulate stage
25	449238	AA428229	Hs.85524	muscle-specific RING-finger protein homo	0.14	2.53	downregulate stage
	449422	AA001373	Hs.59821	ESTs	0.43	2.3	downregulate stage
	449690	AA002140	Hs.33024	ESTs	0.5	2	downregulate stage
	449874	AA135688	Hs.10083	ESTs	0.33	2.7	downregulate stage
	449925	AJ342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	0.11	5.57	downregulate stage
30	450300	AL041440	Hs.59210	ESTs	0.41	2.13	downregulate stage
	450578	AI971773	Hs.232268	ESTs	0.44	2.25	downregulate stage
	450810	BE207588	Hs.25511	transforming growth factor beta 1 induce	0.51	1.86	downregulate stage
	450831	R37974	Hs.25255	ESTs	0.23	1.96	downregulate stage
	451331	AK002039	Hs.28243	Homo sapiens cDNA FLJ11177 fis, clone PL	0.37	2.18	downregulate stage
35	451533	NM_004657	Hs.28530	serum deprivation response (phosphatidyl	0.1	9.36	downregulate stage
	451782	AF233566	Hs.27018	Ris	0.35	2.43	downregulate stage
	451948	AW452473	Hs.211125	ESTs	0.43	1.88	downregulate stage
	452422	AA521416	Hs.22701	ESTs	0.41	1.85	downregulate stage
	452463	R36452	Hs.300817	ESTs	0.09	4.05	downregulate stage
40	452776	AA194540	Hs.13522	ESTs	0.36	2.16	downregulate stage
	452814	AI092790	Hs.55016	hypothetical protein FLJ21935	0.06	4.7	downregulate stage
	453064	RA0334	Hs.301395	Homo sapiens cDNA: FLJ21204 fis, clone C	0.07	4.47	downregulate stage
	453351	AI625721	Hs.61814	Homo sapiens cDNA: FLJ22750 fis, clone K	0.33	3.05	downregulate stage
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	0.03	7.14	downregulate stage
45	453359	AA448787	Hs.24872	ESTs, Weakly similar to aortic carboxype	0.4	1.92	downregulate stage
	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	0.24	3.29	downregulate stage
	453500	AI478427	Hs.43125	ESTs	0.02	11.41	downregulate stage
	453582	AW854339	Hs.33476	hypothetical protein FLJ11937	0.39	2.04	downregulate stage
	453586	AA248089	Hs.50841	ESTs, Weakly similar to tuftelin [M.musc	0.43	1.86	downregulate stage
50	453666	AW015681	Hs.135229	ESTs, Moderately similar to AF107203 1 a	0.28	2.42	downregulate stage
	453698	AA037615	Hs.42746	ESTs	0.2	1.88	downregulate stage
	453702	AA037637	Hs.42128	ESTs	0.32	2.42	downregulate stage
	453725	W28543		gb:48c5 Human retina cDNA randomly prime	0.2	2.06	downregulate stage
	453950	AA156998	Hs.211568	eukaryotic translation initiation factor	0.07	7.86	downregulate stage
55	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	0.16	2.49	downregulate stage
	454471	AW902125		gb:QV0-NN1022-120500-220-h12 NN1022 Homo	0.41	2.45	downregulate stage
	454637	AW811613		gb:CM3-ST0157-300999-017-f06 ST0157 Homo	0.18	2.2	downregulate stage
	454750	AW866285		gb:QV4-SN0024-080400-167-a09 SN0024 Homo	0.49	2.05	downregulate stage
	455073	AW854829		gb:QV2-CT0261-201099-011-f01 CT0261 Homo	0.27	2.09	downregulate stage
60	455485	AA102287	Hs.28756	Homo sapiens cDNA: FLJ20896 fis, clone A	0.32	2.07	downregulate stage
	455611	L06419	Hs.75093	procollagen-lysine, 2-oxoglutarate 5-dio	0.15	2.87	downregulate stage
	456100	AI983981	Hs.189114	ESTs	0.4	2.5	downregulate stage
	456841	AA875863	Hs.152345	poliovirus receptor-related 1 (herpesvir	0.35	1.9	downregulate stage
	457064	AA776743	Hs.191589	ESTs	0.17	2.34	downregulate stage
65	457108	N74724	Hs.108479	ESTs	0.48	2.1	downregulate stage
	457506	AF131757	Hs.274533	Homo sapiens clone 24926 mRNA sequence	0.29	2.59	downregulate stage
	457625	T10073		gb:seq1293 b4HB3MA Cot8-HAP-Ft Homo sapi	0.29	3.45	downregulate stage
	458482	AV648858	Hs.29488	ESTs	0.26	2.17	downregulate stage
	458622	AA972412	Hs.13755	f-box and WD-40 domain protein 2	0.51	1.95	downregulate stage
70	458841	W28965		gb:54d10 Human retina cDNA randomly prim	0.32	3.1	downregulate stage
	459037	AW439497	Hs.290656	EST	0.43	2.35	downregulate stage
	400762				0.71	0.4	early stage
	400937				1.2	0.26	early stage
	400977				0.63	0.48	early stage
75	401024				0.8	0.3	early stage
	401048				1.9	0.22	early stage
	401537				1.3	0.2	early stage
	401619				3.5	0.19	early stage

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	402089			0.39	0.55	early stage
	402176			0.35	0.91	early stage
	402407			1	0.15	early stage
	402430			0.28	1.25	early stage
5	402435			2.15	0.21	early stage
	402522			1.8	0.14	early stage
	402546			0.17	1.66	early stage
	402604			0.41	0.66	early stage
10	402716			0.14	0.86	early stage
	402846			0.61	0.52	early stage
	402922			0.14	0.83	early stage
	403567			0.44	0.49	early stage
	403590			1	0.34	early stage
	404336			0.49	0.44	early stage
15	404345	AA730407	Hs.159156	0.38	0.4	early stage
	404501	AW247252	Hs.75514	0.32	0.8	early stage
	404594			0.37	0.91	early stage
	404874			1.87	0.26	early stage
	404881			0.36	0.5	early stage
20	404896	NM_000429	Hs.106845	1	0.36	early stage
	404999	U58195	Hs.296281	0.19	1.06	early stage
	405071			0.19	0.77	early stage
	405308			0.4	0.55	early stage
	405463			0.41	1	early stage
25	405580			1.89	0.19	early stage
	405600			0.22	0.63	early stage
	405720			0.37	0.61	early stage
	405863			0.53	0.26	early stage
	405867			0.24	1.1	early stage
30	405920			0.39	1.15	early stage
	406036			2.15	0.17	early stage
	406243			0.32	1.23	early stage
	406367			0.38	0.76	early stage
35	406834	AI318680		0.4	0.67	early stage
	406881	D16154		0.14	1.55	early stage
	407411	AF060170		0.39	0.69	early stage
	407639	AW205369	Hs.252936	0.61	0.34	early stage
	408112	AW451982	Hs.248613	0.2	0.54	early stage
40	408732	AL117490	Hs.47225	1	0.32	early stage
	409103	AF251237	Hs.112208	0.33	1.03	early stage
	409840	AW502122		0.56	0.28	early stage
	410128	AW904599		1.26	0.37	early stage
	411474	AW848427		1	0.14	early stage
	412564	X83703	Hs.74019	0.36	0.44	early stage
45	413266	BE300352		1.46	0.25	early stage
	413341	H78472	Hs.191325	0.41	0.48	early stage
	414055	AW818687	Hs.5366	0.33	0.67	early stage
	414170	AA335996	Hs.3743	1.15	0.21	early stage
	414220	BE298094		0.16	0.52	early stage
50	414276	BE297862		1.75	0.2	early stage
	414327	BE408145	Hs.185254	0.1	0.99	early stage
	414366	BE549143		1	0.31	early stage
	414376	BE393856	Hs.66915	0.18	0.96	early stage
	414555	N98569	Hs.76422	0.48	0.67	early stage
55	415199	AA181125	Hs.57893	0.75	0.72	early stage
	417304	H15635		0.6	0.58	early stage
	417371	N74613	Hs.269149	0.3	0.58	early stage
	418133	R43504	Hs.6181	1.28	0.29	early stage
	419273	BE271180	Hs.293490	0.54	0.28	early stage
60	419715	AA553770		0.45	0.66	early stage
	420390	AA330047	Hs.191187	1.45	0.12	early stage
	421745	AF205849	Hs.107740	0.33	0.71	early stage
	421813	BE048255		0.52	0.67	early stage
	422689	H12402	Hs.119122	1	0.26	early stage
65	422743	BE304678	Hs.119598	0.2	0.57	early stage
	422760	BE409561		0.41	0.64	early stage
	422880	AF228704	Hs.121524	3.75	0.1	early stage
	423457	F08208	Hs.155606	0.55	0.54	early stage
	425349	AA425234	Hs.79886	1	0.21	early stage
70	425360	BE547704		0.28	0.85	early stage
	426356	BE536836		0.31	0.69	early stage
	426521	AF161445	Hs.170219	0.11	0.69	early stage
	426670	AA383047	Hs.193718	1	0.55	early stage
	426699	AA383337	Hs.121269	0.33	0.71	early stage
75	427827	AA418577	Hs.189105	1.16	0.41	early stage
	428651	AF196478	Hs.188401	1.85	0.24	early stage
	430727	X75917	Hs.2654	0.78	0.46	early stage

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5	430750	AI650360	Hs.100256	ESTs	2.15	0.17	early stage
	430795	AW971398		gb:EST363487 MAGE resequences, MAGL Homo	1.95	0.21	early stage
	431900	AW972048	Hs.192534	ESTs	0.36	0.73	early stage
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	1.8	0.17	early stage
	432791	NM_014554	Hs.278949	sentrin/SUMO-specific protease	2.8	0.15	early stage
10	433404	T32982	Hs.102720	ESTs	2.2	0.13	early stage
	433782	AF090945		gb:Homo sapiens clone HQ0670	3.3	0.15	early stage
	433877	BE146567	Hs.257475	ESTs	0.65	0.7	early stage
	434483	AA223646	Hs.57222	nurim (nuclear envelope membrane protein	0.38	0.49	early stage
	435752	AF230801	Hs.125180	growth hormone receptor	0.52	0.4	early stage
15	436178	BE152396	Hs.21590	Homo sapiens HSPC304 mRNA, partial cds	1.65	0.14	early stage
	436391	AJ227892	Hs.146274	ESTs	1.35	0.16	early stage
	436602	AI793222	Hs.166817	ESTs	0.17	1.46	early stage
	436777	AA731199	Hs.293130	ESTs	1	0.2	early stage
	436813	AW975714	Hs.129004	ESTs	0.19	1.45	early stage
20	436869	NM_014867	Hs.297661	Homo sapiens YAC clone 377A1 unknown mRNA	0.96	0.2	early stage
	437169	AA309612	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homo	0.07	1.8	early stage
	438649	AA813136	Hs.143014	ESTs	1.38	0.19	early stage
	438681	AW384815	Hs.149208	KIAA1555 protein	0.25	0.54	early stage
	438802	AA825976	Hs.136954	ESTs	1.8	0.14	early stage
25	438887	R68857	Hs.265499	ESTs	1.05	0.32	early stage
	440128	AA962623	Hs.189144	ESTs, Weakly similar to NPT2_HUMAN RENAL	1	0.19	early stage
	440397	AA884448	Hs.157239	ESTs	0.59	0.38	early stage
	440509	BE410132	Hs.134202	ESTs, Weakly similar to B41182 collagen	0.26	0.9	early stage
	440605	Z40094	Hs.185698	ESTs	0.51	0.43	early stage
30	442238	AW135374	Hs.270949	ESTs	1	0.18	early stage
	443258	AF169301	Hs.9098	sulfate transporter 1	0.85	0.49	early stage
	445739	AW136354	Hs.145303	ESTs	0.88	0.4	early stage
	447306	AI373163	Hs.170333	ESTs	0.15	0.8	early stage
	447346	AI525135	Hs.210507	ESTs	1.35	0.27	early stage
35	446265	N46272	Hs.26812	ESTs	0.47	0.26	early stage
	446678	AI580776	Hs.199854	ESTs	0.19	0.68	early stage
	446778	AF074913		gb:Homo sapiens transcription factor Pax	0.57	0.53	early stage
	446871	BE616709		gb:501279937F1 NIH_MGC_39 Homo sapiens c	0.26	0.94	early stage
	449180	AI533836	Hs.195649	ESTs	0.46	0.45	early stage
40	449213	BE616861		gb:501279056F1 NIH_MGC_39 Homo sapiens c	0.73	0.56	early stage
	449231	BE410360		gb:501302340F1 NIH_MGC_21 Homo sapiens c	0.27	0.76	early stage
	449450	AL039852	Hs.256990	ESTs, Moderately similar to ALU7_HUMAN A	1	0.26	early stage
	449815	AI671000	Hs.199739	ESTs	1.2	0.15	early stage
	450972	AW967906	Hs.194617	ESTs	0.28	0.83	early stage
45	451236	AI767406	Hs.207026	ESTs, Weakly similar to B56205 transcrip	0.35	0.77	early stage
	451283	H83979		gb:ys93d11.1.r1 Soares retina N2b5HR Homo	1	0.23	early stage
	451375	AI792066	Hs.283902	Homo sapiens BAC clone RP11-481J13 from	0.16	1.37	early stage
	452530	AI905518		gb:RC-BT091-210195-098 BT091 Homo sapien	1.35	0.21	early stage
	452550	AA026735		gb:za93d05.r1 Soares_fetal_heart_NbHH19W	0.44	0.6	early stage
50	454121	AW090524	Hs.244967	ESTs	2.85	0.17	early stage
	454554	AW847505		gb:RCO-CT0210-280999-021-c10 CT0210 Homo	0.36	0.5	early stage
	454697	AW813728	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC0	0.43	0.6	early stage
	454851	AW835127		gb:RC-LT0011-100100-012-c07 LT0011 Homo	0.77	0.32	early stage
	455040	AW852286		gb:QV0-CT0225-100400-187-d08 CT0225 Homo	0.26	0.52	early stage
55	455225	AW995589		gb:QV3-BN0046-150400-151-g09 BN0046 Homo	1.7	0.18	early stage
	455970	AI733857	Hs.71463	ESTs	0.66	0.45	early stage
	456235	AA203637		gb:zx58b12.1.r1 Soares_fetal_liver_spleen_	0.64	0.43	early stage
	456450	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	0.38	0.76	early stage
	456526	AA782222	Hs.192008	ESTs	0.63	0.43	early stage
60	456855	AF035528	Hs.153663	MAD (mothers against decapentaplegic, Dr	0.49	0.46	early stage
	456983	AI081687	Hs.170225	thymopoietin	0.27	0.75	early stage
	457089	AA416556	Hs.98234	ESTs	0.34	0.48	early stage
	458198	AI286100	Hs.192739	ESTs	0.47	0.48	early stage
	458425	AI084057	Hs.301149	ESTs	0.4	0.37	early stage
65	458660	AI299739	Hs.99601	Homo sapiens cDNA FLJ12553 fis, clone NT	0.79	0.68	early stage
	458703	AW749121	Hs.282901	ESTs	1	0.23	early stage
	458767	T97083	Hs.148355	ESTs	1	0.17	early stage
	459399	BE407712		gb:501299745F1 NIH_MGC_21 Homo sapiens c	0.68	0.56	early stage
	400860				4.9	0.08	late stage
70	408190	AB032963	Hs.43577	ATPase, Class I, type 8B, member 2	0.58	0.84	late stage
	408558	AW015759	Hs.235709	ESTs	1.26	0.45	late stage
	410077	AF097645	Hs.58570	deleted in cancer 1; RNA helicase HDB/DI	6.2	0.12	late stage
	410295	AA741357	Hs.62041	nidogen (enactin)	0.77	0.86	late stage
	410310	J02931	Hs.62152	coagulation factor III (thromboplastin,	1.45	0.27	late stage
75	410614	AI091195	Hs.65029	growth arrest-specific 1	0.4	1.12	late stage
	410867	X63556	Hs.750	fibrillin 1 (Marfan syndrome)	0.71	1.07	late stage
	411573	AB029000	Hs.70823	KIAA1077 protein	3.64	0.19	late stage
	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	5.18	0.13	late stage
	412178	AW898526		gb:RC6-NN0072-040500-011-E05 NN0072 Homo	7.55	0.08	late stage
	412429	AV650262	Hs.75765	GRO2 oncogene	3.37	0.15	late stage
	412652	AI801777	Hs.6774	ESTs	0.49	1.24	late stage

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5	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	3.6	0.11	late stage
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.82	0.14	late stage
	414183	AW957446	Hs.301711	ESTs	3.18	0.16	late stage
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	0.81	0.73	late stage
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	0.37	0.99	late stage
10	414504	AW069181	Hs.293523	ESTs, Weakly similar to transformation-r	0.97	0.65	late stage
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.84	0.1	late stage
	415116	AA160363	Hs.269966	ESTs	7.45	0.07	late stage
	415714	NM_002290	Hs.78672	laminin, alpha 4	0.49	1.39	late stage
	415822	D59243		gb:HUM526E07B Clontech human placenta po	8.15	0.09	late stage
15	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	0.48	1.46	late stage
	417059	AL037672	Hs.81071	extracellular matrix protein 1	1.52	0.44	late stage
	417259	AW903638	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2	0.39	late stage
	417733	AL048678	Hs.82503	syntrophin	0.2	2.67	late stage
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	4.56	0.12	late stage
20	417849	AW291587	Hs.82733	nidogen 2	1.81	0.38	late stage
	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	0.97	0.74	late stage
	418283	S79395	Hs.83942	cathepsin K (pycnodysostosis)	1.21	0.56	late stage
	418875	W19971	Hs.233459	ESTs	2.63	0.33	late stage
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	7.65	0.07	late stage
25	419925	AA159850	Hs.93765	lipoma HMGIC fusion partner	0.91	0.82	late stage
	420411	AI581085	Hs.24678	ESTs	7.3	0.1	late stage
	420943	AI718702	Hs.105341	ESTs	7.05	0.07	late stage
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	0.99	0.42	late stage
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	8.1	0.08	late stage
30	421786	AI188653	Hs.21351	ESTs	8.15	0.08	late stage
	422414	AW875237	Hs.13701	ESTs	1.05	0.69	late stage
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	0.28	1.53	late stage
	422790	AA809875	Hs.25933	ESTs	2.59	0.28	late stage
	423057	AW961597	Hs.130816	ESTs	7.55	0.08	late stage
35	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone C	1.24	0.61	late stage
	423905	AW579560	Hs.135150	lung type-I cell membrane-associated gly	2.12	0.24	late stage
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	0.29	2.45	late stage
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fascilin	4.47	0.17	late stage
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	2.44	0.26	late stage
40	424839	AA740632	Hs.120850	ESTs	2.74	0.23	late stage
	426780	BE242284	Hs.172199	adenylate cyclase 7	8.55	0.09	late stage
	426974	AB002298	Hs.173035	KIAA0300 protein	1.56	0.36	late stage
	427055	AI301740	Hs.173381	dihydropyrimidinase-like 2	0.72	1	late stage
	427882	AA640987	Hs.193767	ESTs	2.25	0.29	late stage
45	428065	AI634046	Hs.157313	ESTs	6.19	0.1	late stage
	428147	AW629965	Hs.234983	ESTs	8.42	0.08	late stage
	428585	AB007863	Hs.185140	KIAA0403 protein	6.85	0.08	late stage
	428825	AI084336	Hs.128783	ESTs	0.9	0.8	late stage
	429490	AI971131	Hs.293684	ESTs, Weakly similar to alternatively sp	1.59	0.39	late stage
50	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	0.77	0.49	late stage
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	0.92	0.3	late stage
	431319	AA873350		gb:ch64h02.s1 NCI_CGAP_Kid5 Homo sapiens	1.36	0.44	late stage
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.69	0.17	late stage
	432314	AA533447	Hs.285173	ESTs	1.75	0.31	late stage
55	432331	W37862	Hs.274368	Homo sapiens mRNA: cDNA DKF2p586I1524 (f	0.35	1.58	late stage
	432559	AW452948	Hs.257631	ESTs	1.37	0.49	late stage
	433470	AW960564	Hs.3337	transmembrane 4 superfamily member 1	2.58	0.24	late stage
	433586	T85301		gb:yd78d06.s1 Soares fetal liver spleen	5.06	0.11	late stage
	436428	AW246900	Hs.283712	hypothetical protein	8.25	0.09	late stage
60	436729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	1.6	0.26	late stage
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.15	0.08	late stage
	439584	AA838114	Hs.221512	ESTs	8.6	0.09	late stage
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	2.21	0.27	late stage
	440524	R71264	Hs.16798	ESTs	3.44	0.21	late stage
65	440624	AF017987	Hs.7306	secreted frizzled-related protein 1	0.42	0.63	late stage
	441976	AA428403	Hs.106131	ESTs	8.5	0.09	late stage
	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	7.95	0.06	late stage
	443852	AI679966	Hs.150603	ESTs	6.84	0.12	late stage
	443896	AI680242	Hs.271587	Homo sapiens cDNA FLJ13527 fis, clone PL	7.95	0.08	late stage
70	444212	AW503976	Hs.10649	basement membrane-induced gene	2.31	0.28	late stage
	444331	AW193342	Hs.24144	ESTs	0.32	1.64	late stage
	445142	AW978484	Hs.93842	Homo sapiens cDNA: FLJ22554 fis, clone H	2.52	0.24	late stage
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	1.43	0.47	late stage
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	0.54	1.39	late stage
75	447526	AL048753	Hs.340	small inducible cytokine A2 (monocyte ch	1.43	0.43	late stage
	447744	AA313230	Hs.19413	S100 calcium-binding protein A12 (calgr	1.35	0.26	late stage
	447818	W79940	Hs.21906	ESTs	6.63	0.13	late stage
	449567	AI990790	Hs.188614	ESTs	4.7	0.13	late stage
	450455	AL117424	Hs.25035	chloride intracellular channel 4	0.64	1.31	late stage
	452239	AW379378	Hs.170121	protein tyrosine phosphatase, receptor t	0.59	1.18	late stage
	452696	NM_001295	Hs.301921	ESTs	2.31	0.26	late stage

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	453212	H15416	Hs.21865	ESTs	2.51	0.26	late stage
	455510	AA422029	Hs.143540	ESTs, Weakly similar to hyperpolarizatio	8.6	0.06	late stage
	400775	R58624	Hs.2186	eukaryotic translation elongation factor	1	1	T2-T4 grade 3 papilloma marker
5	401508				1	1	T2-T4 grade 3 papilloma marker
	403092				1	1	T2-T4 grade 3 papilloma marker
	404232				1	1	T2-T4 grade 3 papilloma marker
	407020	U49973		gb:Human Tigger1 transposable element, c	1	1	T2-T4 grade 3 papilloma marker
	407345	AI053836	Hs.169365	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	1	T2-T4 grade 3 papilloma marker
	407420	AF084362		gb:Homo sapiens lipoteic-protein ligase B	1	1	T2-T4 grade 3 papilloma marker
10	407577	AW131324	Hs.246759	ESTs, Weakly similar to KIAA1074 protein	1	1	T2-T4 grade 3 papilloma marker
	407666	AF071107	Hs.37501	MAD (mothers against decapentaplegic, Dr	1	1	T2-T4 grade 3 papilloma marker
	407916	L09234	Hs.603	ATPase, H ⁺ transporting, lysosomal (vacu	1	1	T2-T4 grade 3 papilloma marker
	407936	AW118147	Hs.270935	ESTs	1	1	T2-T4 grade 3 papilloma marker
	408186	AW168847	Hs.250156	ESTs	1	1	T2-T4 grade 3 papilloma marker
15	408950	AA707814	Hs.7396	ESTs	1	1	T2-T4 grade 3 papilloma marker
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	1.2	0.12	T2-T4 grade 3 papilloma marker
	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	1	1	T2-T4 grade 3 papilloma marker
	409196	NM_001874	Hs.169765	carboxypeptidase M	1	1	T2-T4 grade 3 papilloma marker
	409281	AA069998		gb:zm67b03.r1 Stratagene neuroepithelium	1	1	T2-T4 grade 3 papilloma marker
20	410010	AW572853	Hs.257683	ESTs, Weakly similar to ALU3_HUMAN ALU S	1	0.5	T2-T4 grade 3 papilloma marker
	410157	AW593277	Hs.225056	ESTs	1	0.69	T2-T4 grade 3 papilloma marker
	411112	AW818158		gb:CM1-ST0277-161299-070-g07 ST0277 Homo	1	1	T2-T4 grade 3 papilloma marker
	411335	AW837675		gb:QV2-LT0039-260300-107-b04 LT0039 Homo	1	1	T2-T4 grade 3 papilloma marker
25	412051	T15872	Hs.268713	ESTs, Weakly similar to hypothetical pro	1	1	T2-T4 grade 3 papilloma marker
	413485	N52628		gb:yv37g11.s1 Soares fetal liver spleen	1	1	T2-T4 grade 3 papilloma marker
	413574	BE149158	Hs.129998	Homo sapiens cDNA FLJ14267 fis, clone PL	1	1	T2-T4 grade 3 papilloma marker
	413782	BE546104		gb:601072642F1 NIH_MGC_12 Homo sapiens c	1	1	T2-T4 grade 3 papilloma marker
	414749	H94622	Hs.193358	ESTs, Moderately similar to diabetes mel	1	1	T2-T4 grade 3 papilloma marker
30	415293	R49462	Hs.106541	ESTs	1	1	T2-T4 grade 3 papilloma marker
	415442	F12963	Hs.7045	GLD04 protein	1	1	T2-T4 grade 3 papilloma marker
	416256	T87587	Hs.272082	ESTs	1	1	T2-T4 grade 3 papilloma marker
	417047	AA192640	Hs.1526	ATPase, Ca ⁺⁺ transporting, cardiac muscl	1	1	T2-T4 grade 3 papilloma marker
	417181	L10123	Hs.1071	surfactant protein A binding protein	1	1	T2-T4 grade 3 papilloma marker
	417367	N73877	Hs.171815	ESTs	1	1	T2-T4 grade 3 papilloma marker
35	419721	NM_001660	Hs.288650	aquaporin 4	1	1	T2-T4 grade 3 papilloma marker
	420294	AA808259	Hs.196716	ESTs	1	0.65	T2-T4 grade 3 papilloma marker
	423589	AA328082	Hs.209569	ESTs, Weakly similar to thrombospondin t	1	1	T2-T4 grade 3 papilloma marker
	424549	AI873205	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	1	1	T2-T4 grade 3 papilloma marker
40	425458	H89317	Hs.182839	ESTs	1	1	T2-T4 grade 3 papilloma marker
	425475	AL134728		gb:DKFZp547A1890_r1 547 (synonym: hibr1)	1	1	T2-T4 grade 3 papilloma marker
	429453	AA453195	Hs.124222	ESTs	1	1	T2-T4 grade 3 papilloma marker
	431200	AF044923	Hs.250752	hook1 protein	1	1	T2-T4 grade 3 papilloma marker
	431938	AA938471	Hs.115242	developmentally regulated GTP-binding pr	1	1	T2-T4 grade 3 papilloma marker
45	431944	AI360891	Hs.143619	ESTs	1	1	T2-T4 grade 3 papilloma marker
	432021	AA524470	Hs.58753	ESTs	1	1	T2-T4 grade 3 papilloma marker
	432205	AI806583	Hs.125291	ESTs	1	0.31	T2-T4 grade 3 papilloma marker
	432527	AW975028	Hs.102754	ESTs	1	1	T2-T4 grade 3 papilloma marker
	434069	AF116651	Hs.283058	hypothetical protein PRO0800	1	0.41	T2-T4 grade 3 papilloma marker
50	435278	AW994242	Hs.173495	ESTs	1	1	T2-T4 grade 3 papilloma marker
	435965	AI034368	Hs.132650	ESTs	1	0.36	T2-T4 grade 3 papilloma marker
	436227	AA706937	Hs.120802	ESTs, Moderately similar to A26641 Na ⁺ /K	1	1	T2-T4 grade 3 papilloma marker
	436635	AW104325	Hs.272093	ESTs, Weakly similar to STK2_HUMAN SERIN	1	0.74	T2-T4 grade 3 papilloma marker
	436640	AA724411	Hs.155065	ESTs	1	1	T2-T4 grade 3 papilloma marker
	436884	BE046657		gb:hn42e02.x1 NCL_CGAP_RDF2 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
55	437251	AW976082		gb:EST388191 MAGE rsequences, MAGN Homo	1	1	T2-T4 grade 3 papilloma marker
	437348	AA749149	Hs.163114	ESTs	1	1	T2-T4 grade 3 papilloma marker
	437769	AA767853	Hs.122895	ESTs	1	1	T2-T4 grade 3 papilloma marker
	437771	AA811071	Hs.123349	ESTs	1	1	T2-T4 grade 3 papilloma marker
60	438347	AA909886	Hs.293397	ESTs	1	1	T2-T4 grade 3 papilloma marker
	439171	AA831133	Hs.294128	ESTs	1	0.95	T2-T4 grade 3 papilloma marker
	439914	AA854036	Hs.145394	ESTs	1	1	T2-T4 grade 3 papilloma marker
	440399	AI215527	Hs.125589	ESTs	1	1	T2-T4 grade 3 papilloma marker
	440972	BE044588	Hs.276158	ESTs	1	1	T2-T4 grade 3 papilloma marker
65	442004	AA973568	Hs.128317	ESTs	1	1	T2-T4 grade 3 papilloma marker
	442270	BE585899	Hs.62005	ESTs	1	1	T2-T4 grade 3 papilloma marker
	443413	AI056457	Hs.221642	ESTs	1	1	T2-T4 grade 3 papilloma marker
	443927	AW016726	Hs.134860	ESTs	1	1	T2-T4 grade 3 papilloma marker
	445442	N20392	Hs.42846	ESTs	1	1	T2-T4 grade 3 papilloma marker
70	445611	AW418497	Hs.145593	ESTs	1	0.49	T2-T4 grade 3 papilloma marker
	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	1	1	T2-T4 grade 3 papilloma marker
	446552	AW470827	Hs.156241	ESTs	1	1	T2-T4 grade 3 papilloma marker
	447399	AI815401	Hs.251967	Homo sapiens clone 785627 unknown mRNA	2.9	0.14	T2-T4 grade 3 papilloma marker
	449111	T83109	Hs.196180	ESTs	1	1	T2-T4 grade 3 papilloma marker
	449232	AW192780	Hs.196080	ESTs	1	0.8	T2-T4 grade 3 papilloma marker
75	451373	AI792030		gb:os03e11.y5 NCL_CGAP_Lu5 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	1	1	T2-T4 grade 3 papilloma marker
	452534	AW083022	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1	0.67	T2-T4 grade 3 papilloma marker

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5	452536	BE063380		gb:PMO-BT0275-291099-002-g10 BT0275 Homo	1.65	0.26	T2-T4 grade 3 papilloma marker
	452640	AA027115	Hs.100206	ESTs, Weakly similar to AAAD_HUMAN ARYL A	1	1	T2-T4 grade 3 papilloma marker
	452645	AI911325	Hs.212049	EST	1	1	T2-T4 grade 3 papilloma marker
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1	1	T2-T4 grade 3 papilloma marker
	453472	AL037925		gb:DKFZp564M037_r1 564 (synonym: hibr2)	1	0.8	T2-T4 grade 3 papilloma marker
10	453609	AL045301	Hs.13427	ESTs	1	1	T2-T4 grade 3 papilloma marker
	453677	AL079389		gb:DKFZp434E2116_r1 434 (synonym: htes3)	1	0.77	T2-T4 grade 3 papilloma marker
	453704	R41806	Hs.100884	ESTs	1	1	T2-T4 grade 3 papilloma marker
	455267	AW880861		gb:QV0-DT0033-070300-152-c12 DT0033 Homo	1	1	T2-T4 grade 3 papilloma marker
	455680	BE153208		gb:PMO-HT0335-050400-007-F10 HT0335 Homo	1	1	T2-T4 grade 3 papilloma marker
15	456520	AW835416	Hs.29417	HCF-binding transcription factor Zhangfe	1	1	T2-T4 grade 3 papilloma marker
	456763	AJ271351	Hs.128180	B-cell translocation gene 4	1	0.71	T2-T4 grade 3 papilloma marker
	456912	AI458843	Hs.158112	protein tyrosine phosphatase, receptor t	1	1	T2-T4 grade 3 papilloma marker
	457018	AA761820	Hs.250965	ESTs	1	1	T2-T4 grade 3 papilloma marker
	457323	AW967813	Hs.201064	ESTs	1	1	T2-T4 grade 3 papilloma marker
20	457339	AW971949	Hs.291252	ESTs	1	1	T2-T4 grade 3 papilloma marker
	457340	AA492071		gb:ne97b04.s1 NCI_CGAP_Kid1 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
	457507	AW300248	Hs.181693	ESTs	1	1	T2-T4 grade 3 papilloma marker
	458106	AF086561	Hs.37	acetyl-Coenzyme A acetyltransferase 1 (a	1	1	T2-T4 grade 3 papilloma marker
	458624	AI362790	Hs.181801	ESTs	1	0.34	T2-T4 grade 3 papilloma marker
25	459396	AI907536	Hs.103869	ESTs	1	1	T2-T4 grade 3 papilloma marker
	401002				1	1	T2-T4 grade 3 solid tumor marker
	401866				1.35	0.14	T2-T4 grade 3 solid tumor marker
	403615				1	1	T2-T4 grade 3 solid tumor marker
	403776				1	1	T2-T4 grade 3 solid tumor marker
30	404113				1	0.43	T2-T4 grade 3 solid tumor marker
	404488				1	0.17	T2-T4 grade 3 solid tumor marker
	404653				1	1	T2-T4 grade 3 solid tumor marker
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (fr	1	0.24	T2-T4 grade 3 solid tumor marker
	406471				1	0.42	T2-T4 grade 3 solid tumor marker
35	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	2.75	0.05	T2-T4 grade 3 solid tumor marker
	407624	AW157431	Hs.248941	ESTs	3.05	0.15	T2-T4 grade 3 solid tumor marker
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	3.85	0.03	T2-T4 grade 3 solid tumor marker
	409464	X69115	Hs.54488	zinc finger protein 37a (KOX 21)	1.15	0.29	T2-T4 grade 3 solid tumor marker
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	1	0.24	T2-T4 grade 3 solid tumor marker
40	410025	BE220489	Hs.113592	ESTs	1	0.3	T2-T4 grade 3 solid tumor marker
	410589	AW770768	Hs.266717	ESTs	1	0.28	T2-T4 grade 3 solid tumor marker
	411840	AW866330		gb:QV4-SN0024-080400-167-e01 SN0024 Homo	1.05	0.15	T2-T4 grade 3 solid tumor marker
	412198	AA937111	Hs.69165	ESTs	1	0.26	T2-T4 grade 3 solid tumor marker
	412305	AW936369		gb:QV4-DT0021-301299-071-d07 DT0021 Homo	1	0.53	T2-T4 grade 3 solid tumor marker
45	412753	AI065016	Hs.6390	ESTs	1	0.33	T2-T4 grade 3 solid tumor marker
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	1	0.69	T2-T4 grade 3 solid tumor marker
	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	1	0.29	T2-T4 grade 3 solid tumor marker
	415027	D31010		gb:HUM12147 Human fetal lung Homo sapie	1	1	T2-T4 grade 3 solid tumor marker
	416099	H18626	Hs.22634	ESTs	1	0.74	T2-T4 grade 3 solid tumor marker
50	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8	0.12	T2-T4 grade 3 solid tumor marker
	416329	AW247430	Hs.84152	cystathionine-beta-synthase	2.85	0.08	T2-T4 grade 3 solid tumor marker
	420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	1	0.2	T2-T4 grade 3 solid tumor marker
	421243	AW873803	Hs.102876	pancreatic lipase	1	0.38	T2-T4 grade 3 solid tumor marker
	422660	AW297582	Hs.237062	ESTs	1.05	0.32	T2-T4 grade 3 solid tumor marker
55	422634	AA318334		gb:EST20402 Retina II Homo sapiens cDNA	1	0.38	T2-T4 grade 3 solid tumor marker
	422972	N59319	Hs.145404	ESTs	1	0.61	T2-T4 grade 3 solid tumor marker
	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	2.95	0.12	T2-T4 grade 3 solid tumor marker
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	1	0.05	T2-T4 grade 3 solid tumor marker
	424268	AA397653	Hs.144339	Human DNA sequence from clone 495C10 on	1	0.35	T2-T4 grade 3 solid tumor marker
60	425196	AL037915	Hs.155097	carbonic anhydrase II	2.75	0.05	T2-T4 grade 3 solid tumor marker
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1	0.09	T2-T4 grade 3 solid tumor marker
	430300	U60805	Hs.238648	oncostatin M receptor	1	0.25	T2-T4 grade 3 solid tumor marker
	431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoadenylate	1	0.28	T2-T4 grade 3 solid tumor marker
	431277	AA501806	Hs.249965	ESTs	1	0.22	T2-T4 grade 3 solid tumor marker
65	431750	AA514986	Hs.283705	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	434273	AA913143	Hs.26303	ESTs	1	0.41	T2-T4 grade 3 solid tumor marker
	435505	AF200492	Hs.211238	Interleukin-1 homolog 1	1.8	0.19	T2-T4 grade 3 solid tumor marker
	436281	AW411194	Hs.120051	ESTs	2.05	0.14	T2-T4 grade 3 solid tumor marker
	437010	AA741368	Hs.291434	ESTs	2.4	0.17	T2-T4 grade 3 solid tumor marker
70	437814	AI038192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.8	0.13	T2-T4 grade 3 solid tumor marker
	438361	AA805666	Hs.145217	Homo sapiens cDNA: FLJ23077 fis, clone L	1	0.3	T2-T4 grade 3 solid tumor marker
	438376	BE541211	Hs.34804	Homo sapiens cDNA FLJ11472 fis, clone HE	1	0.57	T2-T4 grade 3 solid tumor marker
	439370	AW274369	Hs.158853	ESTs	1	0.17	T2-T4 grade 3 solid tumor marker
	440021	AW025498	Hs.270842	ESTs, Weakly similar to ALU8_HUMAN ALU S	1	0.65	T2-T4 grade 3 solid tumor marker
75	440404	AI015881	Hs.125616	ESTs	1	0.26	T2-T4 grade 3 solid tumor marker
	441523	AW514263	Hs.168872	ESTs, Weakly similar to ALUF_HUMAN !!!!	1	1	T2-T4 grade 3 solid tumor marker
	442277	AW448914	Hs.202391	ESTs	2.4	0.15	T2-T4 grade 3 solid tumor marker
	442738	AW002370	Hs.131055	ESTs	1	0.29	T2-T4 grade 3 solid tumor marker
	443297	AI049864	Hs.133029	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	444754	T83911	Hs.11381	transmembrane 4 superfamily member 4	1	0.61	T2-T4 grade 3 solid tumor marker
	445550	AI242754	Hs.137306	ESTs	1	0.5	T2-T4 grade 3 solid tumor marker

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	446149	BE242960	Hs.203181	ESTs	1	0.25	T2-T4 grade 3 solid tumor marker
	446163	AA026830	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1	0.21	T2-T4 grade 3 solid tumor marker
	446434	AI823410	Hs.169149	karyopherin alpha 1 (importin alpha 5)	1	1	T2-T4 grade 3 solid tumor marker
	446928	AI694493	Hs.246916	ESTs	1	0.31	T2-T4 grade 3 solid tumor marker
5	448591	AI540111	Hs.171261	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	449121	AI915858	Hs.194980	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	449539	W80363	Hs.58446	ESTs	1	0.33	T2-T4 grade 3 solid tumor marker
	450451	AW591528	Hs.202072	ESTs	1	0.59	T2-T4 grade 3 solid tumor marker
	450469	AI955049	Hs.281326	ESTs	1	0.43	T2-T4 grade 3 solid tumor marker
10	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1	0.05	T2-T4 grade 3 solid tumor marker
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	1.55	0.11	T2-T4 grade 3 solid tumor marker
	451106	BE382701	Hs.25960	v-myc avian myelocytomatosis viral relat	1	0.95	T2-T4 grade 3 solid tumor marker
	451130	AI762250	Hs.211347	ESTs	3.65	0.15	T2-T4 grade 3 solid tumor marker
	451412	AW136378	Hs.208060	ESTs	1	1	T2-T4 grade 3 solid tumor marker
15	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	1.35	0.22	T2-T4 grade 3 solid tumor marker
	452114	N22687	Hs.8236	ESTs	1	0.19	T2-T4 grade 3 solid tumor marker
	452743	AW965082	Hs.61455	ESTs	1	0.44	T2-T4 grade 3 solid tumor marker
	454622	U70071		gb:HSU70071 Human Homo sapiens cDNA clon	1	1	T2-T4 grade 3 solid tumor marker
20	455235	AW875951		gb:CM1-PT0013-131299-067-f09 PT0013 Homo	1	0.31	T2-T4 grade 3 solid tumor marker
	457792	AL046988	Hs.268677	ESTs, Moderately similar to ALU7_HUMANA	1	0.24	T2-T4 grade 3 solid tumor marker
	100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciain	20.531	0.036	upregulate stage
	101193	L20861	Hs.152213	"wingless-type MMTV integration site fam	1	0.526	upregulate stage
	101724	M69225	Hs.620	bulbous pemphigoid antigen 1 (230/240kD)	20.67	0.037	upregulate stage
25	101809	M86849	"Hs.323733	"gap junction protein, beta 2, 26kD (con	20.78	0.019	upregulate stage
	102154	U17760	Hs.75517	"laminin, beta 3 (nicein (125kD), kalini	18.848	0.042	upregulate stage
	102211	U23070	Hs.78776	putative transmembrane protein	2.092	0.28	upregulate stage
	102623	U66083	Hs.37110	"melanoma antigen, family A, 9"	1	0.306	upregulate stage
	102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.27	0.041	upregulate stage
	103036	X54925	"Hs.83169	matrix metalloproteinase 1 (interstitial	13.63	0.034	upregulate stage
30	103119	X63629	Hs.2877	"cadherin 3, type 1, P-cadherin (placent	7.296	0.054	upregulate stage
	103312	X82693	Hs.3185	"lymphocyte antigen 6 complex, locus D"	0.908	0.485	upregulate stage
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	2.928	0.219	upregulate stage
	103587	Z29083	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.156	0.16	upregulate stage
35	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	1.642	0.516	upregulate stage
	107151	AA621169	Hs.8687	ESTs	2.421	0.174	upregulate stage
	107901	AA026418	"Hs.111758	keratin 6A	1.259	0.343	upregulate stage
	107922	AA028028	Hs.61460	"Homo sapiens Ig superfamily receptor LN	14.22	0.049	upregulate stage
	109166	AA179845	Hs.73625	"RAB6 interacting, kinesin-like (rabkine	11.13	0.039	upregulate stage
40	109424	AA227919	"Hs.85962	hyaluronan synthase 3	1.737	0.518	upregulate stage
	110906	N39584	Hs.17404	ESTs	20.93	0.021	upregulate stage
	112244	R51309	Hs.70823	KIAA1077 protein	3.941	0.181	upregulate stage
	115060	AA253214	Hs.198249	"gap junction protein, beta 5 (connexin	1.932	0.502	upregulate stage
	115697	AA411502	Hs.63325	"transmembrane protease, serine 4"	7.394	0.101	upregulate stage
45	115978	AA447522	"Hs.59517	"Homo sapiens, clone MGC:5257, mRNA, com	1.667	0.445	upregulate stage
	116335	AA495830	Hs.41690	desmocollin 3	4.899	0.154	upregulate stage
	118314	N63402	Hs.46692	ESTs	9.75	0.069	upregulate stage
	118336	N63504	Hs.47166	HT021	4.601	0.197	upregulate stage
	119845	W79920	Hs.58561	G protein-coupled receptor 87	1.95	0.123	upregulate stage
50	120486	AA253400	Hs.137559	tumor protein 63 kDa with strong homolog	4.191	0.211	upregulate stage
	121027	AA398470	Hs.99785	"Homo sapiens cDNA: FLJ21245 fis, clone	14.25	0.058	upregulate stage
	124059	F13673	Hs.283713	"ESTs, Weakly similar to ORF YGL050w [S.	4.99	0.168	upregulate stage
	128595	U31875	"Hs.152677	"Homo sapiens cDNA FLJ20338 fis, clone H	2.433	0.306	upregulate stage
	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	4.34	0.14	upregulate stage
55	129041	H58873	"Hs.169902	"solute carrier family 2 (facilitated gl	2.003	0.455	upregulate stage
	129466	L42583	"Hs.111758	keratin 6A	11.584	0.042	upregulate stage
	130627	L23808	Hs.1696	matrix metalloproteinase 12 (macrophage	2.376	0.233	upregulate stage
	132349	Y00705	"Hs.181286	"serine protease inhibitor, Kazal type 1	5.4	0.132	upregulate stage
	132710	W93726	Hs.55279	"serine (or cysteine) proteinase inhibit	3.888	0.187	upregulate stage
60	133391	X57579	Hs.727	"inhibin, beta A (activin A, activin AB	1.517	0.334	upregulate stage
	134110	AA242758	"Hs.79136	"LIV-1 protein, estrogen regulated"	2.221	0.387	upregulate stage
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.85	0.03	upregulate stage
	400297	AI127076	Hs.288381	hypothetical protein DKFZp564C1278	3.54	0.13	upregulate stage
	400346	AB041269	Hs.272263	Homo sapiens mRNA for keratin 19, partia	8.95	0.07	upregulate stage
65	400419	AF084545	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	10.7	0.06	upregulate stage
	400495				1	0.56	upregulate stage
	400509	M97639	Hs.155585	receptor tyrosine kinase-like orphan rec	1.52	0.51	upregulate stage
	400528				3.47	0.23	upregulate stage
	400577				1	0.29	upregulate stage
70	400608				7.2	0.08	upregulate stage
	400644				1	1	upregulate stage
	400666				1.42	0.43	upregulate stage
	400750				8.7	0.1	upregulate stage
	400773				1.11	0.51	upregulate stage
75	400844				9.65	0.04	upregulate stage
	400845				2.3	0.28	upregulate stage
	400846				1.34	0.5	upregulate stage
	400880				9.4	0.06	upregulate stage

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	400887				1	1	upregulate stage
	401086				1	0.51	upregulate stage
	401093				7	0.08	upregulate stage
	401101				1	0.17	upregulate stage
5	401197				5.16	0.14	upregulate stage
	401262				1	1	upregulate stage
	401271				1	1	upregulate stage
	401279				9.1	0.06	upregulate stage
	401342				1.42	0.5	upregulate stage
10	401345	M83738	Hs.147663	protein tyrosine phosphatase, non-recept	1	0.33	upregulate stage
	401365				6.5	0.11	upregulate stage
	401395				1	0.31	upregulate stage
	401420				1	1	upregulate stage
	401439				2.65	0.17	upregulate stage
15	401451				12	0.05	upregulate stage
	401599	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	9.15	0.08	upregulate stage
	401600	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	8.75	0.09	upregulate stage
	401694				1	1	upregulate stage
	401747				29.75	0.02	upregulate stage
20	401759				11.35	0.06	upregulate stage
	401780				6.15	0.07	upregulate stage
	401858	AC005261	Hs.98338	serine/threonine kinase 13 (aurora)/PL1-	1	0.69	upregulate stage
	401994				3.15	0.15	upregulate stage
	402001				4.4	0.14	upregulate stage
25	402230				8.75	0.06	upregulate stage
	402325				1	0.36	upregulate stage
	402408				5.15	0.1	upregulate stage
	402472				9.05	0.08	upregulate stage
	402480				1	1	upregulate stage
30	402490				9.6	0.07	upregulate stage
	402553				9.85	0.09	upregulate stage
	402889				9.4	0.09	upregulate stage
	402901				1.07	0.65	upregulate stage
	402938				1	1	upregulate stage
35	402995				9.6	0.06	upregulate stage
	403005				1.5	0.21	upregulate stage
	403020				5.15	0.12	upregulate stage
	403052	R58624	Hs.2186	eukaryotic translation elongation factor	1	1	upregulate stage
40	403053	R58624	Hs.2186	eukaryotic translation elongation factor	1.5	0.28	upregulate stage
	403073				1	0.37	upregulate stage
	403085				1	0.43	upregulate stage
	403106				1.12	0.57	upregulate stage
	403152	AA576664	Hs.37078	v-crk avian sarcoma virus CT10 oncogene	0.86	1.08	upregulate stage
45	403172				7.7	0.09	upregulate stage
	403212				1.18	0.62	upregulate stage
	403214				6.05	0.1	upregulate stage
	403277				4.5	0.11	upregulate stage
	403331				3.2	0.13	upregulate stage
50	403381				10.7	0.05	upregulate stage
	403485				10.35	0.08	upregulate stage
	403588				1	1	upregulate stage
	403851				2.45	0.34	upregulate stage
	403860				1	1	upregulate stage
55	403894				4.45	0.14	upregulate stage
	403903				1.39	0.58	upregulate stage
	403954	W28077	Hs.79389	nel (chicken)-like 2	1	1	upregulate stage
	404148				9.15	0.08	upregulate stage
	404229				1	1	upregulate stage
60	404258				1	1	upregulate stage
	404274				1.3	0.2	upregulate stage
	404288				1	0.39	upregulate stage
	404403				1	0.28	upregulate stage
	404440				7.05	0.06	upregulate stage
65	404507				1	0.33	upregulate stage
	404516				1	1	upregulate stage
	404639				1	1	upregulate stage
	404684				0.89	0.9	upregulate stage
	404685				2.74	0.26	upregulate stage
70	404704				9.35	0.08	upregulate stage
	404829				1	0.24	upregulate stage
	404860				3.65	0.15	upregulate stage
	404894				2.05	0.16	upregulate stage
75	404939				1	1	upregulate stage
	405034	AL035754	Hs.2474	tol-like receptor 1	1	0.18	upregulate stage
	405059				1	0.56	upregulate stage
	405084				1	0.22	upregulate stage
	405102				9.65	0.08	upregulate stage

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	405167			1	0.67	upregulate stage
	405170			1	0.48	upregulate stage
	405177			1	0.22	upregulate stage
5	405186			3.75	0.1	upregulate stage
	405258			8.85	0.09	upregulate stage
	405281			1	1	upregulate stage
	405379			1	0.87	upregulate stage
	405494			5	0.13	upregulate stage
10	405520			1	0.95	upregulate stage
	405526			8.96	0.08	upregulate stage
	405725			3.3	0.12	upregulate stage
	405738			0.86	0.69	upregulate stage
	405809			2.4	0.18	upregulate stage
15	405838			1	0.22	upregulate stage
	405906			2.6	0.12	upregulate stage
	406137			1.54	0.52	upregulate stage
	406187			3.2	0.14	upregulate stage
	406322			3.95	0.12	upregulate stage
20	406360			4.1	0.1	upregulate stage
	406397			1	0.24	upregulate stage
	406434			7.4	0.07	upregulate stage
	406467			9.1	0.07	upregulate stage
	406511			1	1	upregulate stage
25	406517	W28077	Hs.79389	1	1	upregulate stage
	406588			0.93	0.91	upregulate stage
	406651	AI559224	Hs.277477	10.1	0.07	upregulate stage
	406665	U22961	Hs.75442	1.08	0.81	upregulate stage
	406671	AA129547	Hs.285754	5.7	0.12	upregulate stage
30	406687	M31126	Hs.272620	1.95	0.3	upregulate stage
	406732	AA487229	Hs.2064	1	0.77	upregulate stage
	406747	AI925153	Hs.217493	3.6	0.14	upregulate stage
	406753	AA505665	Hs.217493	5.45	0.13	upregulate stage
	406815	AA833930	Hs.288036	3.65	0.09	upregulate stage
35	406850	AI624300	Hs.172928	1.29	0.62	upregulate stage
	406892	D55643		1	1	upregulate stage
	406944	J04742	Hs.247945	1	1	upregulate stage
	406950	L17325	Hs.278	1	0.36	upregulate stage
	406961	L77563		1	1	upregulate stage
40	406964	M21305	Hs.247946	42.25	0.01	upregulate stage
	406993	S83249		1	1	upregulate stage
	407017	U48697		1	1	upregulate stage
	407073	Y10510		1	0.53	upregulate stage
	407105	S64699	Hs.663	1	1	upregulate stage
45	407128	R83312	Hs.237260	1	1	upregulate stage
	407132	T02871	Hs.228523	1	0.45	upregulate stage
	407137	T97307	Hs.199067	14.3	0.05	upregulate stage
	407158	N49839		1	0.57	upregulate stage
	407175	T86603		1	0.31	upregulate stage
50	407186	AA435610		1	1	upregulate stage
	407189	AA598927		1	1	upregulate stage
	407192	AA609200		6.05	0.12	upregulate stage
	407195	C21124		1	1	upregulate stage
	407202	N58172	Hs.109370	3.7	0.16	upregulate stage
55	407204	R41933	Hs.140237	10.2	0.06	upregulate stage
	407205	R78910	Hs.272620	1.9	0.22	upregulate stage
	407211	T95828	Hs.230070	1	0.59	upregulate stage
	407346	AI090210	Hs.264106	1	1	upregulate stage
	407422	AF116633		1	0.22	upregulate stage
60	407494	U10072		4.1	0.13	upregulate stage
	407547	Y10259		2.45	0.19	upregulate stage
	407564	AA042860	Hs.103005	1	1	upregulate stage
	407603	AW955705	Hs.62604	1.18	0.73	upregulate stage
	407634	AW016569	Hs.301280	9.6	0.06	upregulate stage
65	407668	BE161086	Hs.279617	1	0.39	upregulate stage
	407709	AA456135	Hs.23023	6.8	0.12	upregulate stage
	407710	AW022727	Hs.23616	3.9	0.14	upregulate stage
	407725	BE388094	Hs.21857	9.97	0.07	upregulate stage
	407729	T40707	Hs.270862	9.2	0.09	upregulate stage
70	407774	AA084958		2.65	0.22	upregulate stage
	407788	BE514982	Hs.38991	2.1	0.34	upregulate stage
	407811	AW190902	Hs.40058	8.45	0.06	upregulate stage
	407813	AL120247	Hs.40109	9.1	0.08	upregulate stage
	407833	AW955632	Hs.66666	9.2	0.07	upregulate stage
75	407839	AA045144	Hs.161566	2.11	0.25	upregulate stage
	407853	AA336797	Hs.40499	1	0.34	upregulate stage
	407881	AW072003	Hs.40968	3.52	0.18	upregulate stage
	407882	AI241264	Hs.62772	1	0.26	upregulate stage

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5	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	13.6	0.05	upregulate stage
	407911	AF104922	Hs.41565	growth differentiation factor 8	1	1	upregulate stage
	407912	AW104401	Hs.243489	ESTs, Weakly similar to AF151881 1 CGI-1	10.35	0.07	upregulate stage
	407935	U31986	Hs.41683	cartilage paired-class homeoprotein 1	4.25	0.12	upregulate stage
	407939	W05608		gb:za85e07.r1 Soares_fetal_lung_NbHL19W	8.75	0.09	upregulate stage
10	407944	R34008	Hs.239727	desmocollin 2	9.2	0.06	upregulate stage
	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypep	1.45	0.25	upregulate stage
	407946	AA226495	Hs.154292	ESTs	9.4	0.07	upregulate stage
	407949	W21874	Hs.247057	ESTs	3.32	0.2	upregulate stage
	407974	AW568123	Hs.146401	small inducible cytokine subfamily E, me	3.55	0.14	upregulate stage
15	407983	U40371	Hs.41718	phosphodiesterase 1C, calmodulin-depende	8.95	0.07	upregulate stage
	407994	AW135309	Hs.244331	ESTs	4.5	0.12	upregulate stage
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	2.89	0.19	upregulate stage
	408014	AA723782	Hs.41749	protein kinase, cGMP-dependent, type II	1.31	0.53	upregulate stage
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	3.6	0.17	upregulate stage
20	408046	AW139121	Hs.183643	ESTs	1	0.36	upregulate stage
	408063	BE086548	Hs.42346	caldesmon-binding protein caldesmon-1	10.75	0.05	upregulate stage
	408092	NM_007057	Hs.42650	ZW10 interactor	4.7	0.13	upregulate stage
	408101	AW568504	Hs.123073	CDC2-related protein kinase 7	4.5	0.14	upregulate stage
	408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic b	4.4	0.13	upregulate stage
25	408170	AW204516	Hs.31835	ESTs	5.85	0.13	upregulate stage
	408184	AW168741	Hs.22249	ESTs	1	1	upregulate stage
	408224	AW175997		gb:QV0-BT0078-190899-005-E02 BT0078 Homo	1	0.44	upregulate stage
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.95	0.04	upregulate stage
	408241	AW176546		gb:MR0-CT0063-200899-001-a01 CT0063 Homo	2.8	0.17	upregulate stage
30	408268	AL138247		gb:DKFZp547D237_r1 547 (synonym: hibr1)	1	0.61	upregulate stage
	408277	AW177959		gb:IL3-HT0060-200899-008-D03 HT0060 Homo	1	1	upregulate stage
	408306	BE141991		gb:PM2-HT0134-220999-002-d10 HT0134 Homo	1	1	upregulate stage
	408352	AA053875	Hs.95310	ESTs	1	1	upregulate stage
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	9.15	0.08	upregulate stage
35	408393	AW015318	Hs.23165	ESTs	9.35	0.07	upregulate stage
	408396	AA330496	Hs.40840	ESTs	1	0.61	upregulate stage
	408442	R59608	Hs.21435	ESTs	1	1	upregulate stage
	408514	AW206559	Hs.255903	ESTs	1	0.34	upregulate stage
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	1	0.33	upregulate stage
40	408617	R61736	Hs.124128	ESTs	2.75	0.14	upregulate stage
	408633	AW563372	Hs.46677	PRO2000 protein	3.14	0.25	upregulate stage
	408706	AW438503	Hs.256935	ESTs	8.45	0.09	upregulate stage
	408713	NM_001248	Hs.47042	ecolnucleoside triphosphate diphosphohyd	2.81	0.21	upregulate stage
	408725	AA131539	Hs.15669	ESTs	9.1	0.08	upregulate stage
45	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	3.1	0.11	upregulate stage
	408738	NM_014785	Hs.47313	KIAA0258 gene product	4.4	0.13	upregulate stage
	408739	W01556	Hs.238797	ESTs	5.65	0.11	upregulate stage
	408754	N31256	Hs.161623	ESTs	1	1	upregulate stage
	408765	AA057268	Hs.146013	ESTs	8.75	0.09	upregulate stage
50	408805	H69912	Hs.48269	vaccinia related kinase 1	4.95	0.12	upregulate stage
	408813	AI580090	Hs.46295	RNA helicase family	3.65	0.17	upregulate stage
	408817	AA524525	Hs.279864	PRO1996 protein	6.15	0.12	upregulate stage
	408849	BE219451	Hs.254919	ESTs	1	0.32	upregulate stage
	408902	AW014869	Hs.5510	ESTs	3.3	0.15	upregulate stage
55	408908	BE296227	Hs.48915	serine/threonine kinase 15	5.65	0.1	upregulate stage
	408916	AW295232	Hs.22653	ESTs	10	0.08	upregulate stage
	408933	AA058979	Hs.182133	ESTs, Highly similar to ADP-ribosylation	1	0.91	upregulate stage
	408943	NM_007070	Hs.49105	FKBP-associated protein	3.45	0.16	upregulate stage
	408960	BE158389	Hs.300976	ESTs	6.3	0.1	upregulate stage
60	409032	AW301807	Hs.297260	ESTs	8.4	0.08	upregulate stage
	409093	BE243834	Hs.50441	CGI-04 protein	1.71	0.49	upregulate stage
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	10.1	0.07	upregulate stage
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	11.85	0.05	upregulate stage
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	2.83	0.24	upregulate stage
65	409231	AA446644	Hs.692	tumor-associated calcium signal transduc	9.34	0.08	upregulate stage
	409262	AK000631	Hs.52256	hypothetical protein FLJ20524	8.7	0.09	upregulate stage
	409357	M73628	Hs.54415	casein, kappa	1.6	0.2	upregulate stage
	409402	AF208234	Hs.695	cystatin B (stefin B)	1.57	0.56	upregulate stage
	409405	AA075869	Hs.126400	ESTs, Highly similar to RL39_HUMAN 60S R	2.6	0.12	upregulate stage
70	409408	AW387837		gb:MR4-ST0118-021299-021-f08 ST0118 Homo	4.3	0.15	upregulate stage
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	8.28	0.06	upregulate stage
	409509	AL036523	Hs.127006	ESTs	10.2	0.06	upregulate stage
	409566	AA078899		gb:zm94b01.r1 Striatagene colon HT29 (937	1	0.56	upregulate stage
	409575	AW419225	Hs.256247	ESTs	2.15	0.14	upregulate stage
75	409582	R27430	Hs.271565	ESTs	7.3	0.07	upregulate stage
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	3.78	0.19	upregulate stage
	409642	AW450809	Hs.257347	ESTs	9.55	0.07	upregulate stage
	409674	AI935146	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1	0.29	upregulate stage
	409691	T89583	Hs.246042	ESTs	1	1	upregulate stage
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3	2.22	0.36	upregulate stage
	409727	N63786	Hs.94149	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.57	upregulate stage

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	409760	AA302840		gb:EST10534 Adipose tissue, white I Homo	9.95	0.06	upregulate stage
	409789	BE256027	Hs.180946	ribosomal protein L5	1	0.83	upregulate stage
	409794	AW895891		gb:RC4-OT0071-240300-013-b04 OT0071 Homo	1	1	upregulate stage
5	409977	AW805510	Hs.97056	hypothetical protein FLJ21634	9.65	0.07	upregulate stage
	409985	AW291944	Hs.122139	ESTs	4.35	0.14	upregulate stage
	409989	R37868	Hs.13333	ESTs	1	0.21	upregulate stage
	409995	AW960597	Hs.30164	ESTs	5.05	0.12	upregulate stage
	410013	AF067173	Hs.57904	mago-nashi (Drosophila) homolog, prolif	3.05	0.26	upregulate stage
10	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	3.15	0.09	upregulate stage
	410071	AW582568		gb:RC1-ST0278-080100-011-h04 ST0278 Homo	2.5	0.18	upregulate stage
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	8	0.06	upregulate stage
	410114	AW590540	Hs.271280	ESTs	5.1	0.14	upregulate stage
	410117	AK001566	Hs.58650	hypothetical protein FLJ10724	1	1	upregulate stage
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	4.7	0.11	upregulate stage
15	410181	AI688210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	1	0.23	upregulate stage
	410196	AI936442	Hs.59838	hypothetical protein FLJ10608	6.05	0.09	upregulate stage
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	5.55	0.12	upregulate stage
	410259	AK000337	Hs.61485	hypothetical protein	10.1	0.07	upregulate stage
20	410275	AI554545	Hs.68301	ESTs	2.98	0.25	upregulate stage
	410278	AW614396	Hs.282230	ESTs	1	0.28	upregulate stage
	410325	AB023154	Hs.62264	KIAA0937 protein	6.85	0.13	upregulate stage
	410356	BE244668	Hs.62643	dual adaptor of phosphotyrosine and 3-ph	1	1	upregulate stage
	410388	AA831460	Hs.22039	hepatocyte nuclear factor 3, alpha	1	0.33	upregulate stage
	410399	BE068889	Hs.63236	synuclein, gamma (breast cancer-specific	1.07	0.78	upregulate stage
25	410420	AA224053	Hs.172405	ESTs, Moderately similar to I52835 H-NUC	1	0.14	upregulate stage
	410429	AA310600	Hs.63657	hypothetical protein FLJ11005	11.25	0.07	upregulate stage
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	9.6	0.03	upregulate stage
	410475	AW749927		gb:QV0-BT0537-231299-049-f03 BT0537 Homo	9.8	0.03	upregulate stage
30	410495	N95428		gb:zbB0d09.s1 Soares_senescent_fibroblas	11.3	0.06	upregulate stage
	410501	AI675688	Hs.83286	ESTs	4.75	0.1	upregulate stage
	410503	AW975746	Hs.188662	Homo sapiens cDNA: FLJ23421 fis, clone H	6.5	0.1	upregulate stage
	410520	AW752710		gb:IL3-CT0219-281099-024-A03 CT0219 Homo	1	1	upregulate stage
	410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	3.1	0.16	upregulate stage
35	410537	AW753108		gb:FM1-CT0247-080100-008-e10 CT0247 Homo	10.35	0.08	upregulate stage
	410553	AW016824	Hs.68784	ESTs	1.67	0.41	upregulate stage
	410560	N29220		gb:yx43b05.r1 Soares melanocyte 2NbHM Ho	9	0.07	upregulate stage
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	6.2	0.11	upregulate stage
	410562	AW858528		gb:CM3-CT0341-150300-119-h11 CT0341 Homo	1	1	upregulate stage
40	410579	AK001628	Hs.64691	KIAA0483 protein	11.1	0.06	upregulate stage
	410634	AW888653	Hs.266859	ESTs	1	1	upregulate stage
	410664	NM_006033	Hs.65370	lipase, endothelial	3.95	0.1	upregulate stage
	410668	BE379794	Hs.65403	hypothetical protein	1.82	0.41	upregulate stage
	410730	AW368860	Hs.293950	ESTs	9.25	0.07	upregulate stage
45	410751	AA357918		gb:EST66726 Fetal lung III Homo sapiens	1	1	upregulate stage
	410754	T63840		gb:yc16b10.s1 Stratagene lung (937210) H	3.1	0.14	upregulate stage
	410762	AF226053	Hs.66170	HSKM-B protein	5.55	0.1	upregulate stage
	410764	AW978159	Hs.250164	ESTs, Weakly similar to coded for by C.	1	0.2	upregulate stage
	410782	AW504860	Hs.288836	Homo sapiens cDNA FLJ12673 fis, clone NT	1.75	0.25	upregulate stage
	410794	AA248010	Hs.154669	ESTs	1	0.67	upregulate stage
50	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.2	0.17	upregulate stage
	410844	AW807073		gb:MR4-ST0052-031199-018-d06 ST0062 Homo	1	0.8	upregulate stage
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	6.5	0.12	upregulate stage
	410910	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	9.35	0.08	upregulate stage
55	410973	AW812278		gb:RC0-ST0174-211099-011-h12 ST0174 Homo	1	1	upregulate stage
	410976	R36207	Hs.25092	ESTs	8.35	0.1	upregulate stage
	410997	AW812877		gb:RC3-ST0186-300100-017-e04 ST0186 Homo	1	1	upregulate stage
	410998	W28247	Hs.82007	KIAA0094 protein	2.45	0.18	upregulate stage
	411036	AA857218	Hs.297007	ESTs	4.05	0.14	upregulate stage
60	411110	H93000		gb:yy07f01.s1 Soares fetal liver spleen	1	0.36	upregulate stage
	411132	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	1	1	upregulate stage
	411137	AW819455		gb:RC5-ST0293-021299-031-A04 ST0293 Homo	3.65	0.18	upregulate stage
	411157	AW819867		gb:QV0-ST0294-070300-151-f02 ST0294 Homo	3.2	0.2	upregulate stage
	411159	AW820178		gb:QV0-ST0294-100400-185-e07 ST0294 Homo	1	0.27	upregulate stage
65	411170	AW820503		gb:QV2-ST0298-140200-042-b05 ST0298 Homo	1	1	upregulate stage
	411193	AW821484		gb:IL2-ST0311-211299-028-F12 ST0311 Homo	1	0.24	upregulate stage
	411242	BE146808		gb:QV4-HT0222-181099-013-g03 HT0222 Homo	2.55	0.26	upregulate stage
	411245	AW833441		gb:QV4-TT0008-271099-020-g01 TT0008 Homo	9.62	0.09	upregulate stage
	411263	BE297802	Hs.69360	kinasin-like 8 (mitotic centromere-assoc	2.4	0.32	upregulate stage
70	411282	AW995011		gb:QV0-BN0040-170300-161-d07 BN0040 Homo	1	1	upregulate stage
	411284	N28519	Hs.135191	ESTs, Weakly similar to unnamed protein	3.25	0.12	upregulate stage
	411294	AW859729	Hs.42680	ESTs	1	1	upregulate stage
	411327	AW836922		gb:QV1-LT0036-150200-074-h06 LT0036 Homo	1	0.37	upregulate stage
	411338	AW731782	Hs.116122	ESTs, Weakly similar to unnamed protein	5	0.13	upregulate stage
	411339	BE164598		gb:RC3-HT0470-120200-013-b10 HT0470 Homo	1	0.25	upregulate stage
75	411383	AA001394	Hs.69749	KIAA0087 gene product	3.6	0.18	upregulate stage
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	8.75	0.09	upregulate stage
	411400	AA311919	Hs.69861	GAR1 protein	12.1	0.07	upregulate stage

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5	411425	AW846012		gb:RC2-CT0163-230999-003-E01 CT0163 Homo	1	0.74	upregulate stage
	411461	AW847937		gb:IL3-CT0213-210200-042-D02 CT0213 Homo	1	1	upregulate stage
	411526	AW850327		gb:IL3-CT0219-221199-029-D08 CT0219 Homo	1	1	upregulate stage
	411560	AW851186		gb:IL3-CT0220-150200-071-H05 CT0220 Homo	2.8	0.17	upregulate stage
	411568	BE144593		gb:MR0-HT0167-141199-002-f04 HT0167 Homo	1	1	upregulate stage
10	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.55	0.14	upregulate stage
	411605	AW006831	Hs.20479	ESTs	9.6	0.08	upregulate stage
	411626	AW753453	Hs.71109	KIAA1229 protein	1	1	upregulate stage
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	4.1	0.11	upregulate stage
	411643	AI524519	Hs.192570	Homo sapiens cDNA: FLJ22028 fis, clone H	1	0.28	upregulate stage
15	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	8.9	0.08	upregulate stage
	411727	AW858443		gb:CM0-CT0341-260100-160-f10 CT0341 Homo	1	1	upregulate stage
	411771	AW933247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	2.6	0.14	upregulate stage
	411787	AW863568		gb:MR3-SN0010-240300-102-c10 SN0010 Homo	1	1	upregulate stage
	411788	AW897793		gb:CM1-NN0063-280400-203-f07 NN0063 Homo	3.7	0.15	upregulate stage
20	411826	AW947946		gb:PM0-MT0011-240300-001-a09 MT0011 Homo	3.25	0.13	upregulate stage
	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	1	1	upregulate stage
	411860	T89420		gb:yd98f04.s1 Soares fetal liver spleen	1	0.22	upregulate stage
	411874	AA096106	Hs.20403	ESTs	5.75	0.11	upregulate stage
	411917	AW876360	Hs.3592	Homo sapiens cDNA: FLJ22555 fis, clone H	1	0.33	upregulate stage
25	411928	AA886624	Hs.19121	adaptor-related protein complex 2, alpha	4.75	0.12	upregulate stage
	411932	AW876548		gb:RC3-PT0028-150100-012-h02 PT0028 Homo	1	0.38	upregulate stage
	411943	BE502436	Hs.7962	ESTs, Weakly similar to putative [C.eleg	3.82	0.23	upregulate stage
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	4.65	0.15	upregulate stage
	411991	X58822	Hs.73010	interferon, omega 1	2.45	0.14	upregulate stage
30	412040	D86519	Hs.73085	neuropeptide Y receptor Y6 (pseudogene)	4.6	0.14	upregulate stage
	412088	AI689496	Hs.108932	ESTs	2.82	0.18	upregulate stage
	412134	AW855560		gb:QV4-NN0038-270400-187-g08 NN0038 Homo	6.4	0.1	upregulate stage
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakbines	17.05	0.04	upregulate stage
	412231	AW902491	Hs.289038	heat shock 90kD protein 1, alpha	1	0.91	upregulate stage
35	412296	AW936233		gb:QV0-DT0020-090200-107-a06 DT0020 Homo	1	1	upregulate stage
	412327	AW937355		gb:QV3-DT0043-211299-044-a06 DT0043 Homo	1	1	upregulate stage
	412357	AW939537		gb:QV1-DT0072-110200-066-f05 DT0072 Homo	1	0.24	upregulate stage
	412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	1	0.41	upregulate stage
	412367	AW945954		gb:QV0-ET0001-050500-228-e09 ET0001 Homo	1	0.22	upregulate stage
40	412529	BE271224	Hs.266273	Homo sapiens cDNA FLJ13346 fis, clone OV	4.45	0.14	upregulate stage
	412530	AA766268	Hs.266273	Homo sapiens cDNA FLJ13346 fis, clone OV	9.3	0.08	upregulate stage
	412537	AL031778	Hs.797	nuclear transcription factor Y, alpha	4.25	0.14	upregulate stage
	412547	W27161		gb:23a12 Human retina cDNA randomly prim	1	1	upregulate stage
	412559	T31474		gb:EST33147 Human Embryo Homo sapiens cD	1	0.26	upregulate stage
45	412636	NM_004415	Hs.74316	desmoplakin (DPI, DPLI)	12.05	0.05	upregulate stage
	412648	AA115211	Hs.69653	EST	1	0.28	upregulate stage
	412668	AA456195	Hs.10056	ESTs	10.75	0.07	upregulate stage
	412671	AW977734		gb:EST389963 MAGE resequences, MAGO Homo	2.65	0.3	upregulate stage
	412673	AL042957	Hs.31845	ESTs	4.6	0.11	upregulate stage
50	412723	AA648459	Hs.179912	ESTs	2.55	0.11	upregulate stage
	412739	AA116018	Hs.271809	Homo sapiens cDNA: FLJ22406 fis, clone H	1.6	0.24	upregulate stage
	412744	N31101		gb:yx52a03.r1 Soares melanocyte 2NbHM Ho	2	0.23	upregulate stage
	412778	AA120882	Hs.159244	ESTs	1	1	upregulate stage
	412811	H06382	Hs.21400	ESTs	1	0.49	upregulate stage
55	412838	D61870		gb:HUM218F11B Clontech human aorta polyA	1	0.34	upregulate stage
	412854	BE004149	Hs.31161	ESTs	1	1	upregulate stage
	413075	D59828	Hs.70953	ESTs	1	0.77	upregulate stage
	413109	AW389845	Hs.110355	ESTs	3.93	0.1	upregulate stage
	413117	BE066107	Hs.138484	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.22	upregulate stage
60	413119	BE065941		gb:RC3-BT0319-100100-012-d12 BT0319 Homo	1	0.87	upregulate stage
	413141	BE166323		gb:QV4-HT0492-270100-086-e12 HT0492 Homo	5.45	0.12	upregulate stage
	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PL	2.54	0.19	upregulate stage
	413228	AA127518	Hs.195870	ESTs	1	1	upregulate stage
	413273	U75679	Hs.75257	Hairpin binding protein, histone	5.05	0.11	upregulate stage
65	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.45	0.5	upregulate stage
	413294	BE144034		gb:MR0-HT0165-191199-004-a02 HT0165 Homo	1	1	upregulate stage
	413324	V00571	Hs.75294	corticotropin releasing hormone	6.95	0.03	upregulate stage
	413342	AA128535		gb:z124e04.r1 Soares_pregnant_uterus_NbH	1	1	upregulate stage
	413430	R22479	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT	3	0.18	upregulate stage
70	413707	BE158679		gb:CM0-HT0395-280100-169-c04 HT0395 Homo	1	0.28	upregulate stage
	413743	BE161004		gb:PM0-HT0425-170100-002-h03 HT0425 Homo	1	1	upregulate stage
	413753	U17760	Hs.301103	Human DNA sequence from clone 272L16 on	22.7	0.03	upregulate stage
	413786	AW613780	Hs.13500	ESTs	9.9	0.07	upregulate stage
	413792	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	1	1	upregulate stage
75	413804	T64682		gb:yc48b02.r1 Stratagene liver (S37224)	0.99	0.75	upregulate stage
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.55	0.17	upregulate stage
	413854	BE174300	Hs.44581	heat shock protein hsp70-related protein	1.25	0.24	upregulate stage
	413916	AW015898	Hs.71245	ESTs	4	0.11	upregulate stage
	413968	AW500374	Hs.64056	ESTs	10.85	0.07	upregulate stage
	414091	T83742		gb:yd67g02.s1 Soares fetal liver spleen	8.9	0.1	upregulate stage
	414099	U11313	Hs.75760	sterol carrier protein 2	10.3	0.06	upregulate stage

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	414116	AA587370	Hs.71584	ESTs	1	1	upregulate stage
	414127	AI431863	Hs.135270	ESTs	2.85	0.13	upregulate stage
	414169	AA136169	Hs.149335	ESTs	8.95	0.09	upregulate stage
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	7.05	0.05	upregulate stage
5	414304	AI821276	Hs.165998	DKFZP564M2423 protein	1	0.24	upregulate stage
	414338	N80751	Hs.301471	ESTs	10.3	0.08	upregulate stage
	414447	AA147549	Hs.109909	ESTs	3.4	0.16	upregulate stage
	414494	AA768491	Hs.6783	Homo sapiens cDNA: FLJ22724 fis, clone H	3.4	0.18	upregulate stage
10	414520	AA148806	Hs.204046	ESTs	1	0.21	upregulate stage
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	3.1	0.18	upregulate stage
	414575	H11257	Hs.295233	ESTs	3.1	0.15	upregulate stage
	414597	H67472	Hs.34274	ESTs	4.6	0.11	upregulate stage
	414643	H46177	Hs.119316	ESTs	1	0.28	upregulate stage
15	414658	X58528	Hs.76781	ATP-binding cassette, sub-family D (ALD)	7.75	0.08	upregulate stage
	414661	T97401	Hs.21929	ESTs	1	0.26	upregulate stage
	414683	S78296	Hs.76888	intermedin neuronal intermediate filamen	2.72	0.25	upregulate stage
	414735	BE468016	Hs.281904	ESTs	1	0.38	upregulate stage
	414737	AI160386	Hs.125087	ESTs	5.5	0.1	upregulate stage
20	414747	U30672	Hs.77204	centromere protein F (350/400kD, mitotin	3.19	0.24	upregulate stage
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.45	0.49	upregulate stage
	414783	AW069569	Hs.75839	zinc finger protein 6 (CMPX1)	4.65	0.13	upregulate stage
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	1.7	0.46	upregulate stage
	414833	T07114		gb:EST05003 Fetal brain, Stratagene (cat	4.5	0.13	upregulate stage
	414883	AA926960	Hs.77550	cdc28 protein kinase 1	3.36	0.22	upregulate stage
25	414885	AA157531	Hs.269276	ESTs	2.7	0.21	upregulate stage
	414918	AI219207	Hs.72222	Homo sapiens cDNA FLJ13459 fis, clone PL	0.87	0.69	upregulate stage
	414985	C17372		gb:C17372 Clontech human acrota polyA+ mR	1	0.42	upregulate stage
	415025	AW207091	Hs.72307	ESTs	5.3	0.06	upregulate stage
30	415033	D31476	Hs.301448	Homo sapiens cDNA FLJ12152 fis, clone MA	1	1	upregulate stage
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	6.05	0.1	upregulate stage
	415068	Z19448	Hs.131887	ESTs, Weakly similar to ORF YNL227c [S.c	4.5	0.13	upregulate stage
	415095	D59592	Hs.34745	ESTs	1	0.44	upregulate stage
	415099	AI492170	Hs.77917	ubiquitin carboxyl-terminal esterase L3	2.27	0.29	upregulate stage
35	415104	D60076		gb:HUM084E10A Clontech human fetal brain	3.95	0.13	upregulate stage
	415114	D60468		gb:HUM111A06B Clontech human fetal brain	2.05	0.2	upregulate stage
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	5.8	0.05	upregulate stage
	415139	AW975942	Hs.48524	ESTs	1.15	0.21	upregulate stage
	415148	Z36953	Hs.48527	ESTs	2.5	0.2	upregulate stage
40	415153	C03508	Hs.7000	ESTs	8.95	0.09	upregulate stage
	415178	D80503		gb:HUM080A02B Human fetal brain (TFujiwa	1	0.15	upregulate stage
	415217	H23983	Hs.26922	ESTs	1	0.31	upregulate stage
	415227	AW821113	Hs.72402	ESTs	6.3	0.11	upregulate stage
	415238	R37780	Hs.21422	ESTs	1	1	upregulate stage
45	415241	F02208	Hs.27214	ESTs	1	1	upregulate stage
	415295	R41450	Hs.6546	ESTs	1	0.63	upregulate stage
	415296	F05086		gb:HSC01A011 normalized Infant brain cDN	5.65	0.1	upregulate stage
	415327	H22769	Hs.1861	membrane protein, palmitoylated 1 (55kD)	8.15	0.09	upregulate stage
	415330	Z44693	Hs.21422	ESTs	3	0.2	upregulate stage
50	415336	T77664	Hs.78362	Human clone 23839 mRNA sequence	1	0.87	upregulate stage
	415337	Z44881	Hs.9012	ESTs	8.8	0.07	upregulate stage
	415352	F06565		gb:HSC1CG051 normalized infant brain cDN	1	1	upregulate stage
	415364	F06771		gb:HSC1KD031 normalized infant brain cDN	1	1	upregulate stage
	415371	R15239		gb:y89b02.r1 Soares infant brain 1N1B H	5.1	0.13	upregulate stage
55	415412	F08049	Hs.52132	ESTs	4.25	0.16	upregulate stage
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.1	0.15	upregulate stage
	415462	R52692	Hs.12698	ESTs	4.65	0.11	upregulate stage
	415496	R37637	Hs.12286	ESTs	5.4	0.13	upregulate stage
	415509	R40000	Hs.91968	ESTs	1	0.44	upregulate stage
60	415511	AI732617	Hs.182362	ESTs	9.3	0.03	upregulate stage
	415542	R13474	Hs.290263	ESTs	9.7	0.08	upregulate stage
	415569	Z43930		gb:HSC1OH121 normalized Infant brain cDN	1	0.74	upregulate stage
	415600	F12664		gb:HSC3CG021 normalized infant brain cDN	1	0.43	upregulate stage
	415616	F12945	Hs.12294	ESTs	1	1	upregulate stage
65	415626	Z43847		gb:HSC1MC051 normalized infant brain cDN	1	1	upregulate stage
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	1	0.26	upregulate stage
	415750	AA167712		gb:zq39g08.s1 Stratagene hNT neuron (937	1	0.83	upregulate stage
	415786	AW419196	Hs.257924	Homo sapiens cDNA FLJ13782 fis, clone PL	9	0.08	upregulate stage
	415788	AW628686	Hs.78851	KIAA0217 protein	5.2	0.11	upregulate stage
70	415790	R23574	Hs.23545	ESTs	1	1	upregulate stage
	415799	AA663718	Hs.225841	DKFZP434D193 protein	4.25	0.12	upregulate stage
	415837	H05279	Hs.21758	ESTs	1	0.57	upregulate stage
	415857	AA866115	Hs.301646	Homo sapiens cDNA FLJ11381 fis, clone HE	8.05	0.07	upregulate stage
	415906	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	12.2	0.06	upregulate stage
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	12.2	0.06	upregulate stage
75	415948	AA262226		gb:zs24h06.r1 NCI_CGAP_GCB1 Homo sapiens	1	1	upregulate stage
	415979	H16427	Hs.271501	ESTs	4.85	0.13	upregulate stage
	415989	AI267700	Hs.111128	ESTs	4.45	0.08	upregulate stage

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	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	1	1	upregulate stage
	416052	R12816	Hs.21164	ESTs	1.45	0.24	upregulate stage
	416053	H16359	Hs.130648	ESTs	4.35	0.14	upregulate stage
	416061	R45516	Hs.26119	ESTs	1	1	upregulate stage
5	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	4.72	0.17	upregulate stage
	416097	BE387371	Hs.301304	Homo sapiens cDNA: FLJ21017 fis, clone C	5.75	0.11	upregulate stage
	416111	AA033813	Hs.75018	chromatin assembly factor 1, subunit A (8.4	0.09	upregulate stage
	416135	AW473656	Hs.45119	ESTs	2.29	0.2	upregulate stage
10	416155	AI807264	Hs.205442	ESTs, Weakly similar to AF117610 1 inner	5.1	0.13	upregulate stage
	416173	R52782		gb:yg99d09.r1 Soares infant brain 1N1B H	3.7	0.12	upregulate stage
	416195	AW131940	Hs.104030	ESTs	1.1	0.16	upregulate stage
	416196	W51955	Hs.73372	ESTs	3.25	0.14	upregulate stage
	416203	H27794	Hs.269055	ESTs	1	0.32	upregulate stage
15	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.15	0.12	upregulate stage
	416226	N55342	Hs.34372	ESTs	2.35	0.21	upregulate stage
	416239	AL038450	Hs.48948	ESTs	4.05	0.14	upregulate stage
	416241	N52639	Hs.32683	ESTs	5	0.09	upregulate stage
	416254	H51703	Hs.13640	ESTs	1	0.95	upregulate stage
20	416269	AA177138	Hs.161671	ESTs	4.07	0.2	upregulate stage
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	1.84	0.45	upregulate stage
	416280	H44180	Hs.181789	ESTs	1	1	upregulate stage
	416309	R34694	Hs.79194	cAMP responsive element binding protein	9.35	0.08	upregulate stage
	416324	H47983	Hs.1870	phenylalanine hydroxylase	5.15	0.13	upregulate stage
25	416332	H91284	Hs.244461	ESTs	1	1	upregulate stage
	416343	H49213		gb:yq19e04.r1 Soares fetal liver spleen	1	1	upregulate stage
	416353	T77127	Hs.191297	ESTs, Moderately similar to ALU6_HUMAN A	1.46	0.59	upregulate stage
	416395	R94575		gb:y173e10.s1 Soares fetal liver spleen	9.2	0.09	upregulate stage
	416437	N48990	Hs.37204	ESTs	4.15	0.12	upregulate stage
30	416476	H58137	Hs.268639	ESTs	1	0.22	upregulate stage
	416537	T99086	Hs.144904	nuclear receptor co-repressor 1	5.45	0.12	upregulate stage
	416539	Y07909	Hs.79368	epithelial membrane protein 1	9.45	0.09	upregulate stage
	416575	WC2414	Hs.38383	ESTs	4.95	0.1	upregulate stage
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	1	0.22	upregulate stage
35	416644	H70701	Hs.269135	ESTs	5.65	0.12	upregulate stage
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	9.65	0.05	upregulate stage
	416682	R99700	Hs.36152	ESTs	1	0.25	upregulate stage
	416690	H84078	Hs.108551	ESTs	5.35	0.13	upregulate stage
	416709	R99369	Hs.283108	hemoglobin, gamma G	5.4	0.13	upregulate stage
40	416712	N68576	Hs.81602	ESTs	1	0.25	upregulate stage
	416715	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.32	upregulate stage
	416731	T58115	Hs.10336	ESTs	1	0.4	upregulate stage
	416734	H81213	Hs.14825	ESTs	3.8	0.16	upregulate stage
	416735	R11275	Hs.194485	ESTs	11.5	0.06	upregulate stage
	416738	N29218	Hs.40290	ESTs	1	0.42	upregulate stage
45	416856	N27833	Hs.269028	ESTs	2.6	0.22	upregulate stage
	416883	AW140128	Hs.184902	ESTs	11.3	0.07	upregulate stage
	416923	N32498	Hs.42829	ESTs	1	0.61	upregulate stage
	416936	N21352	Hs.42987	ESTs, Weakly similar to ORF2 [M.musculus	1	1	upregulate stage
50	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	11.3	0.05	upregulate stage
	417079	U65590	Hs.81134	retinoblastoma 1 receptor antagonist	5.04	0.15	upregulate stage
	417134	N51220	Hs.269058	ESTs	1	0.24	upregulate stage
	417185	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	1.98	0.32	upregulate stage
	417218	AA006247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.95	0.21	upregulate stage
55	417265	AL121369	Hs.281117	ESTs	1	0.3	upregulate stage
	417283	N62840	Hs.48648	ESTs	1.05	0.27	upregulate stage
	417308	H60720	Hs.81892	KIAA0101 gene product	9.2	0.09	upregulate stage
	417320	AA195667	Hs.287324	ESTs	2.8	0.16	upregulate stage
	417396	T98987		gb:ye66f02.r1 Soares fetal liver spleen	1	1	upregulate stage
60	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.75	0.09	upregulate stage
	417409	BE272506	Hs.82109	syndecan 1	1.92	0.44	upregulate stage
	417448	AA203135	Hs.130186	ESTs	6.45	0.1	upregulate stage
	417453	H73183	Hs.129885	ESTs, Moderately similar to unnamed prot	4.65	0.13	upregulate stage
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.59	0.49	upregulate stage
65	417540	AA203600	Hs.152250	ESTs	1	1	upregulate stage
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	5.65	0.1	upregulate stage
	417581	R26968	Hs.24104	ESTs, Weakly similar to ALU7_HUMAN ALU S	9.15	0.09	upregulate stage
	417596	R07343	Hs.226823	ESTs	4.35	0.14	upregulate stage
	417599	AA204688	Hs.136201	ESTs, Weakly similar to ALU7_HUMAN ALU S	0.94	0.9	upregulate stage
70	417620	R02530	Hs.191198	ESTs	9.1	0.07	upregulate stage
	417638	R12490	Hs.189779	ESTs	1	0.32	upregulate stage
	417650	T05870	Hs.100640	ESTs	1	0.22	upregulate stage
	417715	AW969587	Hs.86366	ESTs	6.31	0.09	upregulate stage
	417720	AA205625	Hs.208067	ESTs	4.65	0.11	upregulate stage
75	417742	R64719		gb:EST22d11 WATM1 Homo sapiens cDNA clon	4.15	0.13	upregulate stage
	417750	AI267720	Hs.260523	neuroblastoma RAS viral (v-ras) oncogene	9.98	0.08	upregulate stage
	417780	Z43462	Hs.82772	collagen, type XI, alpha 1	2.3	0.14	upregulate stage
	417789	R50978	Hs.267054	ESTs	1.05	0.19	upregulate stage

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5	417791	AW965339	Hs.111471	ESTs	5.35	0.1	upregulate stage
	417850	AA215724	Hs.82741	primase, polypeptide 1 (49kD)	1	1	upregulate stage
	417898	AA826198	Hs.291851	ESTs	2.15	0.21	upregulate stage
	417975	AA641836	Hs.30085	Homo sapiens cDNA: FLJ23188 fis, clone L	3.7	0.13	upregulate stage
	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	1.57	0.5	upregulate stage
10	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	17.9	0.02	upregulate stage
	418027	AB037807	Hs.83293	hypothetical protein	6.6	0.09	upregulate stage
	418030	BE207573	Hs.83321	neuromedin B	12.2	0.04	upregulate stage
	418068	AW971155	Hs.293902	ESTs, Weakly similar to prollyl 4-hydroxy	4.26	0.14	upregulate stage
	418113	AI272141	Hs.83484	SRV (sex determining region Y)-box 4	5.21	0.15	upregulate stage
15	418134	AA397769	Hs.86617	ESTs	1	0.3	upregulate stage
	418153	R13696	Hs.112830	ESTs	1	0.3	upregulate stage
	418180	BE618087	Hs.83724	Human clone 23773 mRNA sequence	8.79	0.09	upregulate stage
	418201	AA214345	Hs.98445	Homo sapiens cDNA: FLJ21652 fis, clone C	3.75	0.13	upregulate stage
	418203	X54942	Hs.83758	CDC28 protein kinase 2	13.85	0.04	upregulate stage
20	418216	AA662240	Hs.283099	ADF15q14 protein	9.75	0.07	upregulate stage
	418236	AW994005	Hs.172572	hypothetical protein FLJ20093	10.75	0.05	upregulate stage
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (iso	6.25	0.12	upregulate stage
	418259	AA215404	Hs.137289	ESTs	11.5	0.07	upregulate stage
	418268	AA810599	Hs.86643	ESTs	1	0.43	upregulate stage
25	418296	C01566	Hs.86671	ESTs	1	0.45	upregulate stage
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	9.04	0.08	upregulate stage
	418379	AA218940	Hs.137516	fidgetin-like 1	3.25	0.15	upregulate stage
	418422	AW440068	Hs.59425	Homo sapiens cDNA: FLJ23323 fis, clone H	8.95	0.1	upregulate stage
	418454	AA315308	Hs.85266	gb:EST167095 Colon carcinoma (HCC) cell	2.5	0.15	upregulate stage
30	418462	BE001596	Hs.85266	Integrin, beta 4	1.33	0.59	upregulate stage
	418469	U34879	Hs.85279	hydroxysteroid (17-beta) dehydrogenase 1	1.21	0.71	upregulate stage
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.69	0.23	upregulate stage
	418480	AA223929	Hs.86902	ESTs	1	1	upregulate stage
	418498	T78248	Hs.85701	gb:yd79f05.r1 Soares fetal liver spleen	1	0.47	upregulate stage
35	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	5.4	0.14	upregulate stage
	418546	AA224827	Hs.85701	gb:nc32g04.s1 NCL_CGAP_Pr2 Homo sapiens	2.72	0.23	upregulate stage
	418573	AA225188	Hs.85701	gb:nc21h04.r1 NCL_CGAP_Pr1 Homo sapiens	9.95	0.07	upregulate stage
	418577	AA225247	Hs.269300	ESTs, Weakly similar to B34087 hypotheti	1	0.77	upregulate stage
	418578	U92459	Hs.86204	glutamate receptor, metabotropic 8	1	1	upregulate stage
40	418590	AI732672	Hs.252507	ESTs	1	0.59	upregulate stage
	418592	X99226	Hs.264153	Fanconi anemia, complementation group A	4.75	0.13	upregulate stage
	418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	1	0.23	upregulate stage
	418624	AI734080	Hs.104211	ESTs	7.95	0.09	upregulate stage
	418661	NM_001949	Hs.1189	Human mRNA for KIAA0075 gene, partial cd	3	0.15	upregulate stage
45	418663	AK001100	Hs.87013	Homo sapiens cDNA FLJ10238 fis, clone HE	17.2	0.04	upregulate stage
	418675	AW299723	Hs.87223	bone morphogenetic protein receptor, typ	1	1	upregulate stage
	418686	Z36830	Hs.87268	annexin A8	2.11	0.3	upregulate stage
	418687	R61850	Hs.22581	ESTs	6.75	0.07	upregulate stage
	418693	AI750878	Hs.87409	thrombospondin 1	4.5	0.08	upregulate stage
50	418704	AA227235	Hs.83286	ESTs	1	0.33	upregulate stage
	418712	Z42183	Hs.83286	gb:HSC0BF041 normalized infant brain cDN	1	0.91	upregulate stage
	418717	AI334430	Hs.86984	ESTs	4.7	0.12	upregulate stage
	418723	AA504428	Hs.10487	ESTs, Weakly similar to Weak similarity	5.85	0.1	upregulate stage
	418738	AW388633	Hs.6682	ESTs	3.6	0.09	upregulate stage
55	418752	AL133556	Hs.88144	hypothetical protein FLJ12476	1	1	upregulate stage
	418757	AI864193	Hs.169728	Homo sapiens cDNA FLJ13150 fis, clone NT	9.15	0.09	upregulate stage
	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	9.25	0.08	upregulate stage
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.83	0.43	upregulate stage
	418876	AA740616	Hs.293874	ESTs	11.3	0.06	upregulate stage
60	418903	AW969665	Hs.154848	ESTs	1	1	upregulate stage
	418915	AI474778	Hs.118977	ESTs	4.75	0.12	upregulate stage
	418939	AW630803	Hs.89497	lamin B1	2.6	0.13	upregulate stage
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	1.45	0.53	upregulate stage
	418976	AA533082	Hs.126883	ESTs	1	0.23	upregulate stage
65	419059	T86216	Hs.89584	gb:yd84a05.r1 Soares fetal liver spleen	1	0.38	upregulate stage
	419078	M93119	Hs.89584	Insulinoma-associated 1	1.25	0.18	upregulate stage
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1	1	upregulate stage
	419169	AW851980	Hs.262346	ESTs, Weakly similar to ORF2: function u	1.59	0.3	upregulate stage
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	3.55	0.05	upregulate stage
70	419218	AI248073	Hs.188723	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.27	upregulate stage
	419226	AI342491	Hs.87413	ESTs	1	0.37	upregulate stage
	419235	AW470411	Hs.288433	neurotrophin	11.9	0.07	upregulate stage
	419286	AA236005	Hs.221303	ESTs	4.85	0.14	upregulate stage
	419327	AA521504	Hs.190179	ESTs	1	1	upregulate stage
75	419355	AA428520	Hs.90061	progesterone binding protein	10.6	0.06	upregulate stage
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	1.84	0.47	upregulate stage
	419413	AA237040	Hs.87589	ESTs	1	1	upregulate stage
	419436	AA991639	Hs.15036	ESTs, Highly similar to AF161358.1 HSPC0	6.6	0.1	upregulate stage
	419452	U33636	Hs.90572	PTK7 protein tyrosine kinase 7	1.31	0.64	upregulate stage
	419472	AW978038	Hs.87648	gb:EST390147 MAGE resequences, MAGO Homo	1	1	upregulate stage
	419475	AA243420	Hs.87648	ESTs	1.1	0.24	upregulate stage

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5	419477	AA826279		gb:cd03g07.s1 NCL_CGAP_GCB1 Homo sapiens	1	0.56	upregulate stage
	419484	AA243474	Hs.272128	Homo sapiens cDNA FLJ13901 fis, clone TH	1	0.22	upregulate stage
	419506	N20912	Hs.42369	ESTs	1	1	upregulate stage
	419554	AI732138	Hs.104318	ESTs	1	0.5	upregulate stage
	419569	AI571651	Hs.91143	jagged 1 (Alagille syndrome)	1	0.91	upregulate stage
10	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	8.1	0.08	upregulate stage
	419651	NM_007023	Hs.91971	cAMP-regulated guanine nucleotide exchan	1	1	upregulate stage
	419666	NM_014810	Hs.92200	KIAA0480 gene product	5.2	0.12	upregulate stage
	419737	H24185	Hs.92918	hypothetical protein	11.7	0.07	upregulate stage
	419743	AW408762	Hs.127478	ESTs	6.1	0.09	upregulate stage
15	419752	AA249573	Hs.152618	ESTs	1.8	0.17	upregulate stage
	419769	H27374	Hs.103483	ESTs	1	0.36	upregulate stage
	419805	AW966945		gb:EST379019 MAGE resequences, MAGJ Homo	1	0.34	upregulate stage
	419807	R77402		gb:y175f11.s1 Soares placenta Nb2HP Homo	1	0.67	upregulate stage
	419831	AW448930	Hs.5415	ESTs	7.05	0.1	upregulate stage
20	419833	AA251131	Hs.220697	ESTs	1.25	0.53	upregulate stage
	419834	AA251139		gb:zs03g12.s1 NCL_CGAP_GCB1 Homo sapiens	1	1	upregulate stage
	419923	AW081455	Hs.120219	ESTs	5.89	0.13	upregulate stage
	419945	AW290975	Hs.118923	ESTs	1	0.24	upregulate stage
	419962	AA830111	Hs.291917	ESTs	1	1	upregulate stage
25	419970	AW612022	Hs.263271	ESTs	9.15	0.09	upregulate stage
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	3.05	0.17	upregulate stage
	419998	AA252691		gb:zs26d09.r1 NCL_CGAP_GCB1 Homo sapiens	1	0.47	upregulate stage
	420016	AW016908	Hs.88025	ESTs	1	0.8	upregulate stage
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	4.8	0.11	upregulate stage
30	420076	AA827860	Hs.293717	ESTs	5.35	0.12	upregulate stage
	420111	AA255652		gb:zs21h11.r1 NCL_CGAP_GCB1 Homo sapiens	5.3	0.11	upregulate stage
	420145	AA809860	Hs.256284	ESTs	1	1	upregulate stage
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	14.8	0.04	upregulate stage
	420161	AI683069	Hs.175319	ESTs	4.7	0.11	upregulate stage
35	420184	AA188408	Hs.95655	hypothetical protein	4.35	0.15	upregulate stage
	420226	AA773709	Hs.152818	ubiquitin specific protease 8	3.1	0.16	upregulate stage
	420230	AL034344	Hs.298020	Homo sapiens cDNA FLJ11796 fis, clone HE	10.35	0.06	upregulate stage
	420236	AA256763	Hs.291111	ESTs	4.45	0.14	upregulate stage
	420270	AA257990		gb:zs35h07.r1 NCL_CGAP_GCB1 Homo sapiens	10.05	0.08	upregulate stage
40	420297	AI628272	Hs.88323	ESTs	9.45	0.09	upregulate stage
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	11.7	0.05	upregulate stage
	420392	AI242930	Hs.97393	KIAA0328 protein	1.7	0.22	upregulate stage
	420413	AW971624	Hs.120605	ESTs	1	1	upregulate stage
	420445	AA262213	Hs.193514	ESTs	1	1	upregulate stage
45	420471	AA262452	Hs.192268	ESTs	3.95	0.13	upregulate stage
	420479	AW183695	Hs.186572	ESTs	4.95	0.12	upregulate stage
	420493	AI635113	Hs.270366	Homo sapiens mRNA; cDNA DKFZp564H0616 (f	4.4	0.15	upregulate stage
	420552	AK000492	Hs.98806	hypothetical protein	11.55	0.06	upregulate stage
	420572	AL035593	Hs.99016	Human DNA sequence from clone 310J6 on c	1.35	0.22	upregulate stage
50	420643	W87731		gb:zh65g10.r1 Soares_fetal_liver_spleen_	1.25	0.25	upregulate stage
	420650	AA455706	Hs.44581	heat shock protein hsp70-related protein	7.3	0.09	upregulate stage
	420654	AA279091	Hs.104420	ESTs	1	0.27	upregulate stage
	420655	R74405	Hs.300886	ESTs	1	1	upregulate stage
	420717	AA284447	Hs.271887	ESTs	9	0.09	upregulate stage
55	420734	AW972872	Hs.293736	ESTs	5.2	0.13	upregulate stage
	420756	AA411800	Hs.189900	ESTs	1	1	upregulate stage
	420789	AI670057	Hs.199882	ESTs	8.85	0.06	upregulate stage
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	4.6	0.12	upregulate stage
	420851	AA281062	Hs.250734	ESTs	8.35	0.08	upregulate stage
60	420880	AI809621	Hs.105620	ESTs	1	1	upregulate stage
	420923	AF097021	Hs.273321	differentially expressed in hematopoiet	10.4	0.03	upregulate stage
	420928	AA281809		gb:zt10e01.r1 NCL_CGAP_GCB1 Homo sapiens	1	1	upregulate stage
	420936	AA456112	Hs.99410	ESTs	8.71	0.07	upregulate stage
	420947	AA491044	Hs.47196	ESTs	1	0.36	upregulate stage
65	421017	AW979181	Hs.293221	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	1	upregulate stage
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	1.26	0.62	upregulate stage
	421070	AA283185	Hs.19327	ESTs	2.2	0.14	upregulate stage
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.69	0.28	upregulate stage
	421102	AI470093	Hs.89217	ESTs	2.65	0.19	upregulate stage
70	421103	AI625835	Hs.271104	ESTs	6	0.1	upregulate stage
	421114	AW975051	Hs.293156	ESTs	4.7	0.12	upregulate stage
	421118	AI471925	Hs.89257	ESTs	1	0.39	upregulate stage
	421155	H87879	Hs.102267	lysyl oxidase	1.15	0.18	upregulate stage
	421159	AW978316	Hs.136649	ESTs	1	0.44	upregulate stage
75	421187	NM_014721	Hs.102471	KIAA0680 gene product	5.7	0.11	upregulate stage
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.07	2.55	upregulate stage
	421221	AW276914	Hs.300877	ESTs	8.75	0.07	upregulate stage
	421229	AI056590	Hs.7066	Homo sapiens cDNA: FLJ23000 fis, clone L	1.64	0.49	upregulate stage
	421261	AA600853	Hs.98133	ESTs	10.9	0.07	upregulate stage
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	2.65	0.16	upregulate stage
	421278	AI367919	Hs.99691	ESTs	1	0.56	upregulate stage

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5	421280	AA811804		gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.34	upregulate stage
	421282	AA286914	Hs.183299	ESTs	9	0.08	upregulate stage
	421306	AA806207	Hs.125889	ESTs	1	0.95	upregulate stage
	421308	AA687322	Hs.192843	ESTs	2.85	0.15	upregulate stage
	421373	AA808229	Hs.167771	ESTs	2.45	0.14	upregulate stage
10	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.6	0.26	upregulate stage
	421381	AA361752		gb:EST71314 T-cell lymphoma Homo sapiens	5.05	0.09	upregulate stage
	421418	AA806639		gb:ob38g05.s1 NCI_CGAP_GCB1 Homo sapiens	6.55	0.1	upregulate stage
	421433	AI829192	Hs.134805	ESTs	9.9	0.07	upregulate stage
	421451	AA291377	Hs.50831	ESTs	11.9	0.06	upregulate stage
15	421491	H99999	Hs.42736	ESTs	3	0.2	upregulate stage
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.51	0.32	upregulate stage
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	9	0.09	upregulate stage
	421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	5.75	0.12	upregulate stage
	421673	HE4384	Hs.36892	ESTs	1	1	upregulate stage
20	421685	AF189723	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	9.45	0.07	upregulate stage
	421708	AW754341		gb:CM0-CT0341-181299-130-h12 CT0341 Homo	1	0.47	upregulate stage
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	1.97	0.33	upregulate stage
	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	7.05	0.1	upregulate stage
	421869	AB003592	Hs.109050	contactin 6	1	1	upregulate stage
25	421925	S80310	Hs.109620	acidic epididymal glycoprotein-like 1	1	1	upregulate stage
	421948	L42583	Hs.111758	keratin 6A	51.9	0.01	upregulate stage
	421958	AA357185	Hs.109918	ras homolog gene family, member H	10.17	0.07	upregulate stage
	421991	NM_014918	Hs.110488	KIAA0990 protein	4.5	0.17	upregulate stage
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	6.5	0.08	upregulate stage
30	422072	AB018255	Hs.111138	KIAA0712 gene product	9.2	0.08	upregulate stage
	422094	AF129535	Hs.272027	F-box only protein 5	6.95	0.09	upregulate stage
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.66	0.17	upregulate stage
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.96	0.1	upregulate stage
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	2.8	0.16	upregulate stage
35	422204	AA339015		gb:EST44247 Fetal brain I Homo sapiens c	1	1	upregulate stage
	422261	AA307595	Hs.119908	nucleolar protein NOP5/NOP58	1	1	upregulate stage
	422271	AB038995	Hs.114159	RAB-8b protein	5.04	0.16	upregulate stage
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	3.46	0.24	upregulate stage
	422282	AF019225	Hs.114309	apolipoprotein L	4.54	0.14	upregulate stage
40	422322	AB022192	Hs.115240	peroxisome biogenesis factor 13	1	0.53	upregulate stage
	422330	D30783	Hs.115263	epiregulin	4.45	0.06	upregulate stage
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.25	0.19	upregulate stage
	422406	AF025441	Hs.116206	Opn-interacting protein 5	9.5	0.07	upregulate stage
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.35	0.04	upregulate stage
45	422491	AA338548	Hs.117546	neuronatin	0.64	1.24	upregulate stage
	422504	AA311407		gb:EST182167 Jurkat T-cells V Homo sapie	3.6	0.11	upregulate stage
	422505	AL120862	Hs.124165	ESTs	2.8	0.14	upregulate stage
	422508	AJ000327	Hs.117852	ATP-binding cassette, sub-family D (ALD)	5.25	0.14	upregulate stage
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.57	0.31	upregulate stage
50	422540	AI050751	Hs.22895	Homo sapiens cDNA: FLJ23548 fis, clone L	1	0.59	upregulate stage
	422588	AA312730		gb:EST183651 Monocytes, stimulated II Ho	3	0.14	upregulate stage
	422678	AA247778	Hs.119155	Homo sapiens mRNA; cDNA DKFZp434B249 (fr	10.7	0.07	upregulate stage
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	5.1	0.13	upregulate stage
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	5.94	0.1	upregulate stage
55	422823	D89974	Hs.121102	vanin 2	10	0.07	upregulate stage
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	1	0.27	upregulate stage
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	7.2	0.08	upregulate stage
	422964	AW439476	Hs.256895	ESTs	11.75	0.07	upregulate stage
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	3.05	0.14	upregulate stage
60	423001	AA320014	Hs.208603	ESTs	9.1	0.09	upregulate stage
	423090	BE387529	Hs.123536	melanoma antigen, family E, 1, cancer/te	1	0.49	upregulate stage
	423100	AA323114		gb:EST25873 Cerebellum II Homo sapiens c	1	1	upregulate stage
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	2.8	0.19	upregulate stage
	423156	AA131493	Hs.124752	fibroblast growth factor 12B	1	0.27	upregulate stage
65	423198	M81933	Hs.1634	cell division cycle 25A	8.95	0.07	upregulate stage
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.2	0.57	upregulate stage
	423262	NM_005479	Hs.126057	frequently rearranged in advanced T-cell	9.75	0.07	upregulate stage
	423296	AW957193	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	4.95	0.12	upregulate stage
	423309	BE006775	Hs.126782	sushi-repeat protein	1.58	0.34	upregulate stage
70	423347	AI660412	Hs.234557	ESTs	1	0.45	upregulate stage
	423359	NM_014170	Hs.127496	HSPC135 protein	1	0.69	upregulate stage
	423368	AA364195		gb:EST75015 Pineal gland II Homo sapiens	1	0.95	upregulate stage
	423389	AI471609	Hs.54347	ESTs	3.95	0.14	upregulate stage
	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	1.62	0.43	upregulate stage
75	423441	R68649	Hs.278359	absent in melanoma 1 like	6.25	0.1	upregulate stage
	423453	AW450737	Hs.128791	CGI-09 protein	8.45	0.09	upregulate stage
	423500	AF020763	Hs.129705	clone 1900 unknown protein	1	0.8	upregulate stage
	423578	AW960454	Hs.222830	ESTs	11.94	0.07	upregulate stage
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.4	0.17	upregulate stage
	423632	AA328624		gb:EST32358 Embryo, 12 week I Homo sapie	1	0.71	upregulate stage
	423642	AW452650	Hs.157148	Homo sapiens cDNA FLJ11883 fis, clone HE	8.35	0.1	upregulate stage

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5	423644	AA329048		gb:EST32875 Embryo, 12 week l Homo sapie	1	0.43	upregulate stage
	423648	AK000456	Hs.130546	hypothetical protein FLJ20449	10.4	0.07	upregulate stage
	423651	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	5.75	0.1	upregulate stage
	423654	AI674253	Hs.35828	ESTs	3.15	0.18	upregulate stage
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	29.7	0.02	upregulate stage
10	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.1	0.16	upregulate stage
	423745	AI809797	Hs.43222	ESTs	1	0.5	upregulate stage
	423748	AJ149048	Hs.30211	hypothetical protein FLJ22313	4.25	0.13	upregulate stage
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	1.18	0.71	upregulate stage
	423758	AA338153	Hs.82124	laminin, beta 1	1	1	upregulate stage
15	423774	L39064	Hs.1702	interleukin 9 receptor	3.08	0.15	upregulate stage
	423818	AA332439		gb:EST36554 Embryo, 8 week l Homo sapien	1	0.38	upregulate stage
	423827	AI472828	Hs.172625	ESTs	1	0.43	upregulate stage
	423837	AW937063		gb:PM3-DT0037-231299-001-g11 DT0037 Homo	1.44	0.55	upregulate stage
	423912	BE091233		gb:PM0-BT0726-300300-001-H07 BT0726 Homo	1	1	upregulate stage
20	423938	AL049328	Hs.135642	Homo sapiens mRNA; cDNA DKFZp564E026 (fr	1	1	upregulate stage
	423942	AF209704	Hs.135723	glycolipid transfer protein	11.65	0.05	upregulate stage
	423944	T91433	Hs.128291	phosphodiesterase 10A	1	0.45	upregulate stage
	423946	AL137344	Hs.135892	Homo sapiens mRNA; cDNA DKFZp7611311 (f	1	1	upregulate stage
	423956	W28203	Hs.136169	Homo sapiens clone 25215 mRNA sequence,	5.35	0.09	upregulate stage
25	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	8.8	0.06	upregulate stage
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	3.14	0.19	upregulate stage
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.6	0.26	upregulate stage
	424073	UC3493	Hs.138959	gap junction protein, alpha 7, 45kD (con	1.8	0.22	upregulate stage
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	9.1	0.06	upregulate stage
30	424087	N69333	Hs.21638	ESTs	1	1	upregulate stage
	424193	AK002005	Hs.142668	Homo sapiens cDNA FLJ11143 fis, clone PL	1	0.23	upregulate stage
	424353	AA339646		gb:EST44755 Fetal brain l Homo sapiens c	1	1	upregulate stage
	424364	AW383226	Hs.201189	ESTs, Weakly similar to DRPLA [H.sapiens	2.18	0.33	upregulate stage
	424406	D54120	Hs.146409	wingless-type MMTV integration site fami	2.05	0.17	upregulate stage
35	424420	BE614743	Hs.146688	prostaglandin E synthase	1.19	0.67	upregulate stage
	424425	AB031480	Hs.146824	SPR1 protein	1.42	0.54	upregulate stage
	424486	BE002477	Hs.278714	chloride intracellular channel 6	1	0.27	upregulate stage
	424490	AJ278016	Hs.55565	ankyrin repeat domain 3	2.02	0.39	upregulate stage
	424492	AI133482	Hs.165210	ESTs	3.15	0.14	upregulate stage
40	424505	AA446131	Hs.124918	Homo sapiens cDNA FLJ13186 fis, clone NT	11.55	0.05	upregulate stage
	424513	BE385864	Hs.145894	mitochondrial translational initiation f	2.65	0.23	upregulate stage
	424575	AL110217	Hs.150751	DKFZP572C163 protein	1	1	upregulate stage
	424583	AF017445	Hs.150926	fructose-1-phosphate guanylyltransferase	1.8	0.26	upregulate stage
	424589	AW854298		gb:RC3-CT0254-100500-211-c03 CT0254 Homo	0.85	0.94	upregulate stage
45	424602	AK002055	Hs.301129	Homo sapiens clone 23859 mRNA sequence	2.85	0.2	upregulate stage
	424625	AW904466	Hs.151310	PDZ domain protein (Drosophila inaD-like	1	0.4	upregulate stage
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	1.41	0.52	upregulate stage
	424643	AF241850	Hs.151428	ret finger protein 2	9.75	0.07	upregulate stage
	424649	BE242035	Hs.151461	embryonic ectoderm development	5.85	0.13	upregulate stage
50	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	1	0.56	upregulate stage
	424670	W61215	Hs.116651	epithelial V-like antigen 1	1.42	0.52	upregulate stage
	424690	BE538356	Hs.151777	Human translation initiation factor eIF-	4.3	0.1	upregulate stage
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	3.85	0.11	upregulate stage
	424702	AF250237	Hs.152009	G protein-coupled receptor 85	1	1	upregulate stage
55	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	4.05	0.09	upregulate stage
	424735	U31875	Hs.152677	Homo sapiens cDNA FLJ20338 fis, clone HE	1.04	0.59	upregulate stage
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	1.11	0.65	upregulate stage
	424749	NM_002451	Hs.152817	methylthioadenosine phosphorylase	1	1	upregulate stage
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	18.5	0.03	upregulate stage
60	424841	AI280215	Hs.96885	ESTs	1	1	upregulate stage
	424860	W60828	Hs.153529	Homo sapiens clone 24540 mRNA sequence	1	1	upregulate stage
	424878	H57111	Hs.221132	ESTs	9.45	0.07	upregulate stage
	424879	AA348013	Hs.159354	ESTs	10.7	0.07	upregulate stage
	424888	AA348126	Hs.24882	ESTs	2.8	0.21	upregulate stage
65	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	7.75	0.07	upregulate stage
	424930	AA885344	Hs.96510	ESTs	1.45	0.38	upregulate stage
	424948	AA348810	Hs.190503	ESTs	3.2	0.12	upregulate stage
	424951	AW964082		gb:EST376155 MAGE resequences, MAGH Homo	8.75	0.09	upregulate stage
	424993	F07625		gb:HSC2CF021 normalized infant brain cDN	1	1	upregulate stage
70	425020	U09368	Hs.154205	zinc finger protein 140 (clone pHZ-35)	1	1	upregulate stage
	425024	R39235	Hs.12407	ESTs	2.65	0.13	upregulate stage
	425057	AA826434	Hs.96544	ESTs	1	0.22	upregulate stage
	425068	AL048716	Hs.154387	KIAA0103 gene product	9.5	0.07	upregulate stage
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	1.66	0.52	upregulate stage
75	425191	AF052146	Hs.155085	Homo sapiens clone 24653 mRNA sequence	1	0.32	upregulate stage
	425216	U81504	Hs.155172	adaptor-related protein complex 3, beta	7.05	0.1	upregulate stage
	425234	AW152225	Hs.165909	ESTs	19.7	0.04	upregulate stage
	425239	BE567924	Hs.155244	pre-mRNA splicing factor similar to S. c	1	0.69	upregulate stage
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	10.45	0.05	upregulate stage
	425304	AA463844	Hs.31339	fibroblast growth factor 11	1.57	0.51	upregulate stage
	425316	AA354977	Hs.191565	ESTs, Moderately similar to NSD1 protein	5.05	0.12	upregulate stage

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	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	14.7	0.05	upregulate stage
	425362	AA355936		gb:EST64410 Jurkat T-cells VI Homo sapie	1	1	upregulate stage
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	8.24	0.09	upregulate stage
5	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	1	0.22	upregulate stage
	425415	M13903	Hs.157091	involucrin	1.19	0.55	upregulate stage
	425420	BE536911	Hs.234545	ESTs, Weakly similar to AF156135 1 novel	2.85	0.13	upregulate stage
	425463	AK000740	Hs.157986	hypothetical protein FLJ20733	9	0.07	upregulate stage
	425465	L18964	Hs.1904	protein kinase C, iota	9.6	0.07	upregulate stage
10	425467	R16484	Hs.190075	ESTs	1	0.83	upregulate stage
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.2	0.15	upregulate stage
	425607	U09860	Hs.158333	protease, serine, 7 (enterokinase)	1	1	upregulate stage
	425608	AA360486	Hs.92448	ESTs	4.7	0.14	upregulate stage
	425614	AI334963	Hs.156256	ESTs	2.65	0.14	upregulate stage
15	425641	D79758	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	4.86	0.1	upregulate stage
	425660	AA521184	Hs.105504	ESTs	1	0.31	upregulate stage
	425665	AK001050	Hs.159066	hypothetical protein FLJ10188	1.25	0.19	upregulate stage
	425672	AA361483		gb:EST70790 T-cell lymphoma Homo sapiens	1	1	upregulate stage
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript)	3.96	0.13	upregulate stage
20	425726	AF085808	Hs.159330	uroplakin 3	0.92	0.79	upregulate stage
	425742	AJ001454	Hs.159425	testican 3	1	1	upregulate stage
	425785	T27017	Hs.159528	Homo sapiens clone 24400 mRNA sequence	1	0.39	upregulate stage
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.89	0.44	upregulate stage
	425843	BE313280	Hs.159627	death associated protein 3	3.1	0.15	upregulate stage
	425852	AK001504	Hs.159651	death receptor 6	1.72	0.47	upregulate stage
25	425883	AL137708	Hs.181031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	0.95	0.68	upregulate stage
	426010	AA136653	Hs.1975	Homo sapiens cDNA: FLJ21007 fis, clone C	1	0.34	upregulate stage
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	14.3	0.04	upregulate stage
	426101	AL049967	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	11.75	0.05	upregulate stage
30	426108	AA622037	Hs.166468	programmed cell death 5	3.23	0.18	upregulate stage
	426115	H08895	Hs.166733	leucyl/cystinyl aminopeptidase	1	0.32	upregulate stage
	426168	NM_003152	Hs.167503	signal transducer and activator of trans	1.97	0.4	upregulate stage
	426257	AL137201	Hs.168625	KIAA0979 protein	1	0.29	upregulate stage
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.8	0.16	upregulate stage
35	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	14.75	0.04	upregulate stage
	426451	AI908165	Hs.169946	GATA-binding protein 3	3.05	0.28	upregulate stage
	426462	U59111	Hs.169993	dermatan sulphate proteoglycan 3	1	0.36	upregulate stage
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	14.17	0.05	upregulate stage
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	1.15	0.47	upregulate stage
40	426561	AA381437		gb:EST94514 Activated T-cells I Homo sap	5.65	0.11	upregulate stage
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	11.05	0.05	upregulate stage
	426731	AW303411	Hs.130332	ESTs	2.4	0.21	upregulate stage
	426759	AI690401	Hs.21213	ESTs	9.5	0.06	upregulate stage
	426786	AA319798	Hs.172247	eukaryotic translation elongation factor	9.25	0.09	upregulate stage
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	5.63	0.14	upregulate stage
45	426818	AA554827	Hs.124841	ESTs, Weakly similar to ALU5_HUMAN ALU S	9	0.08	upregulate stage
	426824	D87717	Hs.172652	KIAA0013 gene product	1	0.87	upregulate stage
	426827	AW067805	Hs.172665	methyleneetetrahydrofolate dehydrogenase	8.95	0.09	upregulate stage
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	1	0.19	upregulate stage
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	1.15	0.72	upregulate stage
50	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	11.06	0.06	upregulate stage
	427071	AA397958	Hs.192719	ESTs	5.75	0.08	upregulate stage
	427126	AA620613	Hs.191827	ESTs	2.55	0.18	upregulate stage
	427134	AA398409	Hs.173561	EST	3.4	0.18	upregulate stage
	427142	AA398510	Hs.133148	ESTs	1	0.25	upregulate stage
55	427259	AA400096		gb:zu69f07.s1 Soares_testis_NHT Homo sap	1	0.22	upregulate stage
	427308	D26067	Hs.174905	KIAA0033 protein	5.9	0.1	upregulate stage
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	6.12	0.11	upregulate stage
	427356	AW023482	Hs.97849	ESTs	2.7	0.13	upregulate stage
60	427370	AI243615	Hs.97740	ESTs	3.6	0.14	upregulate stage
	427376	AA401533	Hs.19440	ESTs	2.1	0.16	upregulate stage
	427387	BE244966	Hs.177584	3-oxoacid CoA transferase	1	0.39	upregulate stage
	427470	AW999924	Hs.178357	Homo sapiens cDNA FLJ13657 fis, clone PL	3.4	0.16	upregulate stage
	427519	AW085233	Hs.180696	ESTs	8.23	0.1	upregulate stage
	427521	AW973352	Hs.299056	ESTs	7.75	0.1	upregulate stage
65	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	5.7	0.15	upregulate stage
	427566	AI743515		gb:wf72b08.x2 Soares_NFL_T_GBC_S1 Homo s	1	1	upregulate stage
	427581	NM_014788	Hs.179703	KIAA0129 gene product	11.45	0.06	upregulate stage
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.25	0.16	upregulate stage
	427603	AI090838	Hs.98006	ESTs	1	1	upregulate stage
70	427646	AI678042	Hs.271953	ESTs	5.7	0.11	upregulate stage
	427652	AI673025	Hs.43874	ESTs	1	0.34	upregulate stage
	427742	AA411880	Hs.190888	ESTs	2.4	0.16	upregulate stage
	427814	W28383	Hs.180900	Williams-Beuren syndrome chromosome regi	9.13	0.08	upregulate stage
	427839	AA606823	Hs.98244	ESTs	1.9	0.19	upregulate stage
75	427878	C05766	Hs.181022	CGI-07 protein	4.1	0.14	upregulate stage
	427922	AK001934	Hs.181112	HSPC126 protein	2.6	0.19	upregulate stage
	427933	AW974643	Hs.190571	ESTs	4.55	0.14	upregulate stage

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5	427934	AA810541	Hs.291866	ESTs	1	1	upregulate stage
	427944	AA417878	Hs.48401	ESTs, Weakly similar to ALU6_HUMAN ALU S	6.15	0.1	upregulate stage
	427961	AW293165	Hs.143134	ESTs	4.85	0.11	upregulate stage
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.55	0.13	upregulate stage
	428003	AL110200	Hs.181384	Homo sapiens mRNA: cDNA DKFZp586B0922 (f	1.45	0.36	upregulate stage
10	428004	AA449563	Hs.300270	ESTs	3.95	0.12	upregulate stage
	428010	AA806554	Hs.185375	ESTs	1	0.38	upregulate stage
	428057	AI343641	Hs.185798	ESTs	10.1	0.06	upregulate stage
	428058	AI821625	Hs.191602	ESTs	1	0.5	upregulate stage
	428071	AF212848	Hs.182339	ets homologous factor	6.4	0.09	upregulate stage
15	428182	BE386042	Hs.293317	ESTs, Weakly similar to JM27 [H.sapiens]	1	0.23	upregulate stage
	428192	AA424051		gb:zv80d03.s1 Soares_total_fetus_Nb2HF8_	2.45	0.16	upregulate stage
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	9.25	0.04	upregulate stage
	428403	AI393048	Hs.239894	leucine rich repeat (in FLII) interactin	9.94	0.06	upregulate stage
	428436	BE080180		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	1	1	upregulate stage
20	428450	NM_014791	Hs.184339	KIAA0175 gene product	4.43	0.16	upregulate stage
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	9.2	0.07	upregulate stage
	428529	AW262022	Hs.106278	Homo sapiens cDNA FLJ12839 fis, clone NT	1	1	upregulate stage
	428576	AW009330	Hs.167621	ESTs	1	0.3	upregulate stage
	428605	AB037862	Hs.186756	KIAA1441 protein	9.25	0.09	upregulate stage
25	428664	AK001666	Hs.189095	similar to SALL1 (sal) (Drosophila)-like	3.8	0.08	upregulate stage
	428685	AF131853	Hs.189527	Homo sapiens clone 25016 mRNA sequence	1	1	upregulate stage
	428716	AL122118	Hs.190614	Homo sapiens mRNA: cDNA DKFZp43401221 (f	1	0.65	upregulate stage
	428783	AW070204	Hs.178176	ESTs	1.6	0.23	upregulate stage
	428788	AF082283	Hs.193516	B-cell CLL/lymphoma 10	9.6	0.08	upregulate stage
30	428829	R14050	Hs.194051	Homo sapiens mRNA: cDNA DKFZp5663213 (fr	5.45	0.11	upregulate stage
	428839	AI767756	Hs.82302	ESTs	10	0.06	upregulate stage
	428881	AI298368	Hs.98918	ESTs	1.4	0.18	upregulate stage
	428954	AF100781	Hs.194678	WNT1 inducible signaling pathway protein	1	1	upregulate stage
	428988	AA442900	Hs.27947	ESTs	3.05	0.13	upregulate stage
35	429042	AW015489	Hs.235520	ESTs	1	0.56	upregulate stage
	429057	AF156557	Hs.194816	stromatin-like protein 1	0.95	0.93	upregulate stage
	429066	AA868555	Hs.178222	ESTs	6	0.11	upregulate stage
	429072	AI376228	Hs.108043	Friend leukemia virus integration 1	1	1	upregulate stage
	429083	Y09397	Hs.227817	BCL2-related protein A1	11.12	0.03	upregulate stage
40	429091	AA935658	Hs.187939	ESTs	8.9	0.08	upregulate stage
	429115	AA446728	Hs.289020	Homo sapiens cDNA FLJ14098 fis, clone MA	4.1	0.17	upregulate stage
	429127	AA749382	Hs.107233	ESTs	1	0.23	upregulate stage
	429135	AA446966	Hs.99090	ESTs, Moderately similar to similar to K	1	1	upregulate stage
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	8.6	0.08	upregulate stage
45	429174	BE559598	Hs.197803	KIAA0160 protein	8.4	0.06	upregulate stage
	429236	AA448407		gb:zw68d11.s1 Soares_testis_NHT Homo sap	1	0.36	upregulate stage
	429268	AA205306	Hs.198481	RAR-related orphan receptor B	2.9	0.16	upregulate stage
	429300	AB011108	Hs.198891	serine/threonine-protein kinase PRP4 hom	4.25	0.15	upregulate stage
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	2.95	0.11	upregulate stage
50	429344	R94038	Hs.199538	inhibin, beta C	2.91	0.28	upregulate stage
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.19	0.68	upregulate stage
	429376	AI867889	Hs.43227	ESTs	1	1	upregulate stage
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	8.15	0.07	upregulate stage
	429450	AA824451	Hs.94292	Homo sapiens cDNA: FLJ23311 fis, clone H	3.3	0.17	upregulate stage
55	429472	AW452421	Hs.15652	ESTs	1	1	upregulate stage
	429482	AF076974	Hs.203952	transformation/transcription domain-asso	1.52	0.59	upregulate stage
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	2.9	0.15	upregulate stage
	429572	AW295375	Hs.39474	ESTs	1	0.95	upregulate stage
	429584	AI817785	Hs.183037	protein kinase, cAMP-dependent, regulato	6.55	0.1	upregulate stage
60	429590	AI219490	Hs.44445	ESTs, Weakly similar to Kelch motif cont	1	1	upregulate stage
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.6	0.14	upregulate stage
	429601	AI804293	Hs.119406	ESTs, Weakly similar to AF143946 1 trans	1.36	0.58	upregulate stage
	429602	AA521463	Hs.183424	ESTs	1	0.34	upregulate stage
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	10.8	0.07	upregulate stage
65	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	3.4	0.12	upregulate stage
	429631	AA455612	Hs.136710	EST	1	1	upregulate stage
	429644	AA455892	Hs.156379	ESTs	3.4	0.15	upregulate stage
	429653	NM_005955	Hs.211581	metal-regulatory transcription factor 1	4.45	0.17	upregulate stage
	429664	L20433	Hs.211588	POU domain, class 4, transcription facto	1.17	0.74	upregulate stage
70	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.19	0.22	upregulate stage
	429699	AI393469	Hs.159300	ESTs	4.4	0.1	upregulate stage
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4.25	0.13	upregulate stage
	429813	AW139678	Hs.180791	ESTs	1	0.95	upregulate stage
	429828	AB019494	Hs.225767	IDN3 protein	4.2	0.14	upregulate stage
75	429838	AW904907	Hs.108241	ESTs, Weakly similar to The KIAA0191 gen	3.25	0.14	upregulate stage
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	1	0.36	upregulate stage
	429913	AA460608	Hs.99552	ESTs	1.35	0.2	upregulate stage
	429917	H80572		gb:yu76c02.r1 Soares fetal liver spleen	4.8	0.13	upregulate stage
	429921	AA526911	Hs.102756	ESTs	1	0.63	upregulate stage
	429950	AW081608	Hs.105053	ESTs	3.7	0.13	upregulate stage
	429971	AF079550	Hs.227098	glial cells missing (Drosophila) homolog	1	0.83	upregulate stage

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5	429979	AA463338		gb:zx97a10.r1 Soares_NhHMPu_S1 Homo sapi	1	0.32	upregulate stage
	429982	AW449534	Hs.99607	Homo sapiens cDNA FLJ13841 fis, clone TH	9.45	0.08	upregulate stage
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolog	0.78	0.58	upregulate stage
	430020	AI535029	Hs.99607	Homo sapiens cDNA FLJ13841 fis, clone TH	1	0.36	upregulate stage
	430021	AA463913	Hs.221160	ESTs	1	0.56	upregulate stage
10	430049	AW277085	Hs.99619	ESTs	3.55	0.17	upregulate stage
	430060	NM_002941	Hs.301198	roundabout (axon guidance receptor, Dros	1	0.59	upregulate stage
	430076	AA465115		gb:aa32c11.r1 NCI_CGAP_GC81 Homo sapiens	5.4	0.12	upregulate stage
	430134	BE380149	Hs.105223	ESTs, Weakly similar to contains similar	3.6	0.13	upregulate stage
	430184	AB013802	Hs.234790	contactin 5	1	1	upregulate stage
15	430195	AW969308	Hs.188594	ESTs	9.15	0.1	upregulate stage
	430279	R85974	Hs.16279	ESTs	1.2	0.52	upregulate stage
	430287	AW182459	Hs.125759	ESTs, Weakly similar to tumor suppressor	4.05	0.15	upregulate stage
	430291	AV660345	Hs.238126	CGI-49 protein	7.2	0.08	upregulate stage
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	11.9	0.06	upregulate stage
20	430350	BE168639		gb:PM1-HT0527-280200-005-a05 HT0527 Homo	7.1	0.09	upregulate stage
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9	0.11	upregulate stage
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.56	0.2	upregulate stage
	430488	D19589	Hs.4220	ESTs, Moderately similar to tetracycline	10.5	0.08	upregulate stage
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	11.2	0.06	upregulate stage
25	430519	AF129534	Hs.49210	F-box only protein 4	5.35	0.11	upregulate stage
	430550	AK000082	Hs.243756	hypothetical protein FLJ20055	1	1	upregulate stage
	430561	BE065227		gb:RC1-BT0314-310300-015-b06 BT0314 Homo	1	1	upregulate stage
	430563	AA481269	Hs.178381	ESTs	1	0.45	upregulate stage
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.75	0.14	upregulate stage
30	430630	AW269920	Hs.2621	cystatin A (stefin A)	2.52	0.25	upregulate stage
	430634	AI860651	Hs.26685	ESTs	1.24	0.61	upregulate stage
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	1.79	0.47	upregulate stage
	430640	AA482636		gb:zv29c06.r1 Soares ovary tumor NbHOT H	9.15	0.08	upregulate stage
	430665	BE350122	Hs.157367	ESTs	9.4	0.08	upregulate stage
35	430726	AL031224	Hs.247850	Human DNA sequence from clone 336H9 on c	1	0.27	upregulate stage
	430733	AW975920	Hs.283361	ESTs	3.5	0.13	upregulate stage
	430781	AW088127	Hs.278536	ESTs	1	1	upregulate stage
	430791	AA486293	Hs.272068	ESTs, Moderately similar to alternative	1.61	0.42	upregulate stage
	430817	AA487242	Hs.185105	ESTs	1	1	upregulate stage
40	430888	BE155293	Hs.76064	ribosomal protein L27a	3.05	0.17	upregulate stage
	430918	NM_000843	Hs.248131	glutamate receptor, metabotropic 6	9.05	0.09	upregulate stage
	430926	L05597	Hs.248136	5-hydroxytryptamine (serotonin) receptor	1	0.91	upregulate stage
	430994	AA490346	Hs.40530	ESTs	1.03	0.89	upregulate stage
	431009	BE149762	Hs.248213	gap junction protein, beta 6 (connexin 3	24.8	0.03	upregulate stage
45	431023	AI283133	Hs.178925	ESTs	2.55	0.15	upregulate stage
	431030	AA830525	Hs.251988	ESTs	1	0.47	upregulate stage
	431041	AA490967	Hs.105276	ESTs	1	0.36	upregulate stage
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.65	0.45	upregulate stage
	431082	AA491600	Hs.161942	ESTs	9.85	0.06	upregulate stage
50	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	43.15	0.01	upregulate stage
	431146	Z83850	Hs.250649	Human DNA sequence from PAC 82J11 and co	1	0.4	upregulate stage
	431173	AW971198	Hs.294068	ESTs	6.3	0.12	upregulate stage
	431245	AA496933	Hs.191687	ESTs	1	1	upregulate stage
	431253	R06428	Hs.226351	ESTs	1	0.8	upregulate stage
55	431267	AW969661	Hs.124047	ESTs	1	0.31	upregulate stage
	431287	BE044989	Hs.274901	ESTs	1	1	upregulate stage
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	10.8	0.06	upregulate stage
	431332	AA503297	Hs.117108	ESTs	6.55	0.1	upregulate stage
	431343	AW970603	Hs.300941	Homo sapiens cDNA FLJ11681 fis, clone HE	5.85	0.09	upregulate stage
60	431346	AA371059	Hs.251636	ubiquitin specific protease 3	1.68	0.52	upregulate stage
	431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	1.12	0.47	upregulate stage
	431381	AA577114	Hs.105727	ESTs	1	0.36	upregulate stage
	431448	AL137517	Hs.288381	hypothetical protein DKFZp564O1278	3.72	0.13	upregulate stage
	431494	AA991355	Hs.129808	ESTs	2.75	0.18	upregulate stage
65	431510	AA580082	Hs.112264	ESTs	3.75	0.13	upregulate stage
	431560	BE244135	Hs.260238	hypothetical protein FLJ10842	9.1	0.08	upregulate stage
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (7.5	0.11	upregulate stage
	431596	T34708	Hs.272927	Sec23 (S. cerevisiae) homolog A	8.2	0.08	upregulate stage
	431610	AK000972	Hs.264363	hypothetical protein FLJ10110	6.4	0.1	upregulate stage
70	431613	AA018515	Hs.264482	Apg12 (autophagy 12, S. cerevisiae)-like	5.8	0.11	upregulate stage
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.3	0.59	upregulate stage
	431663	NM_016569	Hs.267182	TBX3-iso protein	1.6	0.52	upregulate stage
	431670	AW971287		gb:EST383376 MAGE resequences, MAGL Homo	1	1	upregulate stage
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	9.1	0.05	upregulate stage
75	431691	AI208511	Hs.292520	ESTs	4.15	0.12	upregulate stage
	431692	AL021331	Hs.267749	unc93 (C.elegans) homolog A	4.2	0.13	upregulate stage
	431694	AW970112	Hs.292897	ESTs	1	0.83	upregulate stage
	431726	NM_015361	Hs.268053	KIAA0029 protein	10.1	0.07	upregulate stage
	431736	AI912234	Hs.151245	ESTs	9.9	0.08	upregulate stage
	431753	X76029	Hs.2841	neurexophilin U	1	0.23	upregulate stage
	431781	AA515474	Hs.99908	nuclear receptor coactivator 4	1	0.36	upregulate stage

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5	431810	X67155	Hs.270645	kinesin-like 5 (mitotic kinesin-like pro	1	0.65	upregulate stage
	431814	BE256242	Hs.270647	delta-tubulin	3.35	0.18	upregulate stage
	431817	X65233	Hs.271079	zinc finger protein 80 (pT17)	1	1	upregulate stage
	431828	AA572994		gb:nm33f12.s1 NCI_CGAP_Lip2 Homo sapiens	4	0.12	upregulate stage
	431880	AI700238	Hs.187486	ESTs	1	1	upregulate stage
10	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.89	0.27	upregulate stage
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	1	0.18	upregulate stage
	431951	AI086335	Hs.136470	ESTs	6.4	0.11	upregulate stage
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.09	0.07	upregulate stage
	431969	AW972870	Hs.291069	ESTs	1	0.23	upregulate stage
15	431992	NM_002742	Hs.2891	protein kinase C, mu	3.9	0.15	upregulate stage
	432015	AL157504	Hs.159115	ESTs	6.05	0.09	upregulate stage
	432023	AW273128	Hs.214188	ESTs	0.99	0.86	upregulate stage
	432028	AJ272208	Hs.272354	interleukin 1 receptor accessory protein	1	0.48	upregulate stage
	432039	AF220217	Hs.272374	Homo sapiens rsec15-like protein mRNA, p	1	0.24	upregulate stage
20	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	1.38	0.64	upregulate stage
	432069	AW975868	Hs.294100	ESTs	4.25	0.15	upregulate stage
	432072	N62937	Hs.269109	ESTs	5.9	0.09	upregulate stage
	432093	H28383		gb:y52c03.r1 Soares breast 3NbhBst Homo	7.9	0.08	upregulate stage
	432136	AA157632	Hs.272630	vacuolar proton pump delta polypeptide	1	0.28	upregulate stage
25	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	2.5	0.25	upregulate stage
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	6.1	0.11	upregulate stage
	432215	AJ076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.44	0.29	upregulate stage
	432222	AI204995		gb:an03c03.x1 Striatagene schizo brain S1	15	0.02	upregulate stage
	432235	AA531129	Hs.190297	ESTs	9.57	0.06	upregulate stage
30	432237	AK001926	Hs.274132	hypothetical protein FLJ11064	1	0.44	upregulate stage
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	4.3	0.1	upregulate stage
	432261	AK001239	Hs.274263	hypothetical protein FLJ10377	3.95	0.15	upregulate stage
	432338	AA534197	Hs.272693	ESTs	1	1	upregulate stage
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	1.97	0.4	upregulate stage
35	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.16	0.58	upregulate stage
	432407	AA221036	Hs.285026	HERV-H LTR-associating 1	3.75	0.16	upregulate stage
	432410	X68561	Hs.2982	Sp4 transcription factor	1	1	upregulate stage
	432415	T16971	Hs.289014	ESTs	7.3	0.07	upregulate stage
	432432	AA541323	Hs.115831	ESTs	5.35	0.13	upregulate stage
40	432435	BE218886	Hs.282070	ESTs	5.35	0.1	upregulate stage
	432441	AW292425	Hs.163484	ESTs	19.4	0.04	upregulate stage
	432518	AI675836	Hs.94319	ESTs	1	0.59	upregulate stage
	432560	X82018	Hs.3053	zinc finger protein with interaction dom	9.15	0.08	upregulate stage
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	10.15	0.05	upregulate stage
45	432614	AA557153	Hs.185853	ESTs	1	0.33	upregulate stage
	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	10.5	0.07	upregulate stage
	432661	AW973823	Hs.283528	ESTs	1	1	upregulate stage
	432666	AW204069	Hs.129250	ESTs, Weakly similar to unnamed protein	1	0.16	upregulate stage
	432669	AL043482	Hs.267115	ESTs	4.15	0.12	upregulate stage
50	432673	AB028859	Hs.278605	ER-associated DNAJ; ER-associated Hsp40	10.24	0.06	upregulate stage
	432678	AA923424	Hs.135567	ESTs	1	0.69	upregulate stage
	432690	AF181490	Hs.278627	prenylcysteine lyase	4.55	0.12	upregulate stage
	432724	X96266		gb:H.sapiens mRNA for ligase like protei	1	1	upregulate stage
	432758	NM_014091	Hs.278920	PRO1510 protein	1	1	upregulate stage
55	432773	NM_014124	Hs.278935	PRO0255 protein	1	1	upregulate stage
	432789	D26361	Hs.3104	KIAA0042 gene product	3.46	0.22	upregulate stage
	432829	W60377	Hs.57772	ESTs	1.33	0.43	upregulate stage
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	4.5	0.14	upregulate stage
	432900	BE178025	Hs.7942	hypothetical protein FLJ20080	1	0.3	upregulate stage
60	432917	NM_014125	Hs.279812	PRO0327 protein	6.33	0.12	upregulate stage
	432935	AW270239	Hs.213709	ESTs	3.85	0.11	upregulate stage
	432963	AA572859	Hs.225791	ESTs	1	0.19	upregulate stage
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	29.9	0.03	upregulate stage
	433005	AW939074		gb:QV1-DT0069-010200-057-c12 DT0069 Homo	1	0.59	upregulate stage
65	433129	AA577814		gb:nm24d03.s1 NCI_CGAP_Gas1 Homo sapiens	1	1	upregulate stage
	433159	AB035898	Hs.150587	kinesin-like protein 2	6	0.1	upregulate stage
	433201	AB040896	Hs.21104	KIAA1463 protein	9.2	0.09	upregulate stage
	433211	H11850	Hs.12808	MARK	1.6	0.45	upregulate stage
	433218	AJ040372	Hs.278894	KIAA1482 protein	1	0.44	upregulate stage
70	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	5.45	0.12	upregulate stage
	433230	AW136134	Hs.220277	ESTs	7.3	0.09	upregulate stage
	433237	AB040930	Hs.297021	Homo sapiens cDNA FLJ13211 fis, clone NT	1	1	upregulate stage
	433365	AF026944	Hs.293797	ESTs	4.95	0.08	upregulate stage
	433371	T25451		gb:PTH188 HTCDL1 Homo sapiens cDNA 5/3	4.75	0.12	upregulate stage
75	433394	AI907753	Hs.93810	cerebral cavernous malformations 1	4.5	0.11	upregulate stage
	433424	R68252	Hs.163566	ESTs	1	1	upregulate stage
	433440	AF052127		gb:Homo sapiens clone 23850 mRNA sequenc	1	1	upregulate stage
	433452	AW296906	Hs.142869	ESTs	9.82	0.08	upregulate stage
	433456	AA593447	Hs.124296	ESTs	9.45	0.08	upregulate stage
	433467	AI420457	Hs.50955	ESTs	1.11	0.74	upregulate stage
	433479	AW511459	Hs.249972	ESTs	3.35	0.13	upregulate stage

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5	433484	BE264397	Hs.148674	ESTs	1	0.27	upregulate stage
	433515	AA595800	Hs.190246	ESTs	3.05	0.14	upregulate stage
	433602	AI769948	Hs.24906	ESTs	1	1	upregulate stage
	433613	AA836126	Hs.5669	ESTs	2.8	0.12	upregulate stage
	433625	AW955674	Hs.161762	ESTs	1	0.53	upregulate stage
10	433658	L03678	Hs.156110	immunoglobulin kappa constant	9.65	0.05	upregulate stage
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	7.9	0.08	upregulate stage
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.7	0.11	upregulate stage
	433735	AA608955	Hs.109653	ESTs	8.95	0.08	upregulate stage
	433895	AI287912	Hs.3628	mitogen-activated protein kinase kinase	4.43	0.16	upregulate stage
15	433904	AI399956	Hs.208956	ESTs	5.5	0.12	upregulate stage
	433929	AI375499	Hs.27379	ESTs	7	0.09	upregulate stage
	433966	AF113017	Hs.284301	PRO1268 protein	7.95	0.08	upregulate stage
	433967	AF113018	Hs.284302	PRO1621 protein	2.65	0.1	upregulate stage
	434006	AF113668		gb:Homo sapiens clone FLB4630	7.85	0.08	upregulate stage
20	434037	AF1116601	Hs.283048	hypothetical protein PRO0128	8.81	0.09	upregulate stage
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.35	0.09	upregulate stage
	434085	AF116673	Hs.250029	hypothetical protein PRO1925	1	1	upregulate stage
	434092	AA625155		gb:af70d06.r1 Soares_NhHMPu_S1 Homo sapi	1	1	upregulate stage
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	11.5	0.06	upregulate stage
25	434138	AA625804		gb:zu85h01.s1 Soares_testis_NHT Homo sap	3.55	0.11	upregulate stage
	434192	AW387314	Hs.34371	ESTs	1.65	0.22	upregulate stage
	434194	AF119647	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	7.85	0.09	upregulate stage
	434217	AW014795	Hs.23349	ESTs	3.8	0.13	upregulate stage
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	5.95	0.11	upregulate stage
30	434271	AA897778	Hs.201677	ESTs	1	0.38	upregulate stage
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.45	0.07	upregulate stage
	434322	AI125686	Hs.152727	ESTs	2.65	0.18	upregulate stage
	434351	AW974991	Hs.191852	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.61	upregulate stage
	434354	AW974912	Hs.292783	ESTs	1	1	upregulate stage
35	434398	AA121098	Hs.3838	serum-inducible kinase	10.7	0.08	upregulate stage
	434464	BE063921	Hs.295971	ESTs	10.15	0.07	upregulate stage
	434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	7.6	0.09	upregulate stage
	434484	W79839	Hs.104336	hypothetical protein	5.1	0.15	upregulate stage
	434513	AF143888	Hs.18213	Homo sapiens clone IMAGE:121736 mRNA seq	1	1	upregulate stage
40	434534	H90477	Hs.41407	ESTs	1	0.18	upregulate stage
	434540	NM_016045	Hs.5184	TH1 drosophila homolog	12.4	0.06	upregulate stage
	434569	AI311295	Hs.58609	ESTs	1.75	0.38	upregulate stage
	434575	AI133446	Hs.299964	ESTs	9.7	0.06	upregulate stage
	434627	AI221894	Hs.39311	ESTs	1.65	0.17	upregulate stage
45	434629	AA789081	Hs.4029	glioma-amplified sequence-41	9	0.07	upregulate stage
	434663	AA641972	Hs.130058	ESTs	4.55	0.15	upregulate stage
	434731	AA648049	Hs.121518	ESTs	8.5	0.1	upregulate stage
	434765	AA831115	Hs.190473	ESTs	1	0.71	upregulate stage
	434773	AA648962	Hs.152947	ESTs	10.55	0.08	upregulate stage
50	434792	AA649253	Hs.132458	ESTs	5.45	0.11	upregulate stage
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1	0.34	upregulate stage
	434876	AF160477	Hs.245781	Homo sapiens Ig superfamily receptor LN1	1.4	0.57	upregulate stage
	434909	AI479212	Hs.17283	hypothetical protein FLJ10890	1	0.91	upregulate stage
	434926	BE543269	Hs.50252	Homo sapiens HSPC283 mRNA, partial cds	4.9	0.13	upregulate stage
55	434939	AF161422	Hs.21590	Homo sapiens HSPC304 mRNA, partial cds	1	1	upregulate stage
	434953	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	10.75	0.07	upregulate stage
	434970	AW272262	Hs.250468	ESTs	9.05	0.08	upregulate stage
	434980	AW770553	Hs.293640	ESTs	4.95	0.14	upregulate stage
	434997	AW975155	Hs.292163	ESTs	1	0.36	upregulate stage
60	435013	H91923	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.16	0.71	upregulate stage
	435030	AI203316	Hs.148655	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.95	0.14	upregulate stage
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.31	0.2	upregulate stage
	435061	AI851474	Hs.163944	ESTs	1.4	0.2	upregulate stage
	435080	AI831760	Hs.155111	ESTs	9.05	0.08	upregulate stage
65	435087	AW975241	Hs.23567	ESTs	1	1	upregulate stage
	435108	AW975018	Hs.287440	Homo sapiens cDNA FLJ11692 fis, clone HE	1	0.2	upregulate stage
	435136	R27299	Hs.10172	ESTs	8.9	0.07	upregulate stage
	435159	AA668879	Hs.116649	ESTs	1.35	0.25	upregulate stage
	435182	AI911044	Hs.213893	ESTs	1	1	upregulate stage
70	435186	AI391470	Hs.158618	ESTs	5.5	0.12	upregulate stage
	435212	AW300100	Hs.164185	ESTs	1	1	upregulate stage
	435237	AI026836	Hs.114689	ESTs	8.75	0.1	upregulate stage
	435255	W87434	Hs.106015	ESTs, Moderately similar to ALU1_HUMAN A	3.4	0.14	upregulate stage
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.2	0.14	upregulate stage
75	435257	AA677026	Hs.191217	ESTs	4.5	0.12	upregulate stage
	435298	AA677696	Hs.189196	ESTs	1	1	upregulate stage
	435307	W90610	Hs.192003	ESTs	1	0.87	upregulate stage
	435347	AW014873	Hs.116963	ESTs	2.45	0.14	upregulate stage
	435382	N54493		gb:yy40g05.s1 Soares fetal liver spleen	1	0.56	upregulate stage
	435408	H07897	Hs.4302	ESTs	0.84	0.97	upregulate stage
	435491	T98543	Hs.191900	ESTs	1	0.3	upregulate stage

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	435525	AI831297	Hs.123310	ESTs	3.25	0.15	upregulate stage
	435597	AW305188	Hs.163027	ESTs	1	0.57	upregulate stage
	435637	AF220051	Hs.110853	uncharacterized hematopoietic stem/proge	8.76	0.09	upregulate stage
5	435647	AI653240	Hs.49823	ESTs	3.19	0.25	upregulate stage
	435738	AA699633	Hs.269543	ESTs	2.9	0.16	upregulate stage
	435762	AW043836	Hs.212460	ESTs	1	1	upregulate stage
	435809	H90213	Hs.191330	ESTs	1.25	0.23	upregulate stage
	435826	AI554089	Hs.117880	ESTs	6.55	0.08	upregulate stage
10	435854	AJ278120	Hs.4996	DKFZP564D166 protein	2.76	0.29	upregulate stage
	435979	W03698	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.25	upregulate stage
	435981	H74319	Hs.188620	ESTs	6.35	0.11	upregulate stage
	435990	AI015862	Hs.131793	ESTs	4.25	0.08	upregulate stage
	435999	AA703271	Hs.269903	ESTs, Moderately similar to ALU1_HUMAN A	1	1	upregulate stage
15	436018	AA806485	Hs.121536	ESTs	1.45	0.23	upregulate stage
	436023	T81819		gb:yd95f05.s1 Scores fetal liver spleen	9.15	0.07	upregulate stage
	436052	AI021983	Hs.271432	ESTs	1	0.23	upregulate stage
	436115	AW512033	Hs.102004	ESTs	1.9	0.21	upregulate stage
	436118	AI221173	Hs.145080	ESTs	1	1	upregulate stage
20	436120	AI248193	Hs.119860	ESTs	9.61	0.08	upregulate stage
	436149	AI754308	Hs.159452	ESTs	2.4	0.19	upregulate stage
	436156	AA705466	Hs.119900	ESTs	1	0.26	upregulate stage
	436170	AW450381	Hs.14529	ESTs	1	0.91	upregulate stage
	436202	AA706315	Hs.192057	ESTs	1	1	upregulate stage
25	436246	AW450963	Hs.119991	ESTs	3.85	0.11	upregulate stage
	436274	AA732755	Hs.120299	ESTs	2.85	0.13	upregulate stage
	436282	R91913	Hs.272104	ESTs	3.95	0.11	upregulate stage
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	6	0.09	upregulate stage
	436300	AA831601	Hs.275736	ESTs	1	1	upregulate stage
30	436326	BE065236	Hs.181244	major histocompatibility complex, class	2.49	0.28	upregulate stage
	436360	AI962796	Hs.136754	ESTs	2.4	0.17	upregulate stage
	436363	AA843926	Hs.124434	ESTs	3.35	0.1	upregulate stage
	436383	BE065178		gb:RC1-BT0314-020200-012-h01 BT0314 Homo	1	0.67	upregulate stage
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	4	0.15	upregulate stage
35	436408	AW274577	Hs.252954	ESTs	9.1	0.09	upregulate stage
	436422	AA716141	Hs.147027	ESTs	1	0.26	upregulate stage
	436429	AA357003	Hs.17546	hypothetical protein FLJ23499	1	1	upregulate stage
	436463	H06502	Hs.6656	ESTs	5.45	0.12	upregulate stage
	436476	AA326108	Hs.53631	ESTs, Weakly similar to enhancer-of-spli	7.75	0.07	upregulate stage
40	436507	AA721209	Hs.201630	ESTs	2.45	0.18	upregulate stage
	436518	AA766433	Hs.122864	ESTs	3.15	0.21	upregulate stage
	436522	AA721381	Hs.129876	ESTs	4.75	0.1	upregulate stage
	436578	AI091435	Hs.134859	ESTs	3.4	0.12	upregulate stage
	436670	AI690021	Hs.201536	ESTs	6.85	0.11	upregulate stage
45	436740	AW975133		gb:EST387239 MAGE resequences, MAGN Homo	7.4	0.09	upregulate stage
	436764	AW976004	Hs.291731	ESTs	1	1	upregulate stage
	436785	AA745597	Hs.291400	ESTs	1	1	upregulate stage
	436823	AW749865	Hs.293645	ESTs	4.6	0.12	upregulate stage
	436831	AA830173	Hs.291918	ESTs	1.6	0.27	upregulate stage
50	436839	AA767346	Hs.291614	ESTs	1	1	upregulate stage
	436844	AA766458	Hs.122812	ESTs	1.5	0.28	upregulate stage
	436853	BE328074	Hs.148661	ESTs	5.05	0.14	upregulate stage
	436860	H12751	Hs.5327	PRO1914 protein	8.95	0.08	upregulate stage
	436925	AA742327	Hs.292687	ESTs	1	1	upregulate stage
55	437044	AL035884	Hs.69517	ESTs, Highly similar to differentially e	1.61	0.5	upregulate stage
	437087	AA745563		gb:ny60e04.s1 NCI_CGAP_Pr18 Homo sapiens	1	1	upregulate stage
	437144	AL049466	Hs.7859	ESTs	1	0.31	upregulate stage
	437170	R49202	Hs.181694	ESTs	8.7	0.08	upregulate stage
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	4.4	0.05	upregulate stage
60	437207	T27503	Hs.15929	Homo sapiens cDNA FLJ12910 fis, clone NT	1.4	0.22	upregulate stage
	437214	BE092336		gb:IL2-BT0734-240400-072-A12 BT0734 Homo	5.65	0.09	upregulate stage
	437240	AA747537		gb:nx85c05.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.45	upregulate stage
	437257	AI283085	Hs.290931	ESTs, Weakly similar to unknown [S.cerev	3.8	0.14	upregulate stage
	437258	AL041243	Hs.174104	ESTs	9.72	0.08	upregulate stage
	437267	AW511443	Hs.258110	ESTs	4.25	0.12	upregulate stage
65	437274	AA747965		gb:nx79e10.s1 NCI_CGAP_Ew1 Homo sapiens	1	0.19	upregulate stage
	437288	AA748182	Hs.160377	ESTs	1	0.61	upregulate stage
	437311	AA370041	Hs.9456	SW/SNF related, matrix associated, acti	3.1	0.17	upregulate stage
	437324	AL162077		gb:Homo sapiens mRNA; cDNA DKFZp761A219	1	0.25	upregulate stage
70	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	7.95	0.07	upregulate stage
	437356	BE622396	Hs.284252	Homo sapiens mRNA; cDNA DKFZp762Q1615 (f	1	1	upregulate stage
	437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	9.15	0.09	upregulate stage
	437471	AL390169		gb:Homo sapiens mRNA; cDNA DKFZp547D064	1	1	upregulate stage
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	1.1	0.56	upregulate stage
	437567	AW627990	Hs.288954	Homo sapiens cDNA: FLJ21466 fis, clone C	1	1	upregulate stage
75	437575	AW954355	Hs.36529	ESTs	10.25	0.06	upregulate stage
	437717	AA604765	Hs.132853	ESTs	1	0.77	upregulate stage
	437722	AW292947	Hs.122872	ESTs	9.75	0.05	upregulate stage

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	437752	AA767376	Hs.291631	ESTs	6.7	0.08	upregulate stage
	437770	AA767881	Hs.122897	ESTs	2.57	0.24	upregulate stage
	437798	AW811767		gb:RC2-ST0165-300999-011-g02 ST0165 Homo	1	1	upregulate stage
	437799	R51083	Hs.90787	ESTs	1	1	upregulate stage
5	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.77	0.3	upregulate stage
	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	8.8	0.08	upregulate stage
	437887	AA811524	Hs.29263	Homo sapiens cDNA FLJ11896 fis, clone HE	3.8	0.17	upregulate stage
	437889	AA830524	Hs.124357	ESTs	1	0.69	upregulate stage
	437937	AI917222	Hs.121655	ESTs	1	0.38	upregulate stage
10	437938	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	1.37	0.52	upregulate stage
	437983	AI303023	Hs.30211	hypothetical protein FLJ22313	8.82	0.08	upregulate stage
	438011	BE466173	Hs.145696	splicing factor (CC1.3)	9	0.09	upregulate stage
	438032	BE045624	Hs.152992	ESTs	5.65	0.13	upregulate stage
	438069	N80701	Hs.33790	ESTs	3.25	0.13	upregulate stage
15	438077	AA777330	Hs.50429	ESTs	1	1	upregulate stage
	438081	H49546	Hs.298964	ESTs	3.75	0.11	upregulate stage
	438102	AA777793	Hs.137580	xylulokinase (H. influenzae) homolog	1	1	upregulate stage
	438112	W85729	Hs.194279	ESTs	1	0.33	upregulate stage
	438113	AI467908	Hs.8982	ESTs	1.21	0.55	upregulate stage
20	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721.89	11.75	0.07	upregulate stage
	438144	AA778894	Hs.118364	ESTs	1	1	upregulate stage
	438153	AI266632	Hs.146159	ESTs	1	1	upregulate stage
	438171	AW976507	Hs.293515	ESTs	2.82	0.24	upregulate stage
25	438271	L21934	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1	1	upregulate stage
	438290	AA843719	Hs.122341	ESTs	3.9	0.13	upregulate stage
	438321	AA576635	Hs.6153	CGI-48 protein	9.4	0.08	upregulate stage
	438325	AA804258	Hs.123229	ESTs	4.65	0.11	upregulate stage
	438334	AA806992	Hs.291686	ESTs	1	1	upregulate stage
30	438366	AA805760		gb:ns43f01.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.34	upregulate stage
	438370	AA843242	Hs.48523	ESTs	4	0.14	upregulate stage
	438374	AA321866	Hs.6193	Homo sapiens mRNA; cDNA DKFZp434C1717 (f	1	0.84	upregulate stage
	438377	AA806070	Hs.291716	ESTs	1	0.24	upregulate stage
	438378	AW970529	Hs.86434	Homo sapiens cDNA: FLJ21816 fis, clone H	6.65	0.11	upregulate stage
35	438401	AL046321	Hs.197484	ESTs	1	1	upregulate stage
	438403	AA806607	Hs.292206	ESTs	2.75	0.14	upregulate stage
	438412	AA806776	Hs.130814	ESTs	1	1	upregulate stage
	438448	AA807344	Hs.172932	Homo sapiens mRNA for partial 3'UTR, seq	1	0.34	upregulate stage
	438451	AI081972	Hs.220261	ESTs	5.7	0.09	upregulate stage
40	438473	H07986	Hs.136901	ESTs	1	1	upregulate stage
	438487	AI684733	Hs.88920	HDCMC28P protein	1	0.21	upregulate stage
	438529	AW007287	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	1	0.36	upregulate stage
	438534	AW204052	Hs.123644	ESTs	1	0.37	upregulate stage
	438693	AA814360	Hs.249595	ESTs	3.55	0.15	upregulate stage
45	438698	AW297855	Hs.125815	ESTs	3.12	0.22	upregulate stage
	438728	AA815202	Hs.25657	ESTs	1	0.67	upregulate stage
	438746	AI885815	Hs.184727	ESTs	1.5	0.35	upregulate stage
	438805	AA826048	Hs.117887	ESTs	9.35	0.07	upregulate stage
	438812	AA826199	Hs.44287	ESTs	1	0.57	upregulate stage
	438817	AI023799	Hs.163242	ESTs	4.2	0.08	upregulate stage
50	438886	AA827728	Hs.128705	ESTs, Weakly similar to AF149422.2 unkno	4.05	0.12	upregulate stage
	438913	AI380429	Hs.172445	ESTs	5.4	0.11	upregulate stage
	438950	H23789	Hs.144530	ESTs	1	1	upregulate stage
	438961	H42135	Hs.101848	ESTs	7.85	0.08	upregulate stage
55	438990	AF085890		gb:Homo sapiens full length insert cDNA	1	0.83	upregulate stage
	439026	R98978	Hs.117767	ESTs	1	0.27	upregulate stage
	439052	AF085917	Hs.37921	ESTs	1	0.22	upregulate stage
	439057	H59623	Hs.271561	ESTs	1	1	upregulate stage
	439176	AI446444	Hs.190394	ESTs	5.8	0.12	upregulate stage
60	439179	AA831250	Hs.292893	ESTs	1	1	upregulate stage
	439183	AW970600		gb:EST382681 MAGE resequences, MAGK Homo	4.5	0.13	upregulate stage
	439208	AK000299	Hs.180952	dynactin p62 subunit	11.9	0.06	upregulate stage
	439212	AF087995	Hs.134877	ESTs	11.4	0.07	upregulate stage
	439223	AW238299	Hs.23945	ESTs	2.79	0.26	upregulate stage
	439312	AA833902	Hs.270745	ESTs	8.9	0.08	upregulate stage
65	439330	AF086147		gb:Homo sapiens full length insert cDNA	1	0.19	upregulate stage
	439351	W37688	Hs.55158	ESTs, Weakly similar to weak similarity	1	0.31	upregulate stage
	439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	3.9	0.15	upregulate stage
	439444	AI277652	Hs.54578	ESTs	11	0.07	upregulate stage
70	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	12.21	0.05	upregulate stage
	439476	AA836340	Hs.165490	ESTs	1	0.65	upregulate stage
	439492	AF086310	Hs.103159	ESTs	5.43	0.1	upregulate stage
	439527	AW298119	Hs.202536	ESTs	5.25	0.1	upregulate stage
	439550	H10438		gb:ym08d10.s1 Soares infant brain 1N1B H	3.2	0.18	upregulate stage
75	439580	BE565647	Hs.74899	hypothetical protein FLJ12820	1.81	0.32	upregulate stage
	439585	AF086386	Hs.145599	ESTs	8.96	0.07	upregulate stage
	439632	AF086413	Hs.58399	ESTs	1	1	upregulate stage
	439605	AF086431	Hs.134805	ESTs	9.15	0.09	upregulate stage

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	439606	W79123	Hs.58561	ESTs, Weakly similar to K01_HUMAN PROBA	8.45	0.06	upregulate stage
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	5.43	0.14	upregulate stage
	439780	AL109688		gb:Homo sapiens mRNA full length insert	5	0.09	upregulate stage
5	439851	AJ149520	Hs.144453	ESTs	2.75	0.21	upregulate stage
	439862	AI571647	Hs.146170	hypothetical protein FLJ22969	6.3	0.11	upregulate stage
	439926	AW014875	Hs.137007	ESTs	33.5	0.02	upregulate stage
	439942	AW993791	Hs.94881	ESTs	9.9	0.08	upregulate stage
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.59	0.15	upregulate stage
10	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	6.95	0.07	upregulate stage
	439987	AA860116	Hs.223232	ESTs	2.45	0.17	upregulate stage
	439999	AA115811	Hs.6838	ras homolog gene family, member E	8.75	0.07	upregulate stage
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.68	0.41	upregulate stage
	440012	AA861072		gb:ak32e05.s1 Soares_testis_NHT Homo sap	1	1	upregulate stage
15	440126	AA975145	Hs.66194	ESTs	1	1	upregulate stage
	440194	R43809	Hs.22688	ESTs	1	1	upregulate stage
	440228	AF125392	Hs.7089	insulin induced protein 2	1	1	upregulate stage
	440249	AI246590	Hs.125325	ESTs	1.74	0.44	upregulate stage
	440284	AA912032	Hs.181059	ESTs	1	1	upregulate stage
20	440334	BE276112	Hs.7165	zinc finger protein 259	9.45	0.09	upregulate stage
	440348	AW015802	Hs.47023	ESTs	1	0.33	upregulate stage
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.75	0.16	upregulate stage
	440366	F08229	Hs.125273	ESTs	3.5	0.12	upregulate stage
	440462	T71629	Hs.100554	ESTs	1.54	0.52	upregulate stage
25	440527	AV657117	Hs.184164	ESTs	3.75	0.14	upregulate stage
	440613	AI733034	Hs.137079	ESTs	3.9	0.11	upregulate stage
	440705	AA904244	Hs.153205	ESTs	3.9	0.14	upregulate stage
	440856	AW993377	Hs.130390	ESTs	8.95	0.09	upregulate stage
	440899	AW449445	Hs.172690	diacylglycerol kinase, alpha (80kD)	2.55	0.2	upregulate stage
30	440917	AA905651	Hs.160025	ESTs	1	0.17	upregulate stage
	440980	AL042005	Hs.1117	tripeptidyl peptidase II	8.9	0.09	upregulate stage
	440994	AI160011	Hs.193341	ESTs	1.29	0.58	upregulate stage
	441092	T99289	Hs.126556	EST	4.9	0.11	upregulate stage
	441107	AA917075	Hs.190520	ESTs	5.9	0.09	upregulate stage
35	441131	AI733222	Hs.126632	ESTs	9.55	0.09	upregulate stage
	441143	AI027604	Hs.159650	ESTs	3.8	0.13	upregulate stage
	441205	AW137827	Hs.176904	ESTs	4.75	0.12	upregulate stage
	441206	BE552314	Hs.131823	ESTs, Weakly similar to TERA HUMAN [H.sa	1	1	upregulate stage
	441264	AA927170	Hs.23290	ESTs	4.3	0.14	upregulate stage
40	441318	AI078234	Hs.176130	ESTs	1.74	0.45	upregulate stage
	441334	AI700529	Hs.117964	ESTs	1	1	upregulate stage
	441346	AA931077	Hs.186889	Homo sapiens cDNA FLJ12021 fis, clone HE	1	1	upregulate stage
	441378	AA931826	Hs.126846	ESTs	4.5	0.1	upregulate stage
	441383	AW294408	Hs.222068	ESTs	1	1	upregulate stage
45	441421	AA356792	Hs.301786	ESTs	1	0.24	upregulate stage
	441470	BE503874	Hs.301986	ESTs	0.63	0.93	upregulate stage
	441474	AW274946	Hs.144476	ESTs	1	1	upregulate stage
	441484	AA935481	Hs.58972	ESTs	1	0.33	upregulate stage
	441485	AI792988	Hs.189133	ESTs	4.25	0.1	upregulate stage
50	441508	AW015203	Hs.232237	ESTs	1	1	upregulate stage
	441562	AW578981	Hs.52184	hypothetical protein FLJ20618	4.05	0.12	upregulate stage
	441599	AW473362	Hs.127221	ESTs	1	0.29	upregulate stage
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	8.75	0.08	upregulate stage
	441616	BE569122	Hs.74111	RNA-binding protein (autoantigenic)	1.14	0.71	upregulate stage
55	441643	AI740504	Hs.205128	ESTs	1	0.33	upregulate stage
	441677	AW271702	Hs.93739	ESTs	1	0.28	upregulate stage
	441693	AA384673	Hs.7943	RPB5-mediated protein	1	0.43	upregulate stage
	441703	AW390054	Hs.192843	ESTs	9.85	0.08	upregulate stage
	441732	AW298818	Hs.127341	ESTs	4.6	0.14	upregulate stage
60	441759	C16126	Hs.161377	ESTs	4.55	0.13	upregulate stage
	441762	AW592203	Hs.144769	ESTs	1	0.83	upregulate stage
	441790	AW294909	Hs.132208	ESTs	9	0.08	upregulate stage
	441794	AW197794	Hs.253338	ESTs	4.5	0.12	upregulate stage
	441799	AW292276	Hs.127872	ESTs	1	0.22	upregulate stage
65	441801	AW242799	Hs.211874	ESTs	8	0.06	upregulate stage
	441904	AI633206	Hs.128104	ESTs	2	0.19	upregulate stage
	441955	AA972327	Hs.142903	ESTs	0.87	0.96	upregulate stage
	441989	AA306207	Hs.286241	Homo sapiens cDNA: FLJ22698 fis, clone H	9.17	0.07	upregulate stage
	441990	T66139	Hs.113631	ESTs	3.55	0.12	upregulate stage
70	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	4.65	0.14	upregulate stage
	442030	W67167	Hs.109080	ESTs	1	0.35	upregulate stage
	442064	AI422867	Hs.88594	ESTs	8.8	0.08	upregulate stage
	442071	BE048433	Hs.276043	ESTs	9.15	0.09	upregulate stage
	442093	AA976049	Hs.128464	ESTs	1	1	upregulate stage
	442194	AA984389	Hs.205088	ESTs	1	0.83	upregulate stage
75	442202	BE272862	Hs.106534	Homo sapiens cDNA: FLJ22625 fis, clone H	9.9	0.08	upregulate stage
	442203	AI921423	Hs.250146	ESTs	1	1	upregulate stage
	442214	AI681733	Hs.129003	ESTs	2.2	0.26	upregulate stage

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5	442216	AI733468	Hs.129006	ESTs	1	1	upregulate stage
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	1.49	0.31	upregulate stage
	442319	BE048144	Hs.177677	CGI-102 protein	1	0.29	upregulate stage
	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	22.95	0.03	upregulate stage
	442510	AF150179	Hs.249890	ESTs	1	0.63	upregulate stage
10	442518	AF150226		gb:AF150226 Human mRNA from cd34+ stem c	1	1	upregulate stage
	442539	AL119506	Hs.58220	Homo sapiens cDNA: FLJ23005 fis, clone L	1	0.23	upregulate stage
	442552	R20624	Hs.83572	son of sevenless (Drosophila) homolog 1	9	0.08	upregulate stage
	442562	BE379584	Hs.34789	ESTs	6.55	0.1	upregulate stage
	442564	AI590207	Hs.188378	ESTs	1	1	upregulate stage
15	442577	AA292998	Hs.163900	ESTs	1.41	0.52	upregulate stage
	442590	AI002686	Hs.130313	ESTs	1	0.36	upregulate stage
	442597	AI499214	Hs.130825	ESTs	1	1	upregulate stage
	442611	BE077155	Hs.177537	ESTs	4.35	0.15	upregulate stage
	442612	AI005233	Hs.130631	ESTs	1	0.28	upregulate stage
20	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	7.85	0.09	upregulate stage
	442642	R51853	Hs.226429	ESTs	1	1	upregulate stage
	442660	AW138174	Hs.130651	ESTs	4.1	0.09	upregulate stage
	442696	BE569362	Hs.7063	Homo sapiens cDNA: FLJ20913 fis, clone A	2.65	0.16	upregulate stage
	442712	BE465168	Hs.131011	ESTs	2.51	0.23	upregulate stage
25	442760	BE075297	Hs.10067	ESTs, Weakly similar to KIAA1205 protein	8	0.1	upregulate stage
	442769	AW243058	Hs.131155	ESTs	1	0.3	upregulate stage
	442785	AW296625	Hs.131188	ESTs	1	0.27	upregulate stage
	442806	AW294522	Hs.149991	ESTs	9.6	0.08	upregulate stage
	442856	H56735	Hs.282958	Homo sapiens cDNA FLJ13611 fis, clone PL	4.3	0.11	upregulate stage
30	442861	AA243837	Hs.57787	ESTs	3.9	0.12	upregulate stage
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	3.85	0.15	upregulate stage
	442879	AF032922	Hs.8813	syntaxin binding protein 3	3.95	0.14	upregulate stage
	442883	AW195774	Hs.253199	ESTs	1	1	upregulate stage
	442961	BE614474	Hs.289074	Homo sapiens cDNA FLJ13986 fis, clone Y7	11.55	0.07	upregulate stage
35	442965	AI394036	Hs.132237	ESTs, Weakly similar to dual specificity	2.95	0.16	upregulate stage
	442980	AA867025	Hs.8878	kinesin-like 1	1	0.24	upregulate stage
	442992	AI914699	Hs.13297	ESTs	6.1	0.14	upregulate stage
	442994	AI026718	Hs.16954	ESTs	8.9	0.07	upregulate stage
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	5.7	0.11	upregulate stage
40	443113	AI040886	Hs.132908	ESTs	3.9	0.14	upregulate stage
	443119	AA312264	Hs.7980	ESTs, Moderately similar to ALU4_HUMAN A	8.73	0.08	upregulate stage
	443171	BE281128	Hs.9030	TONDU	3.18	0.22	upregulate stage
	443211	AI128388	Hs.143655	ESTs	6.55	0.08	upregulate stage
	443242	BE243910	Hs.9082	nucleoporin p54	11.05	0.06	upregulate stage
45	443243	AI452496	Hs.132056	ESTs	8.9	0.09	upregulate stage
	443247	BE614387	Hs.47378	ESTs, Moderately similar to hypothetical	10.95	0.05	upregulate stage
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	3.75	0.2	upregulate stage
	443299	AI733642	Hs.133042	ESTs	1	0.69	upregulate stage
	443362	AI053464	Hs.166505	ESTs	2.9	0.16	upregulate stage
50	443383	AI792453	Hs.166507	ESTs	5	0.14	upregulate stage
	443411	AW134566	Hs.65320	ESTs	1	0.59	upregulate stage
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.68	0.31	upregulate stage
	443447	AI094222	Hs.166572	ESTs	1	0.38	upregulate stage
	443542	AI927065	Hs.146040	ESTs	5.65	0.13	upregulate stage
55	443557	AV645987	Hs.145681	ESTs	1	1	upregulate stage
	443584	AI807036	Hs.101619	ESTs	1	0.36	upregulate stage
	443606	AI078864	Hs.199424	ESTs	1.15	0.33	upregulate stage
	443634	H73972	Hs.134460	ESTs	3.05	0.16	upregulate stage
	443640	AI872643	Hs.134218	ESTs	3.65	0.12	upregulate stage
60	443715	AI583187	Hs.9700	cyclin E1	5.65	0.11	upregulate stage
	443799	AA150320	Hs.9800	protein kinase Njmu-R1	1.8	0.19	upregulate stage
	443899	AW842283	Hs.79933	cyclin I	4.65	0.13	upregulate stage
	443917	AW503739	Hs.72325	Human DNA sequence from clone RP1-187J11	1	1	upregulate stage
	443919	AI091284	Hs.135224	ESTs	8.05	0.07	upregulate stage
65	443967	AW294013	Hs.200942	ESTs	5.55	0.13	upregulate stage
	443977	AL120986	Hs.150627	ESTs	4	0.14	upregulate stage
	443979	AV647366	Hs.282365	ESTs	1	1	upregulate stage
	444020	R92962	Hs.35052	ESTs	10.45	0.08	upregulate stage
	444105	AW189097	Hs.166597	ESTs	6.29	0.1	upregulate stage
70	444129	AW294292	Hs.256212	ESTs	1	0.77	upregulate stage
	444152	AI125694	Hs.149305	Homo sapiens cDNA FLJ14264 fis, clone PL	1.64	0.48	upregulate stage
	444163	AI126098		gb:gc54g07.x1 Soares_placenta_8to9weeks_	1.12	0.81	upregulate stage
	444166	AV648429	Hs.282393	ESTs	1	1	upregulate stage
	444270	AI138580	Hs.255220	EST	1	0.47	upregulate stage
75	444271	AW452569	Hs.149804	ESTs	3.2	0.12	upregulate stage
	444282	AI138955		gb:qd79b07.x1 Soares_testis_NHT Homo sap	1	1	upregulate stage
	444333	AI262567	Hs.253801	trinucleotide repeat containing 15	1	0.77	upregulate stage
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	6.9	0.06	upregulate stage
	444378	R41339	Hs.12569	ESTs	1	0.32	upregulate stage
	444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	2.85	0.26	upregulate stage
	444431	AW513324	Hs.42280	ESTs	6.27	0.12	upregulate stage

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	444437	AI377961	Hs.44041	ESTs	9.9	0.07	upregulate stage
	444444	AI149332	Hs.14855	ESTs	1.16	0.47	upregulate stage
	444525	AW593778	Hs.259699	ESTs	1	0.5	upregulate stage
	444584	AI168422		gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	3.6	0.15	upregulate stage
5	444599	AI174377	Hs.143796	ESTs	1	0.44	upregulate stage
	444646	AI184565		gb:qd60b08.x1 Soares_testis_NHT Homo sap	1	1	upregulate stage
	444649	AW207523	Hs.197628	ESTs	9.35	0.06	upregulate stage
	444675	AI186380	Hs.244621	ESTs	9.88	0.06	upregulate stage
	444698	AI188139	Hs.147050	ESTs	1	0.36	upregulate stage
10	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moi	2.1	0.15	upregulate stage
	444762	AI733700	Hs.143883	ESTs	3.9	0.14	upregulate stage
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.44	0.53	upregulate stage
	444783	AK001468	Hs.62190	anillin (Drosophila Scraps homolog), act	6.65	0.07	upregulate stage
15	444838	AV651680	Hs.208558	ESTs	4.84	0.14	upregulate stage
	444849	AI199438	Hs.148480	ESTs	3.05	0.17	upregulate stage
	444950	AI950256	Hs.224875	ESTs	1	0.51	upregulate stage
	445027	AV652692	Hs.282498	ESTs	11.1	0.08	upregulate stage
	445091	AI652154	Hs.147294	ESTs	1	1	upregulate stage
20	445098	AL050272	Hs.12305	DKFZP566B183 protein	9.75	0.07	upregulate stage
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	10.9	0.07	upregulate stage
	445250	AI597838	Hs.175621	ESTs	9.8	0.08	upregulate stage
	445258	AI635931	Hs.147613	ESTs	3.05	0.13	upregulate stage
	445390	AI222165	Hs.144923	ESTs	10.6	0.06	upregulate stage
25	445396	BE181792		gb:QV1-HT0639-070500-193-g06 HT0639 Homo	1	0.29	upregulate stage
	445413	AA151342	Hs.12677	CGI-147 protein	4.65	0.12	upregulate stage
	445436	AI224105	Hs.151408	ESTs	1.35	0.22	upregulate stage
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	10.7	0.07	upregulate stage
	445483	AI307150	Hs.148845	ESTs	1	1	upregulate stage
30	445496	AB007860	Hs.12802	development and differentiation enhancin	12.05	0.06	upregulate stage
	445525	BE149866	Hs.14831	ESTs	10.65	0.06	upregulate stage
	445527	W39694	Hs.83286	ESTs	4.85	0.1	upregulate stage
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	9.7	0.06	upregulate stage
	445546	AW468821	Hs.156054	ESTs	4.2	0.13	upregulate stage
35	445576	AI793233	Hs.145608	ESTs	1	0.31	upregulate stage
	445623	AI245366	Hs.149158	ESTs	1	1	upregulate stage
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	4.7	0.13	upregulate stage
	445668	AI557114	Hs.181591	EST	1	0.34	upregulate stage
	445766	AI623607	Hs.282977	Homo sapiens cDNA FLJ13490 fis, clone PL	1	0.23	upregulate stage
40	445770	AL119499	Hs.13285	neuronal potassium channel alpha subunit	1	1	upregulate stage
	445778	AA196443	Hs.86043	Homo sapiens cDNA FLJ13558 fis, clone PL	9.7	0.07	upregulate stage
	445787	AI253167	Hs.145395	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.1	0.13	upregulate stage
	445814	H92020	Hs.101624	ESTs	1	1	upregulate stage
	445818	BE045321	Hs.136017	ESTs	1	1	upregulate stage
45	445829	AI452457	Hs.145526	ESTs	1	0.37	upregulate stage
	445832	AI261545		gb:xz30a07.x1 NCL_CGAP_Kid11 Homo sapien	3.21	0.22	upregulate stage
	445873	AA250970	Hs.251946	Homo sapiens cDNA: FLJ23107 fis, clone L	5.25	0.12	upregulate stage
	445880	AV655474	Hs.131058	ESTs	1.05	0.27	upregulate stage
	445883	AF070559	Hs.13413	Homo sapiens clone 24463 mRNA sequence	1	1	upregulate stage
50	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	3.25	0.15	upregulate stage
	445939	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	8.85	0.08	upregulate stage
	446019	AI362520	Hs.94133	ESTs	9.75	0.06	upregulate stage
	446054	AB014537	Hs.13604	KIAA0637 gene product	10.25	0.07	upregulate stage
	446062	AA211738	Hs.282974	ESTs, Weakly similar to transformation-r	1	1	upregulate stage
55	446080	AI221741	Hs.117777	ESTs	9.75	0.09	upregulate stage
	446082	AI274139	Hs.156452	ESTs	1.37	0.4	upregulate stage
	446099	T93096	Hs.17126	ESTs	2.4	0.31	upregulate stage
	446119	D29527		gb:HUMNK667 Human epidermal keratinocyte	1	1	upregulate stage
60	446120	N26080	Hs.43741	ESTs	1	0.31	upregulate stage
	446126	AW065909	Hs.47413	ESTs	9.35	0.08	upregulate stage
	446127	AA333808	Hs.13980	ubiquitously transcribed tetrapeptid	1	0.25	upregulate stage
	446152	AI292036	Hs.150028	ESTs	4.7	0.12	upregulate stage
	446196	AI744888	Hs.149470	ESTs	1	0.83	upregulate stage
	446229	AI744964	Hs.14449	KIAA1609 protein	2.4	0.36	upregulate stage
65	446248	AI283014	Hs.149638	ESTs	1	1	upregulate stage
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	10.85	0.07	upregulate stage
	446303	X77244	Hs.14732	malic enzyme 1, NADP(+)-dependent, cytos	1	1	upregulate stage
	446312	BE087853		gc:QV1-BT0681-290400-181-h05 BT0681 Homo	11.75	0.06	upregulate stage
	446332	AK001835	Hs.14838	hypothetical protein FLJ10773	6.45	0.1	upregulate stage
	446356	AI816736	Hs.14896	DHHC1 protein	8.9	0.08	upregulate stage
70	446362	AW612481	Hs.255914	ESTs	7.6	0.1	upregulate stage
	446398	AI681317	Hs.150074	ESTs	1	1	upregulate stage
	446411	AI298828	Hs.153439	ESTs	1	0.37	upregulate stage
	446474	AI301227	Hs.150186	ESTs	3.35	0.13	upregulate stage
75	446501	AI302616	Hs.150819	ESTs	4.25	0.12	upregulate stage
	446507	AA352554	Hs.15164	nuclear DNA-binding protein	11.25	0.06	upregulate stage
	446526	H89616	Hs.296290	Homo sapiens cDNA FLJ13357 fis, clone PL	10.25	0.07	upregulate stage
	446555	AV659046	Hs.201847	ESTs	1	1	upregulate stage

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5	446577	AB040933	Hs.15420	KIAA1500 protein	1	0.51	upregulate stage
	446629	AI435046	Hs.156148	Homo sapiens cDNA: FLJ23062 fis, clone L	1	0.25	upregulate stage
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	2.54	0.28	upregulate stage
	446682	AW205632	Hs.211198	ESTs	4	0.18	upregulate stage
	446701	AK001621	Hs.15921	hypothetical protein FLJ10759	1.32	0.69	upregulate stage
10	446718	AV660019	Hs.282676	ESTs	1	1	upregulate stage
	446719	W39500	Hs.47305	ESTs, Weakly similar to LONN_HUMAN MITOC	9.65	0.07	upregulate stage
	446720	AI439136	Hs.140546	ESTs	4.55	0.12	upregulate stage
	446765	AV660348	Hs.282688	ESTs	1	0.91	upregulate stage
	446771	AA128965	Hs.60679	TATA box binding protein (TBP)-associate	11.2	0.06	upregulate stage
15	446821	W03766	Hs.301482	ESTs	6.9	0.09	upregulate stage
	446830	BE179030	Hs.64239	Human DNA sequence from clone RP5-1174N9	10.65	0.07	upregulate stage
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	14.05	0.05	upregulate stage
	446853	AV660630	Hs.87627	disrupter of silencing 10	9.7	0.09	upregulate stage
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ12534 fis, clone NT	11.05	0.06	upregulate stage
20	446922	BE175605	Hs.175605	gb:RC5-HT0580-100500-022-H07 HT0580 Homo	2.75	0.16	upregulate stage
	446950	AA305800	Hs.293454	ESTs, Weakly similar to Similarity to Ye	9.6	0.06	upregulate stage
	446988	AW339533	Hs.272108	ESTs	1	0.29	upregulate stage
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	1.75	0.51	upregulate stage
	447052	AV661911	Hs.282735	ESTs	1	1	upregulate stage
25	447065	AI829014	Hs.158678	ESTs	1	0.25	upregulate stage
	447069	AI359927	Hs.157722	ESTs	1	0.4	upregulate stage
	447078	AW885727	Hs.301570	ESTs	4.4	0.13	upregulate stage
	447080	AI418781	Hs.300144	ESTs	1	0.31	upregulate stage
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	3.55	0.12	upregulate stage
30	447118	AB014599	Hs.17411	KIAA0699 protein	10.15	0.07	upregulate stage
	447153	AA805202	Hs.173912	eukaryotic translation initiation factor	6.2	0.12	upregulate stage
	447154	H52284	Hs.293545	ESTs	1	0.24	upregulate stage
	447159	AI685286	Hs.280386	EST	1.25	0.25	upregulate stage
	447215	BE617056	Hs.283000	ESTs	2.4	0.16	upregulate stage
35	447228	AW192200	Hs.158188	ESTs	1	0.29	upregulate stage
	447258	BE047911	Hs.183858	gb:tz44a05.y1 NCI_CGAP_Bm52 Homo sapien	1.15	0.23	upregulate stage
	447286	AW197097	Hs.36978	transcriptional intermediary factor 1	1	1	upregulate stage
	447289	AW247017	Hs.91109	melanoma antigen, family A, 3	1	1	upregulate stage
	447334	AA515032	Hs.91109	ESTs	9.15	0.08	upregulate stage
40	447342	AI199268	Hs.19322	ESTs	5.95	0.09	upregulate stage
	447343	AA256641	Hs.236894	ESTs, Highly similar to LRP1_HUMAN LOW-D	2.11	0.33	upregulate stage
	447376	AI376747	Hs.18442	gb:tc35h05.x1 Soares_total_fetus_Nb2HF8_	1	0.33	upregulate stage
	447397	BE247676	Hs.18442	E-1 enzyme	5.3	0.14	upregulate stage
	447430	AI742989	Hs.206112	ESTs	3.65	0.13	upregulate stage
45	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	9.2	0.08	upregulate stage
	447519	U46258	Hs.23448	ESTs	14.4	0.05	upregulate stage
	447522	BE143888	Hs.136585	gb:MR0-HTC165-081199-001-b04 HTC165 Homo	1.7	0.18	upregulate stage
	447578	AA912347	Hs.170995	ESTs	1.5	0.3	upregulate stage
	447606	AI588954	Hs.19236	ESTs	2.7	0.16	upregulate stage
50	447688	N87079	Hs.255527	NADH dehydrogenase (ubiquinone) 1 beta s	4.55	0.12	upregulate stage
	447701	BE619526	Hs.167253	ESTs, Weakly similar to unnamed protein	1.63	0.46	upregulate stage
	447741	AI421737	Hs.161338	ESTs	1	1	upregulate stage
	447748	AI422023	Hs.19718	ESTs	3.9	0.11	upregulate stage
	447827	U73727	Hs.23037	protein tyrosine phosphatase, receptor t	1.44	0.59	upregulate stage
55	447881	BE620886	Hs.165900	ESTs	12.15	0.06	upregulate stage
	447963	AI452973	Hs.255906	ESTs, Weakly similar to ALUC_HUMAN !!!!	8.9	0.08	upregulate stage
	447977	AI457097	Hs.280848	ESTs	1	1	upregulate stage
	447978	AI457098	Hs.137551	ESTs	1	1	upregulate stage
	447982	H22953	Hs.246868	ESTs	4.25	0.13	upregulate stage
60	448032	AW511770	Hs.20166	ESTs	1	1	upregulate stage
	448045	AJ297436	Hs.170424	prostate stem cell antigen	2.22	0.29	upregulate stage
	448058	AI458998	Hs.255472	ESTs	1	0.51	upregulate stage
	448062	AW295923	Hs.170736	ESTs	5.9	0.08	upregulate stage
	448138	AW847925	Hs.203230	ESTs	1	1	upregulate stage
65	448154	AL120320	Hs.108923	ESTs	9.85	0.07	upregulate stage
	448165	NM_005531	Hs.22549	meiotic recombination (S. cerevisiae) 11	7.3	0.09	upregulate stage
	448168	AW605999	Hs.20814	hypothetical protein FLJ12799	1	0.77	upregulate stage
	448236	AA890449	Hs.202402	oxysterol 7alpha-hydroxylase	1	0.47	upregulate stage
	448256	BE614149	Hs.20893	CGI-27 protein	11.95	0.07	upregulate stage
70	448289	AW390251	Hs.171055	ESTs	1	0.47	upregulate stage
	448356	AL120837	Hs.196093	high-glucose-regulated protein 8	11	0.07	upregulate stage
	448357	N20169	Hs.21107	ESTs	1.34	0.61	upregulate stage
	448408	AA322866	Hs.269860	neurofilin	1.7	0.24	upregulate stage
	448455	AI252625	Hs.171055	ESTs	8.8	0.09	upregulate stage
75	448459	AW069838	Hs.171055	ESTs	1	0.27	upregulate stage
	448464	AI522053	Hs.171072	ESTs	10.35	0.06	upregulate stage
	448468	BE550361	Hs.239699	ESTs	1	1	upregulate stage
	448502	AW805285	Hs.20104	ESTs	9.3	0.08	upregulate stage
	448552	AW973653	Hs.5064	hypothetical protein FLJ00052	4.75	0.13	upregulate stage
	448556	AW885606	Hs.21486	ESTs	9.8	0.08	upregulate stage
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.14	0.35	upregulate stage

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	448632	BE614269		gb:601504311T1 NIH_MGC_71 Homo sapiens c	1	1	upregulate stage
	448643	AI557531		gb:pt2.1-06.D06.r tumor2 Homo sapiens cD	3.6	0.14	upregulate stage
	448649	T94590	Hs.222855	ESTs	1.95	0.21	upregulate stage
5	448663	BE614599	Hs.106823	H.sapiens gene from PAC 42616, similar t	4.3	0.12	upregulate stage
	448680	AW245890	Hs.21753	JM5 protein	0.97	0.93	upregulate stage
	448725	AA193251	Hs.40289	ESTs	2.6	0.19	upregulate stage
	448729	BE614535	Hs.138580	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.25	0.16	upregulate stage
	448743	AB032962	Hs.21896	KIAA1136 protein	1.9	0.19	upregulate stage
10	448826	AI680252	Hs.293246	ESTs, Weakly similar to putative p150 [H	1.78	0.44	upregulate stage
	448914	AI927656	Hs.196459	ESTs	2.75	0.19	upregulate stage
	448946	AI652855	Hs.155796	ESTs	9.7	0.07	upregulate stage
	448958	AB020651	Hs.22653	KIAA0844 protein	1	0.18	upregulate stage
	448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	5.85	0.11	upregulate stage
15	448979	AI611378	Hs.192610	ESTs	1	1	upregulate stage
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	5.2	0.11	upregulate stage
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	1	0.33	upregulate stage
	449053	AI625777	Hs.270344	ESTs	5.73	0.12	upregulate stage
	449057	AB037784	Hs.22941	KIAA1363 protein	9.25	0.07	upregulate stage
20	449148	AW836677	Hs.287564	Homo sapiens cDNA FLJ13345 fis, clone OV	7.2	0.09	upregulate stage
	449203	AI634578	Hs.282121	ESTs	7	0.1	upregulate stage
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.34	0.36	upregulate stage
	449219	AI637581	Hs.195012	ESTs	1	1	upregulate stage
	449230	BE613348	Hs.23348	S-phase kinase-associated protein 2 (p45	3.08	0.25	upregulate stage
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	4.79	0.16	upregulate stage
25	449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanog	2.8	0.16	upregulate stage
	449328	AI962493	Hs.197647	ESTs	2.55	0.17	upregulate stage
	449343	AI151418	Hs.272458	protein phosphatase 3 (formerly 2B), cat	4.75	0.12	upregulate stage
	449344	AI640355		gb:wa17cd4.x1 NCI_CGAP_Kid11 Homo sapien	2.1	0.22	upregulate stage
30	449351	AW016537	Hs.200760	ESTs	2.45	0.14	upregulate stage
	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	1.55	0.14	upregulate stage
	449424	AW448937	Hs.197030	ESTs	4.05	0.12	upregulate stage
	449425	AW103433	Hs.195684	ESTs	4.6	0.12	upregulate stage
	449434	AW294858	Hs.197641	ESTs	1	0.29	upregulate stage
35	449437	AI702038	Hs.100057	Homo sapiens cDNA: FLJ22902 fis, clone K	2.38	0.34	upregulate stage
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	5.9	0.12	upregulate stage
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.45	0.1	upregulate stage
	449528	H63337	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	2.85	0.18	upregulate stage
	449565	AI824925	Hs.197066	ESTs	1	1	upregulate stage
40	449568	AI157479	Hs.23740	KIAA1598 protein	10.15	0.06	upregulate stage
	449618	AI076459	Hs.14366	Homo sapiens cDNA FLJ12819 fis, clone NT	11.7	0.06	upregulate stage
	449639	AA001968	Hs.59956	ESTs, Highly similar to MGR7_HUMAN METAB	1	1	upregulate stage
	449666	AA002047		gb:zh84e05.r1 Soares_fetal_liver_spleen_	1.85	0.33	upregulate stage
	449704	AK000733	Hs.23900	GTPase activating protein	2.82	0.3	upregulate stage
45	449722	BE280074	Hs.23960	cyllin B1	6.44	0.12	upregulate stage
	449764	N93104	Hs.54895	ESTs, Weakly similar to ZNF91L [H.sapien	1	1	upregulate stage
	449784	AW161319	Hs.12915	ESTs	6.25	0.11	upregulate stage
	449829	N51440	Hs.47261	ESTs	1	0.57	upregulate stage
	449843	R85337	Hs.24030	solute carrier family 31 (copper transpo	10.2	0.07	upregulate stage
50	449892	N73608	Hs.50309	ESTs	6.5	0.1	upregulate stage
	449894	AK001578	Hs.24129	hypothetical protein FLJ10716	4.55	0.12	upregulate stage
	449919	AI674685	Hs.200141	ESTs	5.3	0.11	upregulate stage
	450020	AI680684	Hs.282219	ESTs	1	1	upregulate stage
	450033	R43010	Hs.269452	ESTs, Weakly similar to JH0148 nucleolin	1	0.65	upregulate stage
55	450063	AI681509	Hs.277133	ESTs	4.2	0.17	upregulate stage
	450083	AA131795	Hs.142001	ESTs	3.9	0.16	upregulate stage
	450116	AA005355	Hs.222882	ESTs	1	1	upregulate stage
	450121	AL040174	Hs.238927	Homo sapiens cDNA: FLJ22944 fis, clone K	1	1	upregulate stage
	450135	AI810816	Hs.201142	ESTs	4.95	0.14	upregulate stage
60	450144	T63961	Hs.301851	ESTs	2.75	0.13	upregulate stage
	450149	AW969781	Hs.293440	ESTs, Moderately similar to ZIC2 protein	3.75	0.14	upregulate stage
	450151	AI088196	Hs.295233	ESTs	2.51	0.28	upregulate stage
	450152	AI138635	Hs.22968	ESTs	2.45	0.15	upregulate stage
	450195	AA007352	Hs.256042	ESTs	4.1	0.14	upregulate stage
65	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1	0.3	upregulate stage
	450238	T89693	Hs.138777	ESTs	12.2	0.07	upregulate stage
	450257	AW820313		gb:QV2-ST0296-150200-028-d02 ST0296 Homo	1	1	upregulate stage
	450313	AI038989	Hs.24809	hypothetical protein FLJ10826	4.35	0.15	upregulate stage
	450314	AA574309	Hs.283402	TCR eta	10.1	0.07	upregulate stage
70	450350	T97817	Hs.174880	ESTs	3.85	0.1	upregulate stage
	450411	D61167	Hs.202156	ESTs	1	0.67	upregulate stage
	450447	AF212223	Hs.25010	hypothetical protein P15-2	10.75	0.07	upregulate stage
	450448	D54299	Hs.35244	ESTs	1	1	upregulate stage
	450449	AI696596	Hs.202068	ESTs	1	1	upregulate stage
75	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	11.45	0.05	upregulate stage
	450573	AW964334		gb:EST376407 MAGE resequences, MAGH Homo	1.2	0.2	upregulate stage
	450628	AW362884	Hs.204715	ESTs	4.95	0.13	upregulate stage
	450636	AI703076	Hs.201959	ESTs	1	0.69	upregulate stage

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5	450655	AI707846	Hs.279860	hypothetical protein FLJ20030	1	1	upregulate stage
	450664	AA808358	Hs.35830	ESTs	1	0.34	upregulate stage
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.51	0.09	upregulate stage
	450722	AI732318	Hs.101120	ESTs	1	0.87	upregulate stage
	450751	AI733251	Hs.126853	ESTs, Weakly similar to JU0033 hypotheti	1	1	upregulate stage
10	450772	BE326391	Hs.280146	ESTs, Weakly similar to JU0033 hypotheti	1	1	upregulate stage
	450800	BE395161	Hs.243963	ESTs, Weakly similar to ALU5_HUMAN ALU S	8.7	0.08	upregulate stage
	450824	R09055	Hs.269204	ESTs	3.03	0.22	upregulate stage
	450832	AW970602	Hs.105421	ESTs	6.15	0.08	upregulate stage
	450870	AA011471		gb:z101h08.r1 Soares_fetal_liver_spleen_	1.15	0.23	upregulate stage
15	450937	R49131	Hs.26267	ATP-dependant interferon response protei	9.75	0.08	upregulate stage
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.32	0.26	upregulate stage
	451052	AA281504	Hs.24444	ESTs, Moderately similar to ALUE_HUMAN I	9.25	0.08	upregulate stage
	451067	BE172186	Hs.180789	S164 protein	2.8	0.21	upregulate stage
	451088	AA015600	Hs.82415	ESTs	1	0.32	upregulate stage
20	451094	AI949825	Hs.260395	ESTs	4.45	0.14	upregulate stage
	451096	BE383234	Hs.25925	Homo sapiens clone 23860 mRNA sequence	4.15	0.14	upregulate stage
	451126	H30600	Hs.40910	ESTs	1	1	upregulate stage
	451161	AA211329	Hs.26006	hypothetical protein FLJ10559	2.15	0.16	upregulate stage
	451166	T96171	Hs.185675	ESTs	9.26	0.08	upregulate stage
25	451222	AA018386	Hs.64341	ESTs	1	0.36	upregulate stage
	451225	AI433694	Hs.293608	ESTs	9.19	0.08	upregulate stage
	451228	AI767166	Hs.207025	ESTs	1	1	upregulate stage
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	7.35	0.11	upregulate stage
	451266	AA016292	Hs.290849	ESTs	1	0.33	upregulate stage
30	451276	AW294386	Hs.236533	ESTs, Highly similar to dJ742C19.2 [H.s.a	1	1	upregulate stage
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	11.7	0.06	upregulate stage
	451291	R39288	Hs.6702	ESTs	1	1	upregulate stage
	451326	AW296946	Hs.300967	ESTs	10.55	0.07	upregulate stage
	451347	AI288679	Hs.101139	ESTs	1	1	upregulate stage
35	451359	H85334		gb:ys90e05.r1 Soares retina N2b5HR Homo	2.7	0.15	upregulate stage
	451365	AI791783		gb:op20h10.y5 NCI_CGAP_Co12 Homo sapiens	8.9	0.09	upregulate stage
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	2.45	0.19	upregulate stage
	451440	AA017599	Hs.293817	ESTs	1	1	upregulate stage
	451487	AA018072		gb:ze51g02.r1 Soares retina N2b4HR Homo	5.7	0.1	upregulate stage
40	451492	AA018119	Hs.297824	ESTs, Highly similar to ClK1_HUMAN VOLTA	1	1	upregulate stage
	451495	H86887		gb:y107a01.r1 Soares retina N2b5HR Homo	4.25	0.13	upregulate stage
	451535	AW970577		gb:EST382658 MAGE resequences, MAGK Homo	6.8	0.12	upregulate stage
	451553	AA018454	Hs.269211	ESTs, Weakly similar to B34087 hypotheti	1	1	upregulate stage
	451562	H04150	Hs.107708	ESTs	4.65	0.11	upregulate stage
45	451580	AW138195	Hs.184326	CDC10 (cell division cycle 10, S. cerevi	1	0.42	upregulate stage
	451592	AI805416	Hs.213897	ESTs	2.8	0.17	upregulate stage
	451651	AI097337	Hs.88977	hypothetical protein dJ511E16.2	1	0.18	upregulate stage
	451658	AW195351	Hs.250520	ESTs	9.55	0.07	upregulate stage
	451684	AF216751	Hs.26813	CDA14	3.7	0.15	upregulate stage
50	451690	AW451469	Hs.209990	ESTs	10.86	0.07	upregulate stage
	451724	AI903765		gb:LI-BT037-301298-102 BT037 Homo sapien	8.85	0.09	upregulate stage
	451743	AW074266	Hs.23071	ESTs	2.17	0.35	upregulate stage
	451794	AA019799	Hs.111911	ESTs	1	1	upregulate stage
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	6.5	0.11	upregulate stage
55	451903	W19617	Hs.261003	ESTs, Moderately similar to B34087 hypot	2.2	0.21	upregulate stage
	451914	AI822115	Hs.270618	ESTs, Weakly similar to KIAA0822 protein	11.67	0.07	upregulate stage
	451938	AI354355	Hs.16697	down-regulator of transcription 1, TBP-b	11.65	0.06	upregulate stage
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	1	0.95	upregulate stage
	451971	AA021185	Hs.226306	ESTs	1	1	upregulate stage
60	451998	AW594129	Hs.213666	ESTs	1	0.26	upregulate stage
	452028	AK001859	Hs.27595	hypothetical protein FLJ10997	1	0.21	upregulate stage
	452036	NM_003965	Hs.27621	sema domain, seven thrombospondin repeat	1.76	0.41	upregulate stage
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	8.9	0.07	upregulate stage
	452122	AF216833	Hs.1710	ATP-binding cassette, sub-family B (MDR/	1	0.47	upregulate stage
65	452163	AI863140		gb:tz43h12.x1 NCI_CGAP_Brn52 Homo sapien	1	0.2	upregulate stage
	452179	H16725	Hs.27463	ESTs	3	0.13	upregulate stage
	452198	AI097580	Hs.61210	ESTs	1	0.28	upregulate stage
	452206	AW340281	Hs.33074	ESTs, Moderately similar to ALU1_HUMAN A	12.4	0.07	upregulate stage
	452234	AW084176	Hs.223296	ESTs	6.8	0.09	upregulate stage
70	452240	AI591147	Hs.61232	ESTs	3.75	0.07	upregulate stage
	452247	AL137432	Hs.28564	hypothetical protein DKFZp761E1824	3.9	0.15	upregulate stage
	452250	BE618654	Hs.28607	hypothetical protein A-211C6.1	8.75	0.09	upregulate stage
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	5.2	0.09	upregulate stage
	452266	AI767250	Hs.165240	ESTs	10.45	0.06	upregulate stage
75	452277	AL049013	Hs.28733	KIAA1223 protein	8.9	0.05	upregulate stage
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	8.2	0.04	upregulate stage
	452291	AF015592	Hs.28853	CD7 (cell division cycle 7, S. cerevisi	3.5	0.13	upregulate stage
	452328	AA805679	Hs.61271	ESTs	3.5	0.14	upregulate stage
	452331	AA598509	Hs.29117	H.sapiens mRNA for pur alpha extended 3'	11.75	0.07	upregulate stage
	452345	AA293279	Hs.29173	hypothetical protein FLJ20515	1.08	0.73	upregulate stage
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	10.15	0.07	upregulate stage

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5	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1	0.17	upregulate stage
	452404	AW450675	Hs.212709	ESTs	3.63	0.2	upregulate stage
	452430	AF118083	Hs.29494	PRO1912 protein	1	0.41	upregulate stage
	452436	BE077546	Hs.31447	ESTs	10	0.07	upregulate stage
	452457	AW062499		gb:MR0-CT0065-100899-001-d02 CT0065 Homo	1	0.13	upregulate stage
10	452461	N78223	Hs.108106	transcription factor	8.1	0.06	upregulate stage
	452518	AA280722	Hs.24758	ESTs	9.3	0.08	upregulate stage
	452519	BE006701		gb:RC0-BN0132-270300-021-a03 BN0132 Homo	1	0.19	upregulate stage
	452524	AW136499	Hs.29796	Homo sapiens mRNA; cDNA DKFZp434D1319 (f	1	0.46	upregulate stage
	452531	AA429462	Hs.293946	ESTs	2.94	0.22	upregulate stage
15	452547	AA335295	Hs.74120	adipose specific 2	1.51	0.53	upregulate stage
	452560	BE077084		gb:RC5-BT0603-220200-013-C07 BT0603 Homo	5.35	0.11	upregulate stage
	452571	W31518	Hs.34665	ESTs	2.55	0.11	upregulate stage
	452607	AI160029	Hs.61438	ESTs	4.75	0.11	upregulate stage
	452677	BE167202	Hs.212065	ESTs	1	0.32	upregulate stage
20	452680	AW138410	Hs.45051	ESTs	1	1	upregulate stage
	452724	R84810	Hs.30464	cyclin E2	1	0.27	upregulate stage
	452738	AL133800		gb:DKFZp761A0614_r1 761 (synonym: hamy2)	3.45	0.15	upregulate stage
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ111344 fis, clone PL	3.05	0.16	upregulate stage
	452747	BE153585	Hs.61460	ESTs	2.54	0.28	upregulate stage
25	452761	BE244742	Hs.30532	CGI-77 protein	3.85	0.14	upregulate stage
	452825	AI921523		gb:wo26d09.x1 NCI_CGAP_Gas4 Homo sapiens	1	1	upregulate stage
	452831	AW864089	Hs.135145	ESTs	2.4	0.19	upregulate stage
	452846	AA082160	Hs.204295	ESTs	8.9	0.08	upregulate stage
	452850	H23230	Hs.22481	ESTs	4.75	0.14	upregulate stage
30	452859	AI300555	Hs.288158	Homo sapiens cDNA: FLJ23591 fis, clone L	9.15	0.08	upregulate stage
	452862	AW378065	Hs.8687	ESTs	5.95	0.07	upregulate stage
	452899	M96739	Hs.30956	Human NSCL-1 mRNA sequence	1.04	0.9	upregulate stage
	452902	AI926501	Hs.249729	ESTs	6.8	0.1	upregulate stage
	452909	NM_015368	Hs.30985	pannexin 1	5.6	0.1	upregulate stage
35	452931	AW190011	Hs.158006	hypothetical protein	1	0.53	upregulate stage
	452934	AA581322	Hs.4213	ESTs	1.44	0.55	upregulate stage
	452956	AW003578	Hs.231872	ESTs	1	0.22	upregulate stage
	452974	BE090803	Hs.61506	ESTs	1.75	0.18	upregulate stage
	453011	N62952	Hs.46473	ESTs	1	1	upregulate stage
40	453050	AW136479	Hs.224046	ESTs	1	0.39	upregulate stage
	453074	AA031813	Hs.271880	ESTs	1	1	upregulate stage
	453076	AI978583	Hs.232161	ESTs	3.75	0.14	upregulate stage
	453123	AI953718	Hs.221849	ESTs	6.6	0.11	upregulate stage
	453134	AA032211	Hs.118493	ESTs	1.68	0.42	upregulate stage
45	453135	T07866	Hs.31834	Homo sapiens clone 25129 mRNA sequence	1	1	upregulate stage
	453137	AI954733	Hs.223640	ESTs	1	0.51	upregulate stage
	453144	AW268807	Hs.61646	ESTs	1	0.26	upregulate stage
	453153	N53893	Hs.24360	ESTs	5	0.13	upregulate stage
	453156	BE463762	Hs.223784	ESTs	2.8	0.15	upregulate stage
50	453204	R10799	Hs.191990	ESTs	9.5	0.05	upregulate stage
	453228	AW628325	Hs.232327	ESTs	1	1	upregulate stage
	453274	AA018511	Hs.32769	Homo sapiens mRNA full length insert cDN	1	1	upregulate stage
	453293	AA382267	Hs.10653	ESTs	8.4	0.09	upregulate stage
	453321	AI984381	Hs.232521	ESTs	6.7	0.1	upregulate stage
55	453329	T97205	Hs.17998	ESTs	8.9	0.08	upregulate stage
	453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal kl	1	0.18	upregulate stage
	453437	H10751	Hs.79981	Human clone 23560 mRNA sequence	1	0.83	upregulate stage
	453450	AW797627	Hs.89474	ADP-ribosylation factor 6	7.09	0.08	upregulate stage
	453459	BE047032	Hs.257789	ESTs	2.35	0.3	upregulate stage
60	453476	AI640500	Hs.24633	SAM domain, SH3 domain and nuclear local	2.75	0.16	upregulate stage
	453651	AA971898	Hs.159397	x 010 protein	8.95	0.08	upregulate stage
	453653	AW505554	Hs.300284	ESTs	4.6	0.1	upregulate stage
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.4	0.1	upregulate stage
	453776	R15749	Hs.31677	ESTs	1	1	upregulate stage
65	453846	AL157586		gb:DKFZp761H0216_r1 761 (synonym: hamy2)	1	0.95	upregulate stage
	453884	AA355925	Hs.36232	KIAA0186 gene product	10.25	0.06	upregulate stage
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.75	0.12	upregulate stage
	453913	AW004683	Hs.233502	ESTs	3.65	0.14	upregulate stage
	453925	AW021088	Hs.181614	ESTs	3.7	0.13	upregulate stage
70	453931	AL121278	Hs.25144	ESTs	3.45	0.18	upregulate stage
	453945	NM_005171	Hs.36908	activating transcription factor 1	6.35	0.12	upregulate stage
	454032	W31790	Hs.194293	ESTs	6.15	0.07	upregulate stage
	454049	AW022885		gb:df45e05.y1 Morton Fetal Cochlea Homo	2.8	0.15	upregulate stage
	454069	AW025160	Hs.34161	ESTs, Moderately similar to ALU1_HUMAN A	1	0.32	upregulate stage
75	454099	AW062974		gb:IL1-ST0041-020899-001-H08 ST0041 Homo	1	1	upregulate stage
	454111	AW081681	Hs.269064	ESTs	2.8	0.18	upregulate stage
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	9.4	0.05	upregulate stage
	454259	AL110136	Hs.47679	Homo sapiens mRNA; cDNA DKFZp564I112 (fr	6.2	0.11	upregulate stage
	454327	BE064097		gb:QV3-BT0297-231199-020-h08 BT0297 Homo	1	1	upregulate stage
	454331	AW372937		gb:QV3-BT0381-161299-042-a09 BT0381 Homo	1	0.43	upregulate stage
	454360	AW858722		gb:RC3-CT0347-281199-011-c04 CT0347 Homo	1	0.29	upregulate stage

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5	454524	AW857191	gb:RC2-CT0304-080100-011-b12 CT0304 Homo	10.55	0.08	upregulate stage
	454592	AW810112	gb:MR4-ST0124-100400-006-e07 ST0124 Homo	1	0.37	upregulate stage
	454648	AW811960	gb:RC2-ST0168-240300-017-f09 ST0168 Homo	1	0.4	upregulate stage
	454687	AW814473	gb:MR3-ST0203-010200-109-c11 ST0203 Homo	1	1	upregulate stage
	454692	AW813350	gb:MR3-ST0192-100100-024-g07 ST0192 Homo	4.45	0.14	upregulate stage
10	454702	BE146915	gb:MR0-HT0208-221299-204-h08 HT0208 Homo	9.65	0.08	upregulate stage
	454729	AW817003	gb:QV0-ST0247-040100-081-f03 ST0247 Homo	1	0.8	upregulate stage
	454789	BE156314	gb:QV0-HT0367-150200-114-d02 HT0367 Homo	1	0.31	upregulate stage
	454797	BE161168	gb:PM0-HT0425-170100-002-a10 HT0425 Homo	4.1	0.14	upregulate stage
	454863	AW835610	gb:QV4-LT0016-090200-100-c02 LT0016 Homo	1	1	upregulate stage
15	454893	AW837753	gb:CM1-LT0042-310100-112-g03 LT0042 Homo	4.45	0.18	upregulate stage
	454898	AW838125	gb:QV2-LT0051-240300-097-e12 LT0051 Homo	1	1	upregulate stage
	454951	AW847464	gb:RC3-CT0208-270999-021-h12 CT0208 Homo	7.4	0.1	upregulate stage
	454956	AW847725	gb:IL3-CT0213-180200-041-H10 CT0213 Homo	1	0.23	upregulate stage
	455047	AW852530	gb:PM1-CT0243-071099-001-g06 CT0243 Homo	4.25	0.13	upregulate stage
20	455128	AW861555	gb:RC2-CT0321-110100-013-b05 CT0321 Homo	2.9	0.13	upregulate stage
	455201	AW947884	gb:PM1-MT0010-200300-001-g08 MT0010 Homo	3.15	0.16	upregulate stage
	455207	AW994394	gb:RC3-BN0036-060400-014-h12 BN0036 Homo	1	0.18	upregulate stage
	455331	AW897292	gb:CM0-NN0057-150400-338-b02 NN0057 Homo	1	0.67	upregulate stage
	455351	AW901942	gb:QV0-NN1022-100400-190-b04 NN1022 Homo	1	0.39	upregulate stage
25	455380	BE160188	gb:QV1-HT0413-010200-059-g05 HT0413 Homo	1.96	0.33	upregulate stage
	455414	AW936969	gb:RC1-DT0029-160200-013-f10 DT0029 Homo	1	1	upregulate stage
	455428	AW938204	gb:QV0-DT0048-170200-124-f01 DT0048 Homo	1	0.67	upregulate stage
	455573	BE004988	gb:MR2-BN0114-100500-020-b04 BN0114 Homo	1	1	upregulate stage
	455586	BE070794	gb:RC3-BT0501-130100-011-h02 BT0501 Homo	1	1	upregulate stage
30	455595	BE008343	gb:CM0-BN0154-080400-325-g10 BN0154 Homo	1	1	upregulate stage
	455610	BE011703	gb:CM3-BN0223-100500-177-h09 BN0223 Homo	6.05	0.12	upregulate stage
	455647	BE064415	gb:RC4-BT0311-241199-012-b03 BT0311 Homo	1	1	upregulate stage
	455650	BE064655	gb:RC1-BT0313-301299-012-c09 BT0313 Homo	1	0.67	upregulate stage
	455657	BE065209	gb:RC1-BT0314-310300-015-b12 BT0314 Homo	1.87	0.4	upregulate stage
35	455669	BE065803	gb:RC2-BT0318-241199-011-g02 BT0318 Homo	2.85	0.2	upregulate stage
	455678	BE068007	gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.8	0.18	upregulate stage
	455761	BE080895	gb:QV1-BT0631-280200-084-e01 BT0631 Homo	1	0.48	upregulate stage
	455799	BE169911	Hs.14570 Homo sapiens cDNA: FLJ22530 fls, clone H	5.7	0.11	upregulate stage
	455831	BE144966	gb:RC6-HT0187-201099-031-c04 HT0187 Homo	1	1	upregulate stage
40	455874	BE152283	gb:QV4-HT0316-191199-039-b01 HT0316 Homo	1	0.67	upregulate stage
	455903	BE155185	gb:PM1-HT0350-231299-005-g05 HT0350 Homo	1	0.31	upregulate stage
	455938	BE159432	gb:MR0-HT0407-140200-009-e06 HT0407 Homo	2.4	0.15	upregulate stage
	455950	BE161004	gb:PM0-HT0425-170100-002-h03 HT0425 Homo	1	0.44	upregulate stage
	455951	BE161001	gb:PM0-HT0425-170100-002-f10 HT0425 Homo	1	0.38	upregulate stage
45	455965	BE167014	gb:CM2-HT0502-140200-088-d08 HT0502 Homo	1	1	upregulate stage
	455981	BE177000	gb:RC4-HT0587-070400-015-b07 HT0587 Homo	1	0.57	upregulate stage
	456034	AW450979	gb:U1-H-B13-ala-a-12-0-U1.s1 NCL_CGAP_Su	8.29	0.05	upregulate stage
	456046	R51494	ESTs	3.15	0.17	upregulate stage
	456122	R11813	gb:yyf53a04.r1 Soares infant brain 1N1B H	1.3	0.31	upregulate stage
50	456212	N51636	gb:yyf87b01.s1 Soares_multiple_sclerosis_	4.45	0.14	upregulate stage
	456265	AI968210	ESTs	1	0.34	upregulate stage
	456285	R67585	ESTs	1	0.63	upregulate stage
	456320	AI734064	ESTs	1	1	upregulate stage
	456353	AI042330	ESTs, Weakly similar to similar to YBS4	5.15	0.11	upregulate stage
55	456486	AA676544	HIV-1 Rev binding protein	1	0.27	upregulate stage
	456493	AA261830	gb:zs17g09.r1 NCL_CGAP_GCB1 Homo sapiens	1	0.8	upregulate stage
	456504	AK000532	Homo sapiens cDNA FLJ20525 fls, clone KA	1	0.29	upregulate stage
	456508	AA502764	ESTs, Weakly similar to AF208855 1 BM-01	17.7	0.05	upregulate stage
	456519	AA279917	ESTs, Weakly similar to Unknown [H.sapie	2.3	0.18	upregulate stage
60	456536	AW135986	ESTs	9.45	0.06	upregulate stage
	456592	R91600	gb:yyq10c02.r1 Soares fetal liver spleen	4.5	0.14	upregulate stage
	456621	T35958	DKFZP564I1171 protein	1	0.2	upregulate stage
	456682	AW500321	Homo sapiens cDNA FLJ12360 fls, clone MA	1	0.24	upregulate stage
	456726	H43102	ESTs	1	0.69	upregulate stage
65	456736	AW248217	achaete-scute complex (Drosophila) homol	0.89	0.91	upregulate stage
	456786	AK002084	hypothetical protein FLJ11222	3.2	0.13	upregulate stage
	456800	AL118754	gb:DKFZp761P1910_r1 761 (synonym: hamy2)	1	0.69	upregulate stage
	456823	AL161979	Homo sapiens mRNA: cDNA DKFZp761G1823 (f	8.95	0.07	upregulate stage
	456844	AI264155	CDP-diacylglycerol synthase (phosphatida	5.55	0.1	upregulate stage
70	456999	AA319798	eukaryotic translation elongation factor	11.3	0.07	upregulate stage
	457015	AA688058	ESTs	9.25	0.08	upregulate stage
	457030	AI301740	cytiadipyrimidinase-like 2	2.65	0.17	upregulate stage
	457158	AA135370	Homo sapiens cDNA: FLJ21635 fls, clone C	1	1	upregulate stage
	457190	AI753247	Homo sapiens cDNA FLJ13103 fls, clone NT	1	0.87	upregulate stage
75	457309	AF131843	Homo sapiens clone 24987 mRNA sequence	2.6	0.15	upregulate stage
	457376	AI026984	ESTs	1	1	upregulate stage
	457402	AW452648	activation-induced cytidine deaminase	2.9	0.16	upregulate stage
	457435	AW972024	ESTs, Weakly similar to tyrosine kinase	1	0.36	upregulate stage
	457437	AW369732	gb:EST381810 MAGE resequences, MAGK Homo	2.5	0.14	upregulate stage
	457465	AW301344	ESTs	6.3	0.1	upregulate stage
	457467	AW974815	ESTs	1	1	upregulate stage

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5	457474	AW972935		gb:EST385031 MAGE resequences, MAGM Homo	1	0.29	upregulate stage
	457530	AW973713	Hs.293596	ESTs	1	0.39	upregulate stage
	457637	AI288373	Hs.149875	ESTs	1	1	upregulate stage
	457643	AI375499	Hs.27379	ESTs	3.25	0.19	upregulate stage
	457650	AA649162	Hs.236456	ESTs	8.9	0.08	upregulate stage
10	457661	AA917801	Hs.128596	ESTs	0.96	0.9	upregulate stage
	457692	AA744046	Hs.133350	ESTs	1	1	upregulate stage
	457857	AW814892	Hs.273104	ESTs	1	1	upregulate stage
	457892	AA744389		gb:nys1e10.s1 NCL_CGAP_Pr18 Homo sapiens	8.7	0.06	upregulate stage
	457902	AI624876	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.2	0.21	upregulate stage
15	457943	AA765625	Hs.155690	ESTs	3.55	0.1	upregulate stage
	457948	AI498640	Hs.159354	ESTs	2.65	0.19	upregulate stage
	457964	NM_016353	Hs.5943	rec	1.5	0.17	upregulate stage
	458004	AW976942	Hs.153057	ESTs	1	0.87	upregulate stage
	458027	L49054	Hs.85195	ESTs, Highly similar to t(3;5)(q25.1;p34	3.45	0.12	upregulate stage
20	458079	AI796870	Hs.54277	ESTs	11.5	0.05	upregulate stage
	458158	AW296778	Hs.300357	ESTs, Highly similar to dJ416F21.2 [H.s	1	1	upregulate stage
	458171	AI420016	Hs.192090	ESTs	0.69	1.09	upregulate stage
	458172	BE007237		gb:PM0-BN0139-050500-003-g09 BN0139 Homo	3	0.16	upregulate stage
	458186	AA904244	Hs.153205	ESTs	4.6	0.15	upregulate stage
25	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	3.1	0.16	upregulate stage
	458270	T66139	Hs.113631	ESTs	1	0.67	upregulate stage
	458282	AA984075	Hs.122580	alkylglycerone phosphate synthase	1	1	upregulate stage
	458287	AA987556	Hs.12867	ESTs	5.05	0.13	upregulate stage
	458580	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	1	0.28	upregulate stage
30	458586	AI683479	Hs.653390	ESTs	8.2	0.07	upregulate stage
	458608	AW444662	Hs.202247	ESTs	1	0.27	upregulate stage
	458632	AI744445	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT	1.05	0.23	upregulate stage
	458663	AV658444	Hs.280776	Homo sapiens cDNA FLJ13684 fis, clone PL	5.05	0.13	upregulate stage
	458670	AI301987	Hs.233398	ESTs	8.9	0.08	upregulate stage
35	458680	N73773	Hs.282950	ESTs	1	0.23	upregulate stage
	458720	AV662037	Hs.124740	ESTs	1	0.3	upregulate stage
	458722	AA741545	Hs.282832	ESTs	3.2	0.11	upregulate stage
	458747	BE618395	Hs.257391	ESTs, Weakly similar to GTPase-activatin	3.3	0.14	upregulate stage
	458760	AI498631	Hs.111334	ferritin, light polypeptide	11	0.07	upregulate stage
40	458781	AI444821		gb:RET4B7 subtracted retina cDNA library	6.05	0.12	upregulate stage
	458801	N98648	Hs.276860	ESTs	4.45	0.13	upregulate stage
	458880	AA046742		gb:z48c09.r1 Soares retina N2b4HR Homo	9	0.08	upregulate stage
	458886	AI247487	Hs.103277	ESTs	1	0.3	upregulate stage
	458946	AA009716	Hs.42311	ESTs	8.7	0.08	upregulate stage
45	459023	AW968226	Hs.60798	ESTs	2.95	0.15	upregulate stage
	459028	AI940577		gb:IL5-HT0009-120799-001-G07 HT0009 Homo	2.6	0.17	upregulate stage
	459030	H86658	Hs.107699	ESTs, Weakly similar to hypothetical pro	1	1	upregulate stage
	459058	H85939	Hs.209605	ESTs	1	1	upregulate stage
	459128	AI902169		gb:IL-BT002-221198-051 BT002 Homo sapien	1	0.26	upregulate stage
50	459182	BE178517		gb:PM1-HT0603-090300-001-e09 HT0603 Homo	1	1	upregulate stage
	459204	AW194601	Hs.13219	ESTs	2.85	0.16	upregulate stage
	459256	AW967468	Hs.99821	Homo sapiens mRNA; cDNA DKFZ5664C046 (fr	10.65	0.07	upregulate stage
	459319	NM_000059		gb:Homo sapiens breast cancer 2, early o	1	1	upregulate stage
	459395	Z30300	Hs.281935	ESTs	4.05	0.14	upregulate stage
55	459459	AA460445		gb:zx66h11.r1 Soares_total_fetus_Nb2HF8_	4.8	0.13	upregulate stage
	459464	AA854847		gb:aj77h02.s1 Soares_parathyroid_tumor_N	1	0.38	upregulate stage
	459492	AL118619		gb:DKFZp761E2410_r1 761 (synonym: hamy2)	1	1	upregulate stage
	459530	AW770811		gb:h49d07.x1 NCL_CGAP_Co17 Homo sapiens	1	1	upregulate stage
	401519				12.65	0.06	upregulate stage
60	402474				25.55	0.03	upregulate stage
	402727				16.25	0.05	upregulate stage
	405411				12.95	0.05	upregulate stage
	406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	14.42	0.03	upregulate stage
	406685	M18728		gb:Human nonspecific crossreacting antig	15.75	0.03	upregulate stage
65	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	16.3	0.04	upregulate stage
	407242	M18728		gb:Human nonspecific crossreacting antig	12.56	0.03	upregulate stage
	407347	AA829847	Hs.167347	ESTs, Weakly similar to ALU8_HUMAN ALU S	12.91	0.06	upregulate stage
	407796	AA195509	Hs.272239	lymphocyte activation-associated protein	14.2	0.06	upregulate stage
	408243	Y00787	Hs.624	interleukin 8	18.52	0.02	upregulate stage
70	408380	AF123050	Hs.44532	diubiquitin	16	0.03	upregulate stage
	408618	AK000637	Hs.46624	HSPC043 protein	12.6	0.06	upregulate stage
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	15.5	0.03	upregulate stage
	409417	AA156247	Hs.295908	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.55	0.04	upregulate stage
	410315	AI638871	Hs.17625	ESTs	14	0.05	upregulate stage
75	410324	AW292539	Hs.30177	ESTs	15.55	0.05	upregulate stage
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	12.6	0.05	upregulate stage
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	16.45	0.03	upregulate stage
	413281	AA851271	Hs.34396	ESTs	12.95	0.04	upregulate stage
	414004	AA737033	Hs.7155	ESTs, Weakly similar to 2115357A TYK1 pr	15.25	0.04	upregulate stage
	414161	AA136106	Hs.184852	KIAA1553 protein	13.25	0.06	upregulate stage
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	12.5	0.05	upregulate stage

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	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	12.71	0.05	upregulate stage
	414493	AL133921	Hs.76272	retinoblastoma-binding protein 2	13.05	0.05	upregulate stage
	414522	AW518944	Hs.76325	Homo sapiens cDNA: FLJ23125 fis, clone L	30.45	0.02	upregulate stage
5	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	29	0.02	upregulate stage
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	13.2	0.05	upregulate stage
	416114	AI695549	Hs.183868	glucuronidase, beta	14.7	0.04	upregulate stage
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	13	0.06	upregulate stage
	416391	AI878927	Hs.79284	mesoderm specific transcript (mcuse) hom	13.3	0.04	upregulate stage
10	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	15.55	0.04	upregulate stage
	416980	AA381133	Hs.80684	high-mobility group (nonhistone chromoso	23.85	0.03	upregulate stage
	417258	N58885	Hs.294040	ESTs	15.05	0.06	upregulate stage
	417274	N92036	Hs.81848	RAD21 (S. pombe) homolog	23.05	0.04	upregulate stage
	417353	AA375752	Hs.76362	general transcription factor IIA, 2 (12k	13	0.06	upregulate stage
15	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	19.45	0.04	upregulate stage
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	12.45	0.03	upregulate stage
	417777	AI623763	Hs.72055	ESTs	12.6	0.06	upregulate stage
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	20.8	0.04	upregulate stage
	417928	AA209344	Hs.282973	ESTs	14.65	0.05	upregulate stage
20	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	13	0.05	upregulate stage
	418791	AA935633	Hs.194628	ESTs	12.95	0.06	upregulate stage
	419145	N99638		gb:za39g11.11 Soares fetal liver spleen	13.2	0.05	upregulate stage
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	12.6	0.05	upregulate stage
	422150	AI867118	Hs.2953	ribosomal protein S15a	13.55	0.05	upregulate stage
25	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	15.7	0.05	upregulate stage
	424673	AA345051	Hs.294092	ESTs	16.9	0.04	upregulate stage
	424848	AI263231	Hs.145607	ESTs	15.2	0.05	upregulate stage
	424865	AF011333	Hs.153563	lymphocyte antigen 75	12.85	0.04	upregulate stage
	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homolog	13.25	0.06	upregulate stage
30	425787	AA363867	Hs.155029	ESTs	17.55	0.05	upregulate stage
	426252	BE176980	Hs.28917	ESTs	12.95	0.05	upregulate stage
	426329	AL389951	Hs.271623	nucleoporin 50kD	13.8	0.05	upregulate stage
	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	13.85	0.05	upregulate stage
	427351	AW402593	Hs.123253	Homo sapiens cDNA: FLJ22009 fis, clone H	12.8	0.06	upregulate stage
35	427979	BE379776	Hs.181309	proteasome (prosome, macropain) subunit,	16.95	0.05	upregulate stage
	428044	AA093322	Hs.182225	RNA binding motif protein 3	14.65	0.05	upregulate stage
	428428	AL037544	Hs.194298	cyclin-dependent kinase 7 (homolog of Xe	17.15	0.05	upregulate stage
	428840	M15990	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene	16.8	0.05	upregulate stage
	430191	AI149880	Hs.188809	ESTs	14.5	0.05	upregulate stage
40	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	14.9	0.05	upregulate stage
	430853	AI734179	Hs.105676	ESTs	13.55	0.06	upregulate stage
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	16.2	0.04	upregulate stage
	431211	M86849	Hs.5566	gap junction protein, beta 2, 26kD (conn	27	0.01	upregulate stage
	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	13.45	0.06	upregulate stage
45	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	21.2	0.03	upregulate stage
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	13.05	0.06	upregulate stage
	431863	AA188185	Hs.271871	spindlin	15.6	0.05	upregulate stage
	434263	N34895	Hs.44648	ESTs	14.25	0.05	upregulate stage
	434651	BE616902	Hs.285313	core promoter element binding protein	17.95	0.05	upregulate stage
50	436286	AA804442	Hs.3459	Homo sapiens cDNA: FLJ22003 fis, clone H	14.95	0.05	upregulate stage
	436385	BE551618	Hs.144097	ESTs	13.85	0.06	upregulate stage
	437192	AW975786	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	12.75	0.06	upregulate stage
	438000	AI825880	Hs.5985	non-kinase Cdc42 effector protein SPEC2	15.3	0.04	upregulate stage
	439941	AI392640	Hs.18272	ESTs	17.42	0.05	upregulate stage
55	440086	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom	12.59	0.05	upregulate stage
	440116	AI798851	Hs.9403	ESTs	14.5	0.05	upregulate stage
	441020	W79283	Hs.35962	ESTs	12.4	0.04	upregulate stage
	441633	AW958544	Hs.112242	ESTs	15.85	0.03	upregulate stage
	441980	AK001441	Hs.8055	hypothetical protein FLJ10579	13.6	0.05	upregulate stage
60	442043	BE597620	Hs.99210	ESTs	12.5	0.06	upregulate stage
	442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	12.65	0.06	upregulate stage
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	15.15	0.05	upregulate stage
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	13.4	0.05	upregulate stage
	445033	AV652402	Hs.155145	ESTs	13.3	0.05	upregulate stage
65	446619	AU076943	Hs.313	secreted phosphoprotein 1 (osteopontin,	30.5	0.02	upregulate stage
	446847	T51454	Hs.82845	Human clone 23815 mRNA sequence	13.8	0.04	upregulate stage
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	15.15	0.04	upregulate stage
	448712	W01046	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L	13.2	0.05	upregulate stage
	448772	AW390822	Hs.24639	ESTs	12.75	0.06	upregulate stage
	448926	AI798154	Hs.140903	ESTs, Moderately similar to neuronal thr	13.35	0.06	upregulate stage
70	449962	AA004879	Hs.187820	ESTs	12.79	0.05	upregulate stage
	450139	AK001838	Hs.296323	Homo sapiens cDNA FLJ10976 fis, clone PL	14.76	0.06	upregulate stage
	451035	AU076785	Hs.430	plastin 1 (isoform)	17.65	0.04	upregulate stage
	451334	AI122691	Hs.13268	ESTs	14.7	0.05	upregulate stage
75	452567	D87120	Hs.29382	predicted osteoblast protein	12.45	0.06	upregulate stage
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	13.4	0.05	upregulate stage
	453331	AI240665	Hs.8895	ESTs	12.6	0.05	upregulate stage
	400365	Y10259	Hs.274501	H.sapiens ACTH receptor mRNA 3'UTR	2.2	0.17	upregulate stage

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	401256			2	0.16	upregulate stage
	402075			1	0.1	upregulate stage
	403029			1.75	0.16	upregulate stage
	403047			3.3	0.1	upregulate stage
5	403426			1.7	0.18	upregulate stage
	403754			2.8	0.12	upregulate stage
	403822			1.2	0.14	upregulate stage
	407835	AK002081	Hs.40337	1.9	0.15	upregulate stage
	407980	AA046309		1.35	0.1	upregulate stage
10	408081	AW451597	Hs.167409	2.3	0.18	upregulate stage
	408408	AF070571	Hs.44690	1.65	0.12	upregulate stage
	408920	AL120071	Hs.48998	1	0.2	upregulate stage
	409810	AW500895		2.25	0.2	upregulate stage
15	410094	BE147897	Hs.58593	4.05	0.12	upregulate stage
	410603	AA086219	Hs.68714	1.9	0.18	upregulate stage
	410763	AF279145	Hs.8966	4.15	0.13	upregulate stage
	411418	BE241870		1.6	0.22	upregulate stage
	411691	AW857199		1.45	0.24	upregulate stage
	411750	BE562298	Hs.71827	2.2	0.2	upregulate stage
20	411880	AW872477		1.75	0.06	upregulate stage
	412102	H56435	Hs.75935	1.7	0.2	upregulate stage
	412303	AW936336		1	0.17	upregulate stage
	412312	AW936686		3.4	0.16	upregulate stage
	412598	AI681997	Hs.107057	2.25	0.2	upregulate stage
25	413383	AA128978	Hs.154706	2.3	0.17	upregulate stage
	413406	AW452823	Hs.135268	3.52	0.14	upregulate stage
	413618	BE154078		1	0.18	upregulate stage
	416661	AA634543	Hs.79440	1.05	0.12	upregulate stage
	417708	N74392	Hs.50495	2	0.16	upregulate stage
30	417974	AA210765		1.7	0.18	upregulate stage
	418604	AA225632	Hs.190016	3.75	0.13	upregulate stage
	418631	AA225921	Hs.115105	1.75	0.2	upregulate stage
	418830	BE513731	Hs.88959	3.8	0.09	upregulate stage
	418893	N32264	Hs.44330	2.35	0.14	upregulate stage
35	418950	T78517	Hs.13941	2.15	0.19	upregulate stage
	419044	AI799135	Hs.87164	1.85	0.15	upregulate stage
	420082	N43741	Hs.203148	3.8	0.14	upregulate stage
	420653	AI224532	Hs.88550	2.05	0.16	upregulate stage
40	421112	AW243875	Hs.265427	3.3	0.13	upregulate stage
	421683	AI147535	Hs.143769	2	0.14	upregulate stage
	421799	AW972292	Hs.292998	2.35	0.15	upregulate stage
	422177	AA720878	Hs.201375	3.3	0.14	upregulate stage
	422429	AA310527		3.45	0.12	upregulate stage
45	422956	BE545072	Hs.122579	2.15	0.11	upregulate stage
	424026	AI798295	Hs.124218	3.8	0.14	upregulate stage
	425650	NM_001944	Hs.1925	1	0.09	upregulate stage
	425761	AW664214	Hs.196729	2	0.19	upregulate stage
	426427	M86699	Hs.169840	2.1	0.16	upregulate stage
50	427558	D49493	Hs.2171	2.15	0.14	upregulate stage
	427635	BE397988	Hs.179982	3.9	0.11	upregulate stage
	428766	AA477969	Hs.98800	3.8	0.12	upregulate stage
	429761	AI276780	Hs.135173	1.9	0.17	upregulate stage
	430132	AA204686	Hs.234149	5.05	0.11	upregulate stage
55	430253	AK001514	Hs.236844	3.55	0.15	upregulate stage
	430388	AA356923	Hs.240770	2.5	0.14	upregulate stage
	431187	AW971146	Hs.293187	3.95	0.13	upregulate stage
	431364	AW971382	Hs.294016	1.8	0.15	upregulate stage
	431401	AA504626	Hs.105735	1.65	0.22	upregulate stage
60	431419	AL041844	Hs.277522	1.45	0.16	upregulate stage
	432361	AI378562	Hs.159585	2.15	0.14	upregulate stage
	432810	AA863400	Hs.23054	3.7	0.08	upregulate stage
	432926	AA570416	Hs.32271	2	0.2	upregulate stage
	433108	AB002446		2.35	0.14	upregulate stage
65	434153	AF118072	Hs.283916	1	0.14	upregulate stage
	435202	AI971313	Hs.170204	1.25	0.16	upregulate stage
	435313	AI769400	Hs.189729	2	0.18	upregulate stage
	435359	T60843	Hs.189679	3.6	0.11	upregulate stage
	435488	H57954	Hs.34394	2.2	0.22	upregulate stage
70	436583	AW293909	Hs.156935	1.4	0.19	upregulate stage
	436862	AI821940	Hs.264622	3.2	0.12	upregulate stage
	437485	AI149570	Hs.127363	2.05	0.22	upregulate stage
	437854	AL119723		2.75	0.15	upregulate stage
	438316	AA789249		2.45	0.13	upregulate stage
	438390	AI422017		3.1	0.13	upregulate stage
75	438915	AA280174	Hs.23282	1.35	0.12	upregulate stage
	439983	AA858394	Hs.117955	4	0.13	upregulate stage
	442048	AA974603		5.55	0.09	upregulate stage

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	442369	AI565071	Hs.159983	ESTs	3.85	0.14	upregulate stage
	442748	AI016713	Hs.135787	ESTs	2.35	0.23	upregulate stage
	443717	BE163884	Hs.282331	ESTs	2.5	0.18	upregulate stage
5	445935	AA287537	Hs.167585	ESTs	1	0.2	upregulate stage
	446078	AI339982	Hs.156061	ESTs	2.25	0.24	upregulate stage
	446139	H77395	Hs.39749	ESTs	2.15	0.18	upregulate stage
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	3.45	0.14	upregulate stage
	448253	H25899	Hs.201591	ESTs	1.65	0.18	upregulate stage
10	448956	AK001674	Hs.22630	cofactor required for Sp1 transcriptiona	2.2	0.14	upregulate stage
	449199	AI990122	Hs.196988	ESTs	1.25	0.23	upregulate stage
	449558	AA001765	Hs.157079	KIAA1227 protein	1	0.16	upregulate stage
	449576	AW014631	Hs.225068	ESTs	2.3	0.19	upregulate stage
	449859	T98077	Hs.18214	ESTs	6.3	0.07	upregulate stage
15	450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS [C.e	1.65	0.22	upregulate stage
	450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	1.35	0.19	upregulate stage
	451337	AI400209	Hs.60787	ESTs	1.6	0.16	upregulate stage
	451686	AA059246	Hs.110293	ESTs	3.4	0.14	upregulate stage
	452079	AA830908	Hs.15825	ESTs	1.9	0.23	upregulate stage
20	452220	BE158006	Hs.212296	ESTs	3.1	0.17	upregulate stage
	453918	AW005123	Hs.231975	ESTs	1	0.21	upregulate stage
	455350	AW901809		gb:QV0-NN1020-170400-195-h02 NN1020 Homo	2	0.2	upregulate stage
	456511	AA282330	Hs.145668	ESTs	1.15	0.12	upregulate stage
	456986	D38299	Hs.170917	prostaglandin E receptor 3 (subtype EP3)	1.65	0.18	upregulate stage
25	457427	AW971287		gb:EST383376 MAGE resequences, MAGL Homo	2.35	0.16	upregulate stage
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1	0.27	upregulate stage
	400409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	2.33	0.2	upregulate stage
	400471				7.45	0.09	upregulate stage
	400641				0.71	0.31	upregulate stage
30	400749				7.25	0.1	upregulate stage
	400751				5.35	0.09	upregulate stage
	400761				5.9	0.1	upregulate stage
	400843				5.85	0.07	upregulate stage
	401045				2.42	0.17	upregulate stage
35	401049				1.2	0.19	upregulate stage
	401192				2.47	0.3	upregulate stage
	401203				6.73	0.08	upregulate stage
	401205				6.63	0.1	upregulate stage
	401276				6.95	0.1	upregulate stage
40	401561				2.2	0.13	upregulate stage
	401604				1	0.19	upregulate stage
	402245				7.65	0.09	upregulate stage
	402296				1	0.33	upregulate stage
	402530				5.1	0.13	upregulate stage
45	402812				1.65	0.17	upregulate stage
	402820				1	0.34	upregulate stage
	402892				1	1	upregulate stage
	403344				6.5	0.08	upregulate stage
	404156				3.7	0.11	upregulate stage
50	404290				4.45	0.09	upregulate stage
	404538				8.38	0.09	upregulate stage
	404676				8.3	0.09	upregulate stage
	404977				0.9	0.35	upregulate stage
	405033				1.52	0.31	upregulate stage
55	405109	N47812	Hs.81380	CGI-35 protein	6.2	0.1	upregulate stage
	405654				1.95	0.06	upregulate stage
	406081				3	0.07	upregulate stage
	406270				6.09	0.13	upregulate stage
	406399				1.55	0.41	upregulate stage
60	406475				6.2	0.12	upregulate stage
	406485				1	0.48	upregulate stage
	406741	AA058357	Hs.74486	carcinoembryonic antigen-related cell ad	5.4	0.07	upregulate stage
	406867	AA157857	Hs.182265	keratin 19	2.26	0.37	upregulate stage
65	407173	T64349		gb:yc10d08.s1 Stratagene lung (937210) H	3.35	0.11	upregulate stage
	407230	AA157857	Hs.182265	keratin 19	2.15	0.38	upregulate stage
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	2.1	0.09	upregulate stage
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.25	0.11	upregulate stage
	407825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	6.25	0.08	upregulate stage
	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	4.5	0.12	upregulate stage
70	407877	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	3.3	0.15	upregulate stage
	407968	NM_004863	Hs.59403	serine palmitoyltransferase, long chain	7.35	0.1	upregulate stage
	408162	AA993833	Hs.118527	ESTs	6.2	0.09	upregulate stage
	408363	NM_003389	Hs.44396	coronin, actin-binding protein, 2A	5.36	0.14	upregulate stage
	408576	NM_003542	Hs.46423	H4 histone family, member G	7.28	0.1	upregulate stage
75	408673	BE208517	Hs.184109	ribosomal protein L37a	2.53	0.24	upregulate stage
	408684	R61377	Hs.12727	hypothetical protein FLJ21610	1	0.3	upregulate stage
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	7.7	0.06	upregulate stage
	409592	BE280951	Hs.55058	.EH-domain containing 4	3.95	0.1	upregulate stage

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	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	1.55	0.16	upregulate stage
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	4.1	0.18	upregulate stage
	410232	AW372451	Hs.61184	CGI-79 protein	3.65	0.14	upregulate stage
5	410269	AW613697		gb:hh79g12.x1 NCL_CGAP_GU1 Homo sapiens	7.55	0.09	upregulate stage
	410297	AA148710	Hs.159441	ESTs	3.8	0.1	upregulate stage
	410337	M83822	Hs.62354	cell division cycle 4-like	4.35	0.19	upregulate stage
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.42	0.4	upregulate stage
	410541	AA065003	Hs.64179	hypothetical protein	1.61	0.48	upregulate stage
10	410724	AW799269		gb:RC0-UM0051-210300-012-f01 UM0051 Homo	6.65	0.12	upregulate stage
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	1.4	0.16	upregulate stage
	410968	AA199907	Hs.67397	homeo box A1	3.05	0.1	upregulate stage
	411162	AW819944		gb:QV0-ST0294-240300-172-e03 ST0294 Homo	2	0.23	upregulate stage
	411173	R81571		gb:yj02h10.r1 Soares placenta Nb2HP Homo	7.2	0.1	upregulate stage
15	411243	AB039886	Hs.69319	CA11	0.36	0.93	upregulate stage
	411407	R09093		gb:y87a07.r1 Soares fetal liver spleen	8	0.09	upregulate stage
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	1.75	0.22	upregulate stage
	412121	AB033061	Hs.73287	KIAA1235 protein	5.3	0.11	upregulate stage
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	6.9	0.1	upregulate stage
20	412129	M21984	Hs.73454	troponin T3, skeletal, fast	0.27	1.06	upregulate stage
	412354	AW939148		gb:QV1-DT0069-110200-067-d05 DT0069 Homo	6.9	0.11	upregulate stage
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.88	0.21	upregulate stage
	412700	BE222433	Hs.201262	ESTs	2.85	0.15	upregulate stage
	412706	R97106	Hs.167546	ESTs	3.75	0.16	upregulate stage
25	412935	BE287045	Hs.75064	tubulin-specific chaperone c	7	0.09	upregulate stage
	413402	T24065		gb:seq2245 HMSWMYK Homo sapiens cDNA clo	6.3	0.12	upregulate stage
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	3.45	0.11	upregulate stage
	413445	BE141022		gb:MR0-HT0067-201099-002-d10 HT0067 Homo	3.9	0.13	upregulate stage
	413587	AA156164	Hs.271833	Homo sapiens cDNA FLJ13473 fis, clone PL	7.63	0.09	upregulate stage
30	413800	AI129235		ESTs	3.2	0.18	upregulate stage
	413859	AW992356	Hs.8364	pyruvate dehydrogenase kinase, isoenzyme	2.54	0.33	upregulate stage
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	1.75	0.21	upregulate stage
	413991	H44725	Hs.71300	ESTs	1.3	0.21	upregulate stage
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	8.1	0.07	upregulate stage
35	414203	BE262170		gb:601150419F1 NIH_MGC_19 Homo sapiens c	1.45	0.14	upregulate stage
	414343	AL036166	Hs.75914	coated vesicle membrane protein	1	0.23	upregulate stage
	414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cds	1	0.36	upregulate stage
	414987	AA524394	Hs.165544	ESTs	1.51	0.51	upregulate stage
	414993	AW819403	Hs.77724	KIAA0586 gene product	2.72	0.23	upregulate stage
40	415276	U88666	Hs.78353	SFRS protein kinase 2	6.95	0.1	upregulate stage
	415303	R11813		gb:yf53a04.r1 Soares infant brain 1NIB H	8.1	0.09	upregulate stage
	415392	Z44067		gb:HSC1RF051 normalized infant brain cDN	5.56	0.11	upregulate stage
	415572	F12294		gb:HSC38B051 normalized infant brain cDN	5.7	0.11	upregulate stage
	415773	R21651		gb:yh19g02.r1 Soares placenta Nb2HP Homo	5.3	0.11	upregulate stage
45	416012	AF061959	Hs.78961	protein phosphatase 1, regulatory (inhib	2.19	0.28	upregulate stage
	416074	R40174	Hs.21209	ESTs	7.61	0.11	upregulate stage
	416182	NM_004354	Hs.79069	cyclin G2	1	0.39	upregulate stage
	416518	H60730	Hs.18917	ESTs	6.6	0.1	upregulate stage
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	3.9	0.17	upregulate stage
50	416987	D86957	Hs.80712	KIAA0202 protein	2.54	0.31	upregulate stage
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.26	0.12	upregulate stage
	417275	X63578	Hs.81849	parvalbumin	1	0.12	upregulate stage
	417395	BE564245	Hs.82084	integrin beta 3 binding protein (beta3-e	8.4	0.08	upregulate stage
	417683	AW566008	Hs.239154	Homo sapiens cDNA FLJ12814 fis, clone NT	2.2	0.17	upregulate stage
55	417759	R13567	Hs.12548	ESTs	8.18	0.09	upregulate stage
	417848	AA206581	Hs.39457	ESTs	8.6	0.08	upregulate stage
	417985	AA187545	Hs.83114	crystallin, zeta (quinone reductase)	7	0.11	upregulate stage
	418073	R39789	Hs.119714	EST	6.3	0.11	upregulate stage
60	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	1.63	0.46	upregulate stage
	418406	X73501	Hs.84905	cytokeratin 20	3.5	0.02	upregulate stage
	418555	AI417215	Hs.87159	Homo sapiens cDNA FLJ12577 fis, clone NT	6.75	0.06	upregulate stage
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	4.1	0.11	upregulate stage
	418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	7.5	0.08	upregulate stage
	418827	BE327311	Hs.47166	HT021	5.6	0.13	upregulate stage
65	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	1.5	0.22	upregulate stage
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	2.44	0.29	upregulate stage
	419590	AF005043	Hs.91390	poly (ADP-ribose) glycohydrolase	8.08	0.1	upregulate stage
	419693	AA133749	Hs.92323	FXVD domain-containing ion transport reg	1.64	0.48	upregulate stage
	419712	AA360838	Hs.179909	Homo sapiens cDNA: FLJ22995 fis, clone K	5.4	0.11	upregulate stage
70	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	7.9	0.06	upregulate stage
	419720	AA249131	Hs.143607	hypothetical protein FLJ11068	2.95	0.15	upregulate stage
	419791	AI579909	Hs.105104	ESTs	2.45	0.2	upregulate stage
	419872	AI422951	Hs.146162	ESTs	4.25	0.17	upregulate stage
	419903	T16938	Hs.87902	ESTs	2.5	0.22	upregulate stage
75	419932	AA281594		gb:zl03e01.r1 NCL_CGAP_GCB1 Homo sapiens	6.1	0.12	upregulate stage
	420026	AI831190	Hs.166676	ESTs	3.4	0.14	upregulate stage
	420187	AK001714	Hs.95744	hypothetical protein similar to ankyrin	4.03	0.18	upregulate stage
	420193	AI460060	Hs.202869	ESTs	1	0.28	upregulate stage

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5	420281	AI623693	Hs.191533	ESTs	6.6	0.11	upregulate stage
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	6	0.09	upregulate stage
	420370	Y13645	Hs.97234	uroplakin 2	1.2	0.45	upregulate stage
	420383	T55154	Hs.144880	ESTs	3.8	0.12	upregulate stage
	420450	AW968969	Hs.177726	ESTs	2.75	0.14	upregulate stage
10	420588	AF000982	Hs.147916	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	8.1	0.09	upregulate stage
	420763	AA419392	Hs.178354	ESTs	8	0.09	upregulate stage
	420838	AW118210	Hs.5244	ESTs	8.65	0.07	upregulate stage
	420981	L40904	Hs.100724	peroxisome proliferative activated recep	1.98	0.32	upregulate stage
	421013	M62397	Hs.1345	mutated in colorectal cancers	1	0.29	upregulate stage
15	421072	AI215069	Hs.89113	ESTs	5.8	0.12	upregulate stage
	421110	AJ250717	Hs.1355	cathepsin E	5.45	0.03	upregulate stage
	421141	AW117261	Hs.125914	ESTs	2.75	0.16	upregulate stage
	421338	AA287443		gb:zs52c10.r1 NCL_CGAP_GCB1 Homo sapiens	7.45	0.09	upregulate stage
	421508	NM_004833	Hs.105115	absent in melanoma 2	4.21	0.19	upregulate stage
20	421634	AA437414	Hs.106283	hypothetical protein FLJ10262	7.79	0.08	upregulate stage
	421674	T10707	Hs.296355	neuronal PAS domain protein 2	7.5	0.1	upregulate stage
	421810	AK001718	Hs.108530	hypothetical protein FLJ10856	8.45	0.08	upregulate stage
	421855	F06504	Hs.27384	ESTs	2.9	0.16	upregulate stage
	421898	AA259011	Hs.109268	hypothetical protein FLJ12552	7.06	0.11	upregulate stage
25	422156	N34524	Hs.300893	ESTs, Weakly similar to envelope protein	3.75	0.16	upregulate stage
	422225	BE245652	Hs.118281	zinc finger protein 266	2.95	0.17	upregulate stage
	422243	AW803733	Hs.250655	prothymosin, alpha (gene sequence 28)	8.15	0.08	upregulate stage
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.21	0.17	upregulate stage
	422634	NM_016010	Hs.118821	CGI-82 protein	1.3	0.29	upregulate stage
30	422988	AW673847	Hs.97321	ESTs	4.15	0.11	upregulate stage
	423081	AF262992	Hs.123159	sperm associated antigen 4	2.82	0.3	upregulate stage
	423596	AA328195	Hs.234101	ESTs, Weakly similar to CTL1 protein [H.	2.75	0.19	upregulate stage
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	1.95	0.13	upregulate stage
	423979	AF229181	Hs.136644	CS box-containing WD protein	7.12	0.11	upregulate stage
35	424005	AB033041	Hs.137507	KIAA1215 protein	1.71	0.37	upregulate stage
	424014	AA333653	Hs.24790	KIAA1573 protein	4.85	0.12	upregulate stage
	424028	AF055084	Hs.153692	KIAA0689 protein	8.5	0.07	upregulate stage
	424194	BE245833	Hs.169854	hypothetical protein SP192	6.1	0.1	upregulate stage
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.59	0.11	upregulate stage
40	424550	AI650541	Hs.115298	ESTs	3.25	0.12	upregulate stage
	424631	AA688021	Hs.179808	ESTs	5.45	0.11	upregulate stage
	424659	AW891293	Hs.301877	ESTs, Weakly similar to hSIAH2 [H.sapien	3.55	0.15	upregulate stage
	424704	AI263293	Hs.152096	cytochrome P450, subfamily IIJ (arachido	8.45	0.06	upregulate stage
	424775	AB014540	Hs.153026	SWAP-70 protein	6.65	0.11	upregulate stage
45	424800	AL035588	Hs.153203	MyoD family inhibitor	1.94	0.3	upregulate stage
	425066	M82882	Hs.154365	E74-like factor 1 (els domain transcript	2.85	0.19	upregulate stage
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.2	0.1	upregulate stage
	425277	NM_001241	Hs.155478	cyclin T2	6	0.13	upregulate stage
	425508	AA991551	Hs.97013	ESTs	5.67	0.1	upregulate stage
50	425689	W16480	Hs.24283	ESTs	4.55	0.13	upregulate stage
	425721	AC002115	Hs.159309	uroplakin 1A	0.71	0.8	upregulate stage
	426069	H10807	Hs.30998	ESTs	3.4	0.17	upregulate stage
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	6.84	0.09	upregulate stage
	426110	NM_002913	Hs.165563	replication factor C (activator 1) 1 (14	6.7	0.1	upregulate stage
55	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	3.05	0.14	upregulate stage
	426603	AA382291		gb:EST95683 Testis 1 Homo sapiens cDNA 5	1.8	0.26	upregulate stage
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.96	0.36	upregulate stage
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig).	1.32	0.49	upregulate stage
	426902	AI125334	Hs.97408	ESTs	5.05	0.07	upregulate stage
60	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	2.95	0.12	upregulate stage
	427001	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	4.9	0.13	upregulate stage
	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	0.57	0.86	upregulate stage
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	1.86	0.31	upregulate stage
	427399	NM_014883	Hs.177664	KIAA0514 gene product	5	0.13	upregulate stage
65	427450	AB014526	Hs.178121	KIAA0626 gene product	5.3	0.09	upregulate stage
	427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	6.37	0.13	upregulate stage
	427737	AA435988	Hs.178066	ESTs, Weakly similar to AF068289 5 HDCME	5.7	0.11	upregulate stage
	428042	AA419529		gb:zv03d12.r1 Soares_NhHMPu_S1 Homo sapi	1.65	0.14	upregulate stage
	428336	AA503115	Hs.183752	microseminoprotein, beta-	5.37	0.05	upregulate stage
70	428337	AA644508		gb:af73c01.r1 Soares_NhHMPu_S1 Homo sapi	3.4	0.13	upregulate stage
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	1	0.17	upregulate stage
	428471	X57348	Hs.184510	stratifin	1.81	0.39	upregulate stage
	428583	AA430589	Hs.301374	ESTs, Moderately similar to ALU5_HUMAN A	7.55	0.11	upregulate stage
	428670	AA431682	Hs.134832	ESTs	8.05	0.1	upregulate stage
75	428785	AI015953	Hs.125265	ESTs	1.65	0.15	upregulate stage
	429332	AF030403	Hs.199263	Ste-20 related kinase	2.64	0.26	upregulate stage
	429343	AK000785	Hs.199480	epsin 3	3.15	0.27	upregulate stage
	429556	AW139399	Hs.98988	ESTs	1.87	0.31	upregulate stage
	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	0.61	1.02	upregulate stage
	429624	AA296363	Hs.121520	Human BAC clone GS1-99H8	2.03	0.39	upregulate stage
	429666	BE081342	Hs.226799	HSPC039 protein	7.85	0.08	upregulate stage

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	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	1	0.61	upregulate stage
	430042	AB023170	Hs.227850	KIAA0953 protein	2.5	0.17	upregulate stage
	430168	AW968343	Hs.300896	ESTs, Highly similar to AF128113 1 promi	1.98	0.4	upregulate stage
	430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	6.7	0.09	upregulate stage
5	430399	AI916284	Hs.199671	ESTs	8.09	0.08	upregulate stage
	430763	AA485468	Hs.106658	ESTs	3.18	0.24	upregulate stage
	431474	AL133990	Hs.190642	ESTs	0.37	0.51	upregulate stage
	431567	N51357	Hs.260855	Homo sapiens mRNA; cDNA DKFZp781G2311 (f	1.74	0.39	upregulate stage
10	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.55	0.15	upregulate stage
	431683	AK001749	Hs.267604	hypothetical protein FLJ10450	8.55	0.08	upregulate stage
	431709	AF220185	Hs.267923	uncharacterized hypothalamus protein HT0	7.95	0.1	upregulate stage
	431846	BE019924	Hs.271580	uroplakin 1B	1.33	0.5	upregulate stage
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	4.15	0.12	upregulate stage
15	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	3.7	0.13	upregulate stage
	432520	AI075978	Hs.188007	ESTs	2.05	0.22	upregulate stage
	432524	AI458020	Hs.293287	ESTs	5.15	0.14	upregulate stage
	432540	AI821517	Hs.105866	ESTs	5.5	0.11	upregulate stage
	432623	AA557351	Hs.152448	ESTs, Moderately similar to PUR5_HUMAN M	8.43	0.09	upregulate stage
20	432632	AW973801	Hs.134656	ESTs	2.45	0.16	upregulate stage
	432820	AI554057	Hs.152477	ESTs	8.29	0.09	upregulate stage
	432945	AL043663	Hs.271357	ESTs, Weakly similar to unnamed protein	3.22	0.23	upregulate stage
	433027	AF191018	Hs.279923	putative nucleotide binding protein, est	2.15	0.39	upregulate stage
	433037	NM_014158	Hs.279938	HSPC067 protein	5.1	0.11	upregulate stage
25	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	7.9	0.1	upregulate stage
	433171	AA579425		gb:nf37c08.s1 NCL_CGAP_Pr2 Homo sapiens	3.54	0.14	upregulate stage
	433311	AA688149		gb:nv16h12.s1 NCL_CGAP_Pr22 Homo sapiens	6.6	0.08	upregulate stage
	433383	AF034837	Hs.192731	double-stranded RNA specific adenosine d	2.45	0.21	upregulate stage
	433409	AI278802	Hs.25661	ESTs	4.75	0.1	upregulate stage
	433650	AA603472	Hs.28456	ESTs	1.6	0.18	upregulate stage
30	433675	AW977653	Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H	3.88	0.17	upregulate stage
	434328	BE564937	Hs.15984	pp21 homolog	3	0.15	upregulate stage
	434476	AW868520	Hs.271825	ESTs	4.6	0.1	upregulate stage
	434683	AW298724	Hs.202639	ESTs	2.1	0.19	upregulate stage
35	434726	AF062719	Hs.139053	ESTs	1.76	0.34	upregulate stage
	435124	AA725362	Hs.120456	ESTs	7.7	0.09	upregulate stage
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	5.8	0.09	upregulate stage
	435899	W89093	Hs.189914	ESTs	1.32	0.42	upregulate stage
	436026	AI349764	Hs.217081	ESTs	1	0.22	upregulate stage
40	436154	AA764950	Hs.119898	ESTs	8.4	0.05	upregulate stage
	436293	AI601188	Hs.120910	ESTs	2.42	0.2	upregulate stage
	436361	AA825814	Hs.149065	ESTs	6.95	0.09	upregulate stage
	436455	AI027959	Hs.132300	ESTs	3.25	0.15	upregulate stage
	436577	W84774	Hs.17643	ESTs	6.3	0.06	upregulate stage
45	436684	AW976319	Hs.94806	KIAA1062 protein	4.75	0.12	upregulate stage
	437036	AI571514	Hs.133022	ESTs	1.4	0.13	upregulate stage
	437146	AA730977		gb:nw55f05.s1 NCL_CGAP_Ew1 Homo sapiens	1	0.37	upregulate stage
	437262	BE250537	Hs.174838	Homo sapiens cDNA FLJ14192 fis, clone NT	3.25	0.17	upregulate stage
	437277	AA748016	Hs.123370	ESTs	6.75	0.09	upregulate stage
50	437882	AI243203	Hs.131572	ESTs	8.12	0.09	upregulate stage
	438392	AA806395	Hs.123205	ESTs	1	0.34	upregulate stage
	438416	N76398	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	8.1	0.1	upregulate stage
	438739	AA815391		gb:ai61c02.s1 Soares_testis_NHT Homo sap	4.69	0.12	upregulate stage
	439211	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	6.65	0.11	upregulate stage
55	439394	AA149250	Hs.56105	ESTs, Weakly similar to WDNM RAT WDNM1 P	3.19	0.11	upregulate stage
	439544	W26354	Hs.28891	hypothetical protein FLJ11360	2.3	0.34	upregulate stage
	439569	AW602165	Hs.222399	CEGPI protein	0.73	0.51	upregulate stage
	439586	AA922936	Hs.110039	ESTs	4.3	0.1	upregulate stage
	439706	AW872527	Hs.59761	ESTs	1	0.14	upregulate stage
60	439897	NM_015310	Hs.6763	KIAA0942 protein	8.4	0.08	upregulate stage
	439898	AW505514	Hs.209561	ESTs, Weakly similar to C05E11.1 gene pr	7.35	0.1	upregulate stage
	439949	AW979197	Hs.292073	ESTs	8.55	0.08	upregulate stage
	440035	BE561589	Hs.285122	hypothetical protein FLJ21839	6	0.11	upregulate stage
	440619	AW408586	Hs.91052	ESTs, Moderately similar to ALU5_HUMAN A	7.95	0.07	upregulate stage
65	440635	AW610331		gb:RC4-ST0316-190100-011-c08 ST0316 Homo	5.95	0.11	upregulate stage
	440787	AW292043	Hs.209433	ESTs	5.05	0.12	upregulate stage
	441233	AA972965	Hs.135568	ESTs	1.7	0.12	upregulate stage
	441528	AI003797	Hs.130815	hypothetical protein FLJ21870	7.2	0.09	upregulate stage
	441670	AW874090	Hs.127392	ESTs, Moderately similar to p33ING1 [H.s	2.45	0.19	upregulate stage
70	441683	BE564214	Hs.102946	ESTs	5.9	0.13	upregulate stage
	441847	AI215564	Hs.220972	ESTs	6.95	0.11	upregulate stage
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	3	0.19	upregulate stage
	442299	AW467791	Hs.155561	ESTs	5.05	0.13	upregulate stage
	442315	AA173992	Hs.7956	ESTs	3.97	0.17	upregulate stage
	442528	AF150317	Hs.134217	ESTs	1.4	0.34	upregulate stage
75	442571	C06338	Hs.165464	ESTs	8	0.08	upregulate stage
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	6.7	0.1	upregulate stage
	442652	AI005183	Hs.201378	ESTs, Weakly similar to KIAA0944 protein	7.15	0.11	upregulate stage

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	442947	R40800	Hs.21303	ESTs	8.5	0.08	upregulate stage
	442993	BE018682	Hs.44343	ESTs	1.91	0.34	upregulate stage
	443015	R33261	Hs.6614	ESTs	8.5	0.09	upregulate stage
5	443085	AI032660	Hs.164711	ESTs	4	0.13	upregulate stage
	443228	W24781	Hs.293798	ESTs	1.61	0.47	upregulate stage
	443367	AW071349	Hs.215937	ESTs	1.75	0.29	upregulate stage
	443371	AI792888	Hs.145489	ESTs	5.85	0.11	upregulate stage
	443564	AI921685	Hs.199713	ESTs	1.4	0.18	upregulate stage
10	443638	AW028596	Hs.145679	ESTs	3.25	0.15	upregulate stage
	443677	AV646096	Hs.293776	ESTs, Weakly similar to 1207289A reverse	6.45	0.11	upregulate stage
	443861	AW449462	Hs.134743	ESTs	6.72	0.09	upregulate stage
	444097	AW517412	Hs.150757	ESTs	4.25	0.11	upregulate stage
	444171	AB018249	Hs.10458	small inducible cytokine subfamily A (Cy	8.45	0.09	upregulate stage
15	444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	8.1	0.1	upregulate stage
	444385	BE278964	Hs.11085	CGI-111 protein	8.6	0.09	upregulate stage
	444624	AV650476	Hs.282936	ESTs	7.52	0.1	upregulate stage
	444631	AW995395	Hs.84520	ESTs	1.25	0.21	upregulate stage
	444707	AI188613	Hs.143866	ESTs	2.1	0.21	upregulate stage
20	444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	6.8	0.1	upregulate stage
	444779	AI192105	Hs.147170	ESTs	0.94	0.6	upregulate stage
	444823	BE262989	Hs.12045	putative protein	8.09	0.1	upregulate stage
	444858	AI199738	Hs.208275	ESTs, Weakly similar to unnamed protein	4.6	0.09	upregulate stage
	444875	AI200759	Hs.44737	ESTs	6.85	0.11	upregulate stage
25	444888	AI651039	Hs.148559	ESTs	3.15	0.18	upregulate stage
	445076	AI206888	Hs.154131	ESTs	7.81	0.09	upregulate stage
	445182	AW189787	Hs.147474	ESTs	2	0.07	upregulate stage
	445189	AI936450	Hs.147482	ESTs	2.65	0.12	upregulate stage
	445320	AA503887	Hs.167011	Homo sapiens cDNA: FLJ21362 fis, clone C	1.47	0.46	upregulate stage
30	445594	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	6.2	0.07	upregulate stage
	445674	BE410347	Hs.13063	transcription factor CA150	3.8	0.15	upregulate stage
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	5.6	0.1	upregulate stage
	445871	AI702901	Hs.145582	ESTs	2.3	0.33	upregulate stage
	446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone H	2.15	0.18	upregulate stage
35	446553	AB021179	Hs.15299	HMBA-inducible	2.55	0.18	upregulate stage
	446651	AA393907	Hs.97179	ESTs	8.05	0.07	upregulate stage
	447086	AI421397	Hs.161321	ESTs	6.9	0.1	upregulate stage
	447290	AI476732	Hs.263912	ESTs	2.35	0.18	upregulate stage
	447379	AI554946	Hs.158794	ESTs	6.3	0.09	upregulate stage
40	447390	X95384	Hs.18426	translational inhibitor protein p14.5	7.25	0.08	upregulate stage
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	1	0.24	upregulate stage
	447548	N53388	Hs.7222	ESTs	8.6	0.07	upregulate stage
	447731	AA373527	Hs.19385	CGI-58 protein	7.3	0.08	upregulate stage
	447853	AI434204	Hs.164285	ESTs, Weakly similar to Atg1p [S.cerevis	6.75	0.11	upregulate stage
45	447857	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	2.2	0.24	upregulate stage
	447965	AW292577	Hs.94445	ESTs	3.6	0.13	upregulate stage
	448072	AI459306	Hs.24908	ESTs	5.8	0.11	upregulate stage
	448474	AI792014	Hs.13809	ESTs	2.72	0.28	upregulate stage
	448513	AA344741	Hs.61773	Homo sapiens cDNA FLJ11648 fis, clone HE	4.8	0.12	upregulate stage
50	448601	R61666	Hs.293690	ESTs	2.65	0.2	upregulate stage
	448625	AW970786	Hs.178470	Homo sapiens cDNA: FLJ22662 fis, clone H	1.68	0.44	upregulate stage
	448735	AW473830	Hs.171442	ESTs	2.95	0.19	upregulate stage
	448807	AI571940	Hs.7549	ESTs	2.3	0.14	upregulate stage
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	8.6	0.08	upregulate stage
55	449448	D60730	Hs.57471	ESTs	1	0.13	upregulate stage
	449517	AW500106	Hs.23543	serine/threonine protein kinase MASK	6.4	0.11	upregulate stage
	449585	AI655321	Hs.197693	ESTs	1	0.16	upregulate stage
	449619	AI655992	Hs.300647	ESTs	8.35	0.09	upregulate stage
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	6.65	0.11	upregulate stage
60	449689	AF228421	Hs.301039	Human DNA sequence from clone RP1-132F21	8.35	0.06	upregulate stage
	449901	AI674072		gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	5.8	0.1	upregulate stage
	449964	AW001741	Hs.273193	hypothetical protein FLJ10706	8.7	0.09	upregulate stage
	450170	AI685366	Hs.32775	ESTs	6.77	0.12	upregulate stage
	450193	AI916071	Hs.224623	ESTs	5.73	0.1	upregulate stage
65	450336	AA046814	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, clone H	8.2	0.08	upregulate stage
	450341	N90956	Hs.17230	hypothetical protein FLJ22087	4.2	0.19	upregulate stage
	450353	AI244661	Hs.103296	ESTs	4.71	0.15	upregulate stage
	450737	AW007152	Hs.203330	ESTs	2.14	0.25	upregulate stage
	450795	AW173371	Hs.60435	ESTs	6	0.1	upregulate stage
70	450928	AI744417		gb:tr10h12.x1 NCI_CGAP_Ov23 Homo sapiens	1.75	0.18	upregulate stage
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	4.3	0.1	upregulate stage
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	4.75	0.16	upregulate stage
	451593	AF151879	Hs.26706	CGI-121 protein	5.8	0.11	upregulate stage
	451618	AA115639	Hs.26764	KIAA0546 protein	5.8	0.13	upregulate stage
	451668	Z43948	Hs.26789	hypothetical protein FLJ10320	0.73	0.26	upregulate stage
75	451790	AA927403	Hs.43897	ESTs, Weakly similar to P2CA_HUMAN PROTE	3.2	0.25	upregulate stage
	452001	AI827675	Hs.297735	Homo sapiens cDNA: FLJ22094 fis, clone H	3.7	0.13	upregulate stage
	452039	AI922988	Hs.172510	ESTs	1	0.65	upregulate stage

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5	452046	AB018345	Hs.27657	KIAA0602 protein	1.13	0.39	upregulate stage
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.2	0.15	upregulate stage
	452278	AL037715	Hs.28785	Homo sapiens mRNA; cDNA DKFZp586F0219 (f	8.25	0.07	upregulate stage
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.34	upregulate stage
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	4.97	0.13	upregulate stage
10	452714	AW770994	Hs.30340	hypothetical protein KIAA1165	7.6	0.09	upregulate stage
	453078	AF053551	Hs.31584	melanin 2	5.3	0.09	upregulate stage
	453370	AI470523	Hs.182356	ESTs, Moderately similar to translation	3.78	0.13	upregulate stage
	453765	BE279901	Hs.35091	hypothetical protein FLJ10775	3.95	0.11	upregulate stage
	453972	AW137224	Hs.245869	ESTs	6	0.09	upregulate stage
15	454044	AW022393		gb:df37h12.y1 Morton Fetal Cochlea Homo	1.15	0.18	upregulate stage
	454289	AL137554	Hs.49927	Homo sapiens mRNA; cDNA DKFZp434H1720 (f	7.05	0.1	upregulate stage
	454314	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	1	0.37	upregulate stage
	454315	AW373564	Hs.251928	nuclear pore complex interacting protein	2.7	0.13	upregulate stage
	454775	BE160229		gb:QV1-HT0413-090200-062-a12 HT0413 Homo	8.5	0.09	upregulate stage
20	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	1.15	0.14	upregulate stage
	454792	AW820794	Hs.252406	hypothetical protein FLJ12296 similar to	3.65	0.12	upregulate stage
	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	5.7	0.07	upregulate stage
	455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	1	0.25	upregulate stage
	456141	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 f1s, clone H	8.35	0.09	upregulate stage
25	456258	AW976410	Hs.289069	Homo sapiens cDNA: FLJ21016 f1s, clone C	4.85	0.14	upregulate stage
	456279	AW006783	Hs.6886	ESTs	7.25	0.1	upregulate stage
	457518	AA825350	Hs.143805	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.84	0.11	upregulate stage
	457570	AA579426	Hs.190226	ESTs	2.6	0.2	upregulate stage
	457982	AW856093	Hs.183617	ESTs	1	0.25	upregulate stage
30	458080	BE142728		gb:MR0-HT0157-021299-004-d08 HT0157 Homo	2.05	0.27	upregulate stage
	458340	AI457102	Hs.121583	Human glucose transporter pseudogene t	2.25	0.18	upregulate stage
	458440	AI095468	Hs.135254	ESTs, Weakly similar to thrombospondin t	2.35	0.13	upregulate stage
	458771	AW295151	Hs.163612	ESTs	1	0.19	upregulate stage
	459092	AA722012	Hs.255757	ESTs, Weakly similar to KIAA0611 protein	6.95	0.1	upregulate stage

TABLE 1B

35	Pkey:	Unique Eos probaset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

	Pkey	CAT	Accessions
40	407774	101538_1	AA084958 AA214034 AA044587 AA130152 AA130116 D81924
	407939	1027688_1	W05608 AW118352 AW196215
	407980	103087_1	AA046309 AI263500 AA046397
	408224	1048369_1	AW175997 AW176000 AW175999 AW175994 AW176004 AW175989
	408241	1048867_1	AW176546 AW178965 BE141057
45	408268	104987_1	AL138247 AA053529 BE173313
	408277	1050131_1	AW177559 AW177960 AW178066 AW178022
	408306	1050863_1	BE141991 AW178855 BE141990 BE141993 BE141994 BE062405 BE062404 AW178850
	409281	111502_1	AA069998 AA075659 AA075660 AA069828
	409408	1128045_1	AW387837 AW387874 AW387826 AW387758 AW387864 AW809268 AW387754
50	409566	114012_1	AA078899 AA078782 AA075788
	409760	115373_1	AA302840 T93016 T92950 AA077551
	409794	1154785_1	AW886691 BE185989 BE185940 AW500322 H10282
	409810	1155339_1	AW500895 AW937549
	409840	1156071_1	AW502122 AW502125 AW501663 AW501720
55	410071	1174764_1	AW582568 AW818656 AW818647 AW818655 AW818637 AW818234
	410128	117773_1	AW904599 AA325920 AW964919 AA081786 T05150
	410269	1189983_1	AW613597 BE080235 BE080168
	410475	1204788_1	AW749927 AW749938 AW749986 AW749986 R87124 AW860547
	410495	1205826_1	N95428 W24040 AW751366 H81987
60	410520	1206965_1	AW752710 BE180336 BE180186
	410534	1207247_1	AW905138 AW753008 R13818 Z43519
	410537	1207336_1	AW753108 AW852909 N36993 AW894327 AW903629
	410560	1208311_1	N29220 AW754225 AW754224
	410562	1208415_1	AW858528 AW754362 H74000
65	410724	1218202_1	AW799269 AW799385 AW799501 AW799386 AW799270 AW799467
	410751	121964_1	AA357918 AA089516 AA357917
	410754	1219733_1	T63840 AW801569 AW801568
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	410910	1226517_1	AW810204 AW810555 AW810196 AW810619 AW810507
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411788 125879_1 AW897793 R20054 H23321
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413792 1389912_1 T64882 BE168190 BE168256
413804 1390710_1 T83742 AW672882 AA135378
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414203 1425510_2 BE298094 BE267860
414220 1426940_1 BE297862
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5	414366	1438636_1	BE549143 BE390613 BE277344
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	414985	1511215_1	C17372 D63180 D78908 D63262
	415027	1515978_1	D31010 D30991 D31168 D31166 D31465
	415104	1522649_1	D60076 D60259 D61037
10	415114	1523035_1	D60468 D60950 D61218 N98936
	415178	1527354_1	D80503 D81739 N95691
	415296	1533528_1	F05086 F05091 R17158
	415303	153360_1	R11813 AA164376 T56632
	415352	1534744_1	F05565 Z43466 R18417 F06477 F06476 F07098
15	415364	1535008_1	F06771 H04895 Z42778
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	415392	1535746_1	Z44067 F07617 R34555
	415569	1539911_1	Z43930 F12170 H10681 T65261
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	415626	1540758_1	Z43847 F13068 T75331
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	415948	156264_1	AA262228 A1984175 AA171807
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	454637	1227707_1	AW811613 AW811611 AW811610
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	458880	80785_1	AI444821 W26012
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	459182	922744_1	AI940577 AI940580 AI940568 AI940578 AI940569 AI795858 AI795867 AI940572
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			BE178517 AI908132 BE142437

75 TABLE 1C

Pkey: Unique number corresponding to an Eos probelet

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Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NI_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NI_position
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10	400471	9931670	Minus	105629-105760
	400495	9714773	Minus	61902-62137
	400528	6981824	Plus	472381-472528,474170-474277,475328-475542,475878-476000
	400577	7960401	Plus	101535-101881
	400608	9887666	Minus	96756-97558
15	400641	8117693	Plus	4786-4992
	400644	8117693	Plus	27682-27840
	400666	8118496	Plus	17982-18115,20297-20456
	400749	7331445	Minus	9162-9293
	400750	8115067	Plus	198991-199168,199316-199548
20	400751	7331445	Minus	35395-35533
	400761	8131609	Minus	114220-115164
	400762	8131616	Plus	7235-7605
	400773	8131629	Minus	44116-44238,48208-48321
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
25	400844	9188605	Plus	24746-24872,25035-25204
	400845	9188605	Plus	34428-34612
	400846	9188605	Plus	39310-39474
	400860	9757499	Minus	151830-152104,152649-152744
	400880	9931121	Plus	29235-29336,36363-36580
	400887	9958187	Plus	119239-121542
30	400888	9958187	Minus	199600-199875
	400937	7652890	Minus	89519-89905
	400977	8072510	Plus	73950-74364
	401002	8117251	Minus	77898-78050
35	401024	8117489	Plus	60551-60802
	401045	8117619	Plus	90044-90184,91111-91345
	401048	7232177	Plus	132430-132761
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40	401093	8516137	Minus	22335-23166
	401101	8568122	Plus	77081-77226
	401192	9719502	Minus	69559-70101
	401197	9719705	Plus	176341-176452
	401203	9743387	Minus	172961-173056,173868-173928
45	401205	9743388	Plus	167373-167433,167936-168031
	401256	9796573	Minus	45482-45620
	401262	9796963	Plus	35662-35799
	401271	9797373	Minus	61292-61911
	401276	8954274	Minus	15919-16096
50	401279	9800062	Minus	13535-13669
	401342	9908882	Plus	3096-3242
	401365	9796180	Minus	119572-119672
	401395	7327842	Minus	11502-11771,46357-46489,58720-58916
	401420	7452889	Minus	141362-141502
55	401439	8246737	Plus	92993-94026
	401451	6634068	Minus	119926-121272
	401508	7534110	Minus	110779-110983
	401519	6649315	Plus	157315-157950
	401537	7960358	Minus	186786-187029,190607-190779,198218-198348
60	401561	8224660	Minus	10652-10838,19815-20018
	401566	8469090	Minus	96277-96420,96979-97160
	401604	7689963	Minus	119835-120185
	401619	8516761	Minus	141309-143576
	401669	9801805	Plus	25414-26310
	401691	3582311	Plus	162333-162715
65	401694	3540172	Minus	64056-64168
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401759	9929699	Plus	59811-60665
70	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401866	8018106	Plus	73126-73623
	401905	8671966	Plus	153965-154441,156599-156819
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
	402001	9501818	Plus	68052-68223
75	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
	402076	8117410	Plus	128316-128627
	402089	7249154	Plus	101610-101819
	402110	8131678	Minus	173889-174062

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	402176	7543687	Minus	10-750
	402230	9966312	Minus	29782-29932
	402245	7690231	Minus	88253-88417
	402296	6598824	Plus	22587-23723
5	402325	7636348	Minus	60658-60738,61677-61803
	402407	3962498	Minus	115812-116187
	402408	9796239	Minus	110326-110491
	402430	9796372	Minus	62382-62552
10	402435	9796462	Plus	114593-115588
	402472	9797116	Plus	53716-54470
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	402480	9797375	Plus	59708-59999
	402490	9797648	Plus	149982-150929
15	402522	9798493	Plus	20605-20731
	402530	7630937	Minus	1524-2003
	402546	7637348	Plus	24673-25170
	402553	9863566	Plus	48292-48398,49564-49944
	402604	9909420	Plus	20393-20767
20	402716	8969253	Minus	84065-84242
	402727	9211324	Plus	54596-54777
	402812	6010110	Plus	25026-25091,25844-25920
	402820	6456853	Minus	82274-82443
	402846	9408716	Minus	5726-5850
25	402889	9931133	Plus	89392-89498,90358-90571
	402892	8086844	Minus	194384-194645
	402901	8894222	Minus	175426-175667
	402922	8216969	Minus	19036-19401,19589-19849,19951-20102
	402938	8953442	Plus	22365-22473
30	402995	2996643	Minus	5962-6216
	403005	5791501	Minus	16945-17053,20018-20403
	403020	6984114	Minus	96644-97021,97462-97868
	403029	7768593	Minus	44568-44766
	403047	3540153	Minus	59793-59968
35	403073	8954241	Plus	142964-143260
	403085	8954241	Plus	165035-165334,165420-165713
	403092	8954241	Plus	174720-175016,175104-175406,175508-175813
	403106	7331404	Plus	77162-77350,81338-81511
	403172	7464784	Minus	64007-64275
40	403212	7630897	Minus	156037-156210
	403214	7630945	Minus	76723-77027,79317-79484
	403277	8072597	Minus	27494-27642
	403331	8567936	Plus	169793-169966
	403344	8569726	Plus	70823-70990
45	403362	8571772	Plus	64099-64260
	403381	9438267	Minus	26009-26178
	403426	9719529	Minus	157156-158183
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403567	8101141	Plus	35349-35614
50	403588	8101227	Minus	197672-197944
	403590	8101229	Plus	405-1296
	403615	8567964	Plus	107671-107866
	403687	7387384	Plus	9009-9534
	403754	7229815	Minus	163899-164726
55	403776	7770611	Minus	1414-1513,1624-1756
	403822	9369510	Minus	142803-142922
	403851	7708872	Plus	22733-23007
	403860	7708960	Minus	95755-96045
	403894	7381715	Minus	1442-2224
60	403903	7710671	Minus	101165-102597
	403959	8224399	Minus	175363-177474
	404015	8655948	Minus	587821-588222
	404059	3548785	Plus	104326-106788
	404113	9588571	Minus	13446-13646
65	404148	9863703	Plus	78218-78418,79571-79709
	404152	9884757	Plus	41111-41281,45495-45716,47801-47910
	404156	9886577	Plus	127319-127754
	404229	7159766	Plus	16607-16841
	404232	8218045	Minus	71800-71956
70	404268	9711362	Plus	33238-33463
	404274	9885189	Plus	104127-104318
	404288	2769644	Plus	3512-3691
	404290	2769644	Plus	36651-36813
	404336	9838028	Plus	157951-158129
75	404403	7272157	Minus	72053-72238
	404440	7528051	Plus	80430-81581
	404488	8113286	Minus	64835-64994
	404498	8151654	Plus	13292-13497

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	404507	8151803	Plus	146359-146739
	404516	8151987	Plus	114153-114322
	404538	8247909	Minus	192748-192945
	404594	9958262	Minus	15310-15510
5	404639	9796778	Plus	5779-14387
	404653	9796999	Plus	164997-165230
	404676	9797204	Minus	56167-56342,58066-58189,58891-59048,60452-60628
	404684	9797403	Minus	110881-111020
10	404685	9797437	Minus	153217-153315,154043-154124,159185-159353,161290-161420,163544-163669,166127-166207,167654-167734
	404704	9800728	Minus	88841-89018
	404819	4678240	Plus	16223-16319,16427-16513,16738-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
	404829	6624702	Minus	4913-5093,7310-7469,9472-9621,9951-10082
	404860	8979555	Plus	65852-66081
15	404874	9650523	Minus	96066-96192
	404881	5931510	Minus	36360-36608
	404894	6850447	Plus	102822-103127
	404939	6862697	Plus	175318-175476
	404977	3738341	Minus	43081-43229
20	405033	7107731	Minus	142358-142546
	405059	7658683	Plus	349-822
	405064	7658416	Plus	81207-81416
	405071	7708797	Minus	11115-11552
	405102	8076881	Minus	120922-121296
25	405167	9966316	Plus	43796-43981,48245-48427,54141-54317
	405170	9966524	Plus	37047-37198
	405177	7139696	Minus	118466-118663
	405186	7229793	Plus	161475-161581,162930-163067
	405258	7329310	Plus	129930-130076
30	405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
	405308	3638954	Plus	40778-41034,41383-41573
	405349	2914717	Minus	85552-85806
	405379	6513908	Minus	22332-22473,24333-24439
35	405390	6606064	Minus	94007-94177
	405411	3451356	Minus	17503-17778,18021-18290
	405463	7715630	Minus	123097-123260
	405494	8050952	Minus	70284-70518
	405520	9454643	Plus	60849-60981
40	405526	9558556	Minus	132704-133277
	405580	4512267	Plus	169232-169647
	405600	5923640	Plus	26662-27225
	405654	4895155	Minus	53624-53759
	405720	9797144	Plus	13409-13861
45	405725	9838299	Minus	106417-106521
	405735	9931101	Minus	29854-29976
	405738	9943998	Plus	44370-45410
	405809	5304920	Minus	6655-6883,8687-8859
	405838	5686575	Plus	3460-3717
50	405863	7657810	Plus	49410-49620
	405867	6758731	Minus	74553-75173
	405906	7705124	Minus	10835-11059
	405920	6758795	Plus	120621-120971
	405968	8247789	Plus	14893-15148
55	406017	8272661	Minus	46271-46874
	406036	6758919	Plus	17942-18163
	406081	9123861	Minus	38115-38691
	406137	9166422	Minus	30487-31058
	406187	7289992	Plus	8044-8877
60	406243	7417725	Plus	38899-39369
	406270	7534217	Plus	13136-13591
	406320	9211754	Minus	20170-20511
	406322	9212102	Minus	130230-130418
	406360	9258107	Minus	7513-7673
65	406367	9258126	Minus	58313-58489
	406397	9258243	Minus	127317-127454
	406399	9258288	Minus	63448-63554
	406434	9258651	Minus	17803-17931
	406467	9795651	Plus	182212-182958
70	406471	9795666	Plus	87383-87589
	406475	9797684	Plus	125417-125663,128052-128180
	406485	7711305	Plus	125036-125422
	406511	7711412	Plus	177277-177384
	406588	8189273	Minus	135629-135848

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TABLE 2A: 485 GENES UP-REGULATED IN BLADDER CANCER

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of mRNA expression in bladder tumors compared to normal bladder			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
15	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	3.473
	412841	AI751157	Hs.101395	hypothetical protein MGC11352	2.279
	421066	AU076725	Hs.101408	branched chain aminotransferase 2, mito	3.052
	435136	R27299	Hs.10172	ESTs	4.717
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	0.003
20	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	188.231
	421318	U63973	Hs.103501	rhodopsin kinase	1.381
	421359	AK001589	Hs.103816	hypothetical protein FLJ10727	1.000
	459462	AA481396	Hs.105167	ESTs	1.000
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypothe	1.000
25	433227	AB040923	Hs.106808	kelch (Drosophila)-like 1	1.000
	421742	AW970004	Hs.107528	androgen induced protein	1.514
	417366	BE186289	Hs.1076	small proline-rich protein 1B (cornifin)	2.782
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	20.064
	451686	AA059246	Hs.110293	ESTs	0.033
30	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	56.751
	458760	AI498631	Hs.111334	ferritin, light polypeptide	2.512
	422119	AI277829	Hs.111862	KIAA0590 gene product	2.634
	422170	AI791949	Hs.112432	anti-Mullerian hormone	0.055
	441877	AW273802	Hs.11340	hypothetical protein FLJ23047	0.008
35	445958	BE326257	Hs.114536	ESTs	0.002
	434288	AW189075	Hs.116265	fibrillin3	11.401
	435347	AW014873	Hs.116963	ESTs	0.003
	453134	AA032211	Hs.118493	ESTs	262.962
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	5.336
40	436154	AA764950	Hs.119898	ESTs	103.154
	436246	AW450963	Hs.119991	ESTs	0.071
	436293	AI601188	Hs.120910	ESTs	29.129
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	274.769
	438181	AW978608	Hs.122121	ESTs, Weakly similar to I38022 hypothe	0.024
45	449399	AA760681	Hs.122408	ESTs	1.000
	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypothe	4.314
	457465	AW301344	Hs.122908	DNA replication factor	0.264
	409757	NM_001898	Hs.123114	cystatin SN	1.390
	439907	AA853978	Hs.124577	ESTs	0.010
50	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	0.344
	440304	BE159984	Hs.125395	ESTs	0.025
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	0.014
	441495	AW294603	Hs.127039	ESTs	0.198
	435376	AW770956	Hs.127280	ESTs	0.008
55	427685	AI751124	Hs.127311	ESTs	3.244
	423349	AF010258	Hs.127428	homeo box A9	0.134
	445457	AF166793	Hs.12743	carnitine O-octanoyltransferase	7.255
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.000
	441875	AI435973	Hs.128056	ESTs	0.013
60	441940	AW298115	Hs.128152	ESTs	6.075
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	0.137
	429983	W92620	Hs.128656	ESTs	162.590
	445600	AF034803	Hs.12953	PTPRF interacting protein, binding prote	0.969
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	9.163
65	459204	AW194601	Hs.13219	ESTs	1.000
	439842	AI910896	Hs.132413	ESTs	1.000
	443113	AI040686	Hs.132908	ESTs	0.069
	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	0.100
	420792	AA280321	Hs.13392	telomeric factor SEC34	16.103
70	427719	AI393122	Hs.134726	ESTs	0.667
	443861	AW449462	Hs.134743	ESTs	5.100
	447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314 CDC28/cdc	1.691
	445550	AI242754	Hs.137306	ESTs	0.006
	454284	AW297935	Hs.138493	ESTs, Moderately similar to ALU7_HUMAN A	0.003
75	418937	T71508	Hs.13861	ESTs, Weakly similar to T42383 probable	0.042
	424098	AF077374	Hs.139322	small proline-rich protein 3	1.347
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	0.186
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	47.549
	425900	AW163564	Hs.142375	ESTs	0.404
	439337	AA448718	Hs.142505	ESTs	0.012

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	427961	AW293165	Hs.143134	ESTs	0.073
	419888	AI243493	Hs.144049	ESTs	11.958
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 lis, clone NT	77.269
	445871	AI702901	Hs.145582	ESTs, Weakly similar to FOR4 MOUSE FORMI	183.782
5	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.362
	424395	AA165082	Hs.146388	microtubule-associated protein 7	203.038
	424411	NM_005209	Hs.146549	crystallin, beta A2	1.808
	444517	AI939339	Hs.146883	ESTs	0.004
10	445020	AI205655	Hs.147221	ESTs	0.307
	422109	S73265	Hs.1473	gastrin-releasing peptide	1.000
	445352	AI221087	Hs.147761	ESTs	0.015
	444444	AI149332	Hs.14855	ESTs	140.859
	444152	AI125894	Hs.149305	hypothetical protein MGC2603	2.037
15	446248	AI283014	Hs.149638	ESTs	0.018
	433159	AB035898	Hs.150587	kinesin-like protein 2	0.110
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.179
	456840	H03754	Hs.152213	wingless-type MMTV integration site fami	0.005
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	1.111
20	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	257.949
	446082	AI274139	Hs.156452	ESTs	0.779
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	1.919
	446536	AC002563	Hs.15757	citron (rho-interacting, serine/threonin	0.417
	447073	AW204821	Hs.157726	ESTs	10.349
25	422755	AW409701	Hs.15778	baculoviral IAP repeat-containing 5 (sur	1.839
	446873	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	1.591
	447475	AI380797	Hs.158992	ESTs	44.641
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	0.340
	418343	AA216372	Hs.159501	ESTs	0.023
30	441143	AI027604	Hs.159650	ESTs	0.280
	440917	AA909651	Hs.160025	ESTs	1.000
	418355	AW014345	Hs.161590	ESTs	0.056
	431839	AW020280	Hs.162025	ESTs	0.005
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	0.506
35	438817	AI023799	Hs.163242	ESTs	2.202
	432441	AW292425	Hs.163484	ESTs	2.305
	442577	AA292998	Hs.163900	ESTs	688.038
	435212	AW300100	Hs.164185	ESTs	0.002
	425048	H05468	Hs.164502	ESTs	0.083
40	442083	R50192	Hs.165062	ESTs	3.844
	423536	L22075	Hs.1655	guanine nucleotide binding protein (G pr	0.157
	418678	NM_001327	Hs.167379	cancer/testis antigen	269.487
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	0.208
	456967	AW004056	Hs.168357	T-box 2	160.397
45	447979	AI457197	Hs.170348	ESTs	0.016
	458814	AI498957	Hs.170851	ESTs, Weakly similar to Z195_HUMAN ZINC	1.036
	446312	BE087853	Hs.171802	ESTs, Weakly similar to T08729 RING zinc	1.334
	426783	Z19084	Hs.172210	MUF1 protein	1.554
	423915	AW993496	Hs.17235	Homo sapiens clone TOCCIA00176 mRNA sequ	154.064
50	409092	AI735283	Hs.172608	ESTs	0.007
	426853	U32974	Hs.172777	baculoviral IAP repeat-containing 4	0.009
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	0.002
	407581	R48402	Hs.173508	P3ECSL	0.856
	427239	BE270447	Hs.174070	ubiquitin carrier protein	15.708
55	427268	X78520	Hs.174139	chloride channel 3	207.936
	436577	W84774	Hs.17643	ESTs	62.333
	420875	AA918425	Hs.177744	ESTs	32.959
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	1.171
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmidt metaph	1.000
60	427747	AW411425	Hs.180655	serine/threonine kinase 12	12.445
	429813	AW139678	Hs.180791	ESTs	0.013
	439806	AA848824	Hs.180908	ESTs	0.561
	427878	C05766	Hs.181022	CGI-07 protein	0.002
65	440284	AA912032	Hs.181059	ESTs, Weakly similar to Z108276A ssDNA-b	0.030
	427922	AK001934	Hs.181112	HSPC126 protein	0.039
	427972	AA854870	Hs.181304	putative gene product	0.004
	428071	AF212848	Hs.182339	ets homologous factor	4.321
	428336	AA503115	Hs.183752	microseminoprotein, beta-	145.128
	428450	NM_014791	Hs.184339	KIAA0175 gene product	0.370
70	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	0.632
	438746	AI858815	Hs.184727	ESTs	0.339
	420557	AA960844	Hs.186579	Homo sapiens, clone IMAGE:4081483, mRNA	0.006
	431014	W67730	Hs.187573	ESTs	0.344
	428651	AF195478	Hs.188401	annexin A10	1.459
75	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	0.502
	432497	AA551104	Hs.189048	ESTs, Moderately similar to ALUC_HUMAN I	2.499
	431474	AL133990	Hs.190642	ESTs	0.044
	427742	AA411880	Hs.190888	ESTs	0.158

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	428058	AI821625	Hs.191602	ESTs	0.006
	431245	AA496933	Hs.191687	ESTs	0.006
	453204	R10799	Hs.191990	ESTs	1.734
5	436608	AA628980	Hs.192371	down syndrome critical region protein DS	115.500
	447342	AI199288	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	0.152
	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	60.103
	449121	AI915858	Hs.194980	ESTs	0.003
	447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor t	305.974
10	438401	AL046321	Hs.197484	ESTs, Weakly similar to JC4295 ring fing	0.002
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.011
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	9.390
	429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	178.436
	429276	AF056065	Hs.198612	G protein-coupled receptor 51	0.729
15	449818	AW594365	Hs.199365	ESTs	1.000
	429345	R11141	Hs.199695	hypothetical protein	7.339
	443564	AI921685	Hs.199713	ESTs	0.001
	449847	AW204447	Hs.199750	organic anion transporter polypeptide-re	1.000
	449351	AW016537	Hs.200760	ESTs	0.005
20	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	381.474
	434411	AA632649	Hs.201372	ESTs	0.039
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.337
	446555	AV659046	Hs.201847	ESTs	0.024
	450411	D61167	Hs.202156	ESTs	0.004
25	442282	AW451086	Hs.202390	ESTs	1.000
	427587	BE348244	Hs.202628	ESTs, Weakly similar to I78885 serine/th	228.705
	429485	AF155827	Hs.203963	hypothetical protein FLJ10339	0.133
	426582	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.070
	426745	J03625	Hs.2057	uridine monophosphate synthetase (orotid	0.528
30	448275	BE514434	Hs.20830	kinesin-like 2	19.718
	459058	H85939	Hs.209605	EST	0.005
	441795	N58115	Hs.21137	AD024 protein	1.000
	451592	AI805416	Hs.213897	ESTs	0.012
	443367	AW071349	Hs.215937	ESTs	0.003
35	415949	H10562	Hs.21691	ESTs	0.072
	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLIC	213.962
	432548	AW973399	Hs.22133	hypothetical protein FLJ20121	0.250
	427867	NM_005073	Hs.2217	solute carrier family 15 (oligopeptide t	0.010
40	453123	AI953718	Hs.221849	ESTs	0.566
	439569	AW602166	Hs.222399	CEGP1 protein	10.625
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	27.603
	435956	AF269255	Hs.22604	lysosomal apyrase-like protein 1	127.564
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptiona	2.216
45	431253	R06428	Hs.226351	ESTs	0.023
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.103
	430034	X60155	Hs.227767	zinc finger protein 41	1.000
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	0.024
	417997	AA418189	Hs.23017	Homo sapiens cDNA: FLJ22747 fis, clone K	1.635
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	120.167
50	452956	AW003578	Hs.231872	ESTs	1.000
	446009	AI939885	Hs.231926	ESTs	4.000
	430499	AW959408	Hs.231991	ESTs	0.014
	448560	BE613183	Hs.23213	ESTs	285.090
	441508	AW015203	Hs.232237	ESTs	0.261
55	453228	AW628325	Hs.232327	ESTs	1.000
	442167	H18740	Hs.23248	hypothetical protein from EUROIMAGE 2005	0.240
	453321	AI984381	Hs.232521	ESTs	0.609
	449207	AL044222	Hs.23255	nucleoporin 155kD	0.551
	430152	AB001325	Hs.234642	aquaporin 3	1.040
60	439239	AI031540	Hs.235331	ESTs	0.598
	435087	AW975241	Hs.23567	ESTs	0.007
	451276	AW294386	Hs.236533	ESTs, Highly similar to dJ742C19.2 [H,sa	0.012
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	1.280
	431011	AA490631	Hs.23783	ESTs	0.016
65	430307	BE513442	Hs.238944	hypothetical protein FLJ10631	284.526
	444371	BE540274	Hs.239	forkhead box M1	3.691
	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	0.255
	449722	BE280074	Hs.23960	cyclin B1	0.467
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	13.419
70	430168	AW988343	Hs.24255	DKFZP434I1735 protein	1.192
	452292	AW139588	Hs.244369	ESTs	1.000
	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	2.500
	455582	AW500321	Hs.246766	Homo sapiens cDNA FLJ12360 fis, clone MA	0.014
	457343	NM_013936	Hs.247862	olfactory receptor, family 12, subfamily	0.233
75	430978	U53583	Hs.248182	olfactory receptor, family 1, subfamily	1.000
	431020	AF097874	Hs.248226	caspase 14, apoptosis-related cysteine p	5.866
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.838
	431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoadenylate	0.004

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	454170	AW177225	Hs.250158	ESTs	0.243
	439223	AW238299	Hs.250618	UL16 binding protein 2	0.516
	438081	H49546	Hs.251391	claudin 16	0.080
5	431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	843.974
	450663	H43540	Hs.25282	ribonuclease HI, large subunit	5.928
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.000
	413094	H24184	Hs.25413	TOLLIP protein	268.885
	450796	NM_001988	Hs.25482	envoplakin	1.643
10	408827	AW275730	Hs.254825	ESTs	0.008
	444129	AW294292	Hs.256212	ESTs	0.002
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	3.240
	436138	H53323	Hs.25717	Homo sapiens cDNA: FLJ23454 fis, clone H	0.679
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	280.231
15	453459	BE047032	Hs.257789	ESTs	2.133
	456636	AW135986	Hs.257859	ESTs	98.795
	438424	AI912498	Hs.25895	hypothetical protein FLJ14996	1.882
	451161	AA211329	Hs.26006	hypothetical protein FLJ10559	0.012
	430634	AI860651	Hs.26685	calcyphosine	9.561
20	435562	AL046988	Hs.268677	ESTs, Moderately similar to ALU7_HUMAN A	0.957
	417964	R71449	Hs.268760	ESTs	0.004
	445703	AV654845	Hs.27	glycine dehydrogenase (decarboxylating;	1.324
	431846	BE015924	Hs.271580	uroplakin 1B	303.679
	453074	AA031813	Hs.271880	ESTs	0.004
25	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.828
	435182	AA669386	Hs.272035	ESTs, Weakly similar to gonadotropin ind	0.013
	430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU S	8.978
	432136	AA157632	Hs.272630	vacuolar proton pump delta polypeptide	0.316
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	0.014
30	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	26.348
	423031	AI278995	Hs.27457	ESTs	53.288
	455612	BE042896	Hs.274848	ESTs	21.013
	452046	AB018345	Hs.27657	KIAA0802 protein	129.013
	436567	AI492860	Hs.276904	ESTs	0.007
35	459006	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	0.031
	430157	BE348706	Hs.278543	ESTs	99.244
	452012	AA307703	Hs.279766	kinesin family member 4A	0.408
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.721
	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	38.231
40	450020	AI680684	Hs.282219	ESTs	0.003
	435858	AF254260	Hs.283009	tufelin 1	1.516
	430733	AW975920	Hs.283361	ESTs	1.000
	446024	AB040946	Hs.284227	KIAA1513 protein	9.424
	433967	AF113018	Hs.284302	PRO1621 protein	0.008
45	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	0.030
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.058
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	273.013
	432097	X51730	Hs.2905	progesterone receptor	0.002
	452345	AA293279	Hs.29173	hypothetical protein FLJ20515	4.010
50	457733	AW974812	Hs.291971	ESTs	1.000
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	1.000
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	0.006
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	0.003
	433365	AF026944	Hs.293797	ESTs	0.049
55	417151	AA194055	Hs.293858	ESTs	6.593
	424242	AA337476	Hs.293984	hypothetical protein MGC13102	1.656
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	17.094
	422424	AI186431	Hs.296638	prostate differentiation factor	2.646
	432410	X68561	Hs.2982	Sp4 transcription factor	0.007
60	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	0.005
	454054	AI336329	Hs.301519	Homo sapiens cDNA FLJ12536 fis, clone NT	0.488
	452142	AB028947	Hs.301654	KIAA1024 protein	0.009
	449773	R76294	Hs.302383	ESTs	0.001
	438366	AA805780	Hs.303567	ESTs	1.000
65	452724	R84810	Hs.30464	cyclin E2	1.000
	429343	AK000785	Hs.307036	Homo sapiens, Similar to epsin 3, clone	0.494
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	0.022
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	16.744
	432789	D26361	Hs.3104	KIAA0042 gene product	0.302
70	432666	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	0.001
	453028	AB006532	Hs.31442	RacQ protein-like 4	13.392
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.766
	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	553.782
	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	84.115
75	443247	BE614387	Hs.333893	c-Myc target JPO1	79.385
	439632	AW410714	Hs.334437	hypothetical protein MGC4248	337.474
	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	0.842
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	402.500

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	433958	AW043909	Hs.334707	aminoacylase 1	191.179
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	313.462
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	21.744
5	451359	H85334	Hs.336623	ESTs	0.038
	440249	AI246590	Hs.337275	ESTs	0.432
	434487	AF143867	Hs.337688	ESTs, Moderately similar to S56657 alpha	1.102
	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	0.483
	447519	U46258	Hs.339665	ESTs	1.032
10	434192	AW387314	Hs.34371	ESTs	0.003
	453765	BE279901	Hs.35091	hypothetical protein FLJ10775	0.056
	441020	W79283	Hs.35962	ESTs	75.141
	453884	AA355925	Hs.36232	KIAA0186 gene product	0.138
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	0.008
15	453945	NM_005171	Hs.36908	activating transcription factor 1	0.044
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	0.002
	407625	U39196	Hs.37169	potassium inwardly-rectifying channel, s	0.009
	423620	N71320	Hs.39938	ESTs	1.000
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	0.042
20	407845	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	1.810
	443133	AI033878	Hs.41379	ESTs	0.534
	434534	H90477	Hs.41407	ESTs	0.013
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	3.679
	434952	T10269	Hs.4285	Homo sapiens cDNA: FLJ22505 fis, clone H	2.885
25	432237	AK001926	Hs.44143	polybromo 1	0.010
	420900	AL045633	Hs.44269	ESTs	10.436
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	3.393
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	385.256
	431009	BE149782	Hs.48956	gap junction protein, beta 6 (connexin 3	0.922
30	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	0.003
	435647	AI653240	Hs.49823	ESTs	175.910
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prole	2.584
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	0.610
	455505	AA703584	Hs.5105	hypothetical protein FLJ10569	0.008
35	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.089
	408287	AL080213	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	16.910
	435047	AA454985	Hs.54973	cadherin-like protein VR20	0.612
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	5.938
	439462	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	1.000
40	439482	W70045	Hs.58089	ESTs	0.118
	439605	W79123	Hs.58561	G protein-coupled receptor 87	0.095
	439705	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	0.055
	452240	AI591147	Hs.61232	ESTs	0.221
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	2.595
45	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.677
	434875	AF160477	Hs.61460	Ig superfamily receptor LNIR	7.587
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	0.046
	438779	NM_003787	Hs.6414	nucleolar protein 4	0.030
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	12.016
50	440125	AA975145	Hs.66194	ESTs	0.008
	451291	R39288	Hs.6702	ESTs	0.012
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	1.653
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	8.628
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	140.908
55	418107	R41726	Hs.7284	ESTs	0.146
	436326	BE085236	Hs.75313	aldo-keto reductase family 1, member B1	0.649
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	0.237
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.242
	414430	AI346201	Hs.75118	ubiquitin carboxyl-terminal esterase L1	0.202
60	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	2.318
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.622
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	246.564
	451575	AA767622	Hs.78893	KIAA0244 protein	1.000
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	4.552
65	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	5.128
	456921	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	0.246
	409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypotheti	7.249
	440371	BE268550	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	0.792
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	360.782
70	417003	AL036170	Hs.80756	betaine-homocysteine methyltransferase	60.590
	407584	W25945	Hs.8173	hypothetical protein FLJ10803	9.988
	417312	AW888411	Hs.81915	leukemia-associated phosphoprotein p18 (402.705
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	10.806
	428839	AI757756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	1.051
75	436315	R56795	Hs.82419	ESTs	0.226
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	26.260
	417933	X02308	Hs.82962	thymidylate synthetase	221.080
	418057	AI127958	Hs.83393	cystatin E/M	2.396

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5	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	1.000
	418205	L21715	Hs.83760	troponin I, skeletal, fast	0.159
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.490
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.527
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.077
10	458027	L49054	Hs.85195	myeloid leukemia factor 1	0.008
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.813
	418583	AA604379	Hs.86211	hypothetical protein	125.769
	441801	AW242799	Hs.86366	ESTs	55.026
	414792	BE314949	Hs.87128	hypothetical protein FLJ23309	8.139
15	407246	S70348	Hs.87149	integrin, beta 3 (platelet glycoprotein	0.020
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	313.141
	445060	AA830811	Hs.88808	ESTs	1.000
	453450	AW797627	Hs.89474	ADP-ribosylation factor 6	137.718
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	0.006
20	401464	AF039241	Hs.9028	histone deacetylase 5	6.846
	443162	T49951	Hs.9029	DKFZP434G032 protein	14.057
	431024	AA713666	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.507
	419559	Y07828	Hs.91096	ring finger protein	0.025
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	684.577
25	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	0.363
	424457	AI249036	Hs.94292	hypothetical protein FLJ23311	175.667
	410348	AW182663	Hs.95469	ESTs	0.011
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	428.231
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	0.005
30	443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	1.168
	426902	AI126334	Hs.97408	ESTs	37.467
	444874	AI218496	Hs.97515	BRCA1-interacting protein 1; BRCA1-assoc	0.067
	427356	AW023482	Hs.97849	ESTs	1.000
	430000	AW205931	Hs.99598	hypothetical protein MGC5338	0.812
35	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	0.342
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	19.785
	421934	AA300625		gb:EST13476 Testis tumor Homo sapiens cD	103.769
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	0.258
	424040	AA334400		gb:EST38610 Embryo, 9 week Homo sapiens	0.011
40	433108	AB002446		gb:Homo sapiens mRNA from chromosome 5q2	0.023
	458829	AI557368		gb:PT2.1_6_G03.r tumor2 Homo sapiens cDN	1.000
	455169	AI905517		gb:RC-BT091-210199-105 BT091 Homo sapien	0.773
	400300	X03363		HER2 receptor tyrosine kinase (c-erb-b2,	468.462
	440012	AA961072		gb:ak32e05.s1 Soares_testis_NHT Homo sap	0.002
45	412799	AI267605		gb:an91h03.x1 Stanley Frontal SB pool 1	0.010
	412964	BE019688		gb:bb28g08.x1 NIH_MGC_5 Homo sapiens cDN	0.003
	406992	S82472		gb:beta-pol=DNA polymerase beta (exon a	0.005
	414969	C16195		gb:C16195 Clontech human aorta polyA mRN	0.023
	413158	BE068098		gb:CM1-BT0368-061299-050-c09 BT0368 Homo	0.007
50	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hany2)	0.994
	453846	AL157586		gb:DKFZp761H0216_r1 761 (synonym: hany2)	0.004
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	0.037
	415204	T27434		gb:hbc2294 Human pancreatic islet Homo s	76.500
	434572	AF147340		gb:Homo sapiens full length insert cDNA	0.030
55	438990	AF085890		gb:Homo sapiens full length insert cDNA	1.000
	439780	AL109688		gb:Homo sapiens mRNA full length insert	0.256
	413671	Z43712		gb:HSC1JA121 normalized infant brain cDN	0.009
	406974	M57293		gb:Human parathyroid hormone-related pep	0.004
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.616
60	455807	BE141140		gb:MR0-HT0075-021299-008-d07 HT0075 Homo	0.413
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	0.015
	443309	AI821874		gb:nt58f10.x5 NCL_CGAP_Pr3 Homo sapiens	0.007
	437240	AA747537		gb:nx85c05.s1 NCL_CGAP_GCB1 Homo sapiens	0.006
	455189	AW864176		gb:PM0-SN0014-250400-002-b08 SN0014 Homo	0.069
65	444163	AI126098		gb:xq54g07.x1 Soares_placenta_8to9weeks_	394.282
	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	0.757
	454789	BE155314		gb:QV0-HT0367-150200-114-d02 HT0367 Homo	1.000
	433005	AW939074		gb:QV1-DT0069-010200-057-c12 DT0069 Homo	0.013
	455380	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	0.249
70	455650	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	1.000
	436383	BE065178		gb:RC1-BT0314-020200-012-h01 BT0314 Homo	1.000
	413100	BE055208		gb:RC1-BT0314-310300-015-b09 BT0314 Homo	271.372
	428436	BE080180		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	0.002
	455631	BE144966		gb:RC6-HT0187-201099-031-c04 HT0187 Homo	0.011
75	434414	AI798376		gb:tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens	293.654
	414221	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCL_CGAP_Su	0.807
	409488	AW402825		gb:U1-HF-BK0-aaq-d-08-0-U1.r1 NIH_MGC_36	0.965
	437938	AI950087		gb:wq05c02.x1 NCL_CGAP_Kid12 Homo sapien	2.952
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	7.341
	449325	AA001162		gb:ze48b06.r1 Soares retina N2b4HR Homo	0.004
	413316	W91931		gb:zh47c01.r1 Soares_fetal_liver_spleen_	0.004

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	401016	0.342
	401335	0.256
	401555	1.000
5	401760	301.372
	401781	247.141
	401961	1.722
	402239	5.180
	402305	0.917
10	402424	551.141
	402777	153.231
	402778	0.006
	402837	0.367
	402948	154.103
	402952	17.038
15	403142	0.196
	403297	12.744
	403637	0.304
	403657	0.032
20	404136	0.008
	404249	0.065
	404875	1.105
	404917	69.590
	404983	1.000
25	405238	1.000
	405364	294.141
	405531	1.747
	405601	145.551
	405621	0.224
	405932	1.968
30	406117	0.333
	406354	1.000
	406548	0.002
	406599	0.010
35	459702	0.449

TABLE 2B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409468	1134791_1	AW402825 BE544338
412799	132817_1	AI267606 AA121045 AA126521
412964	1339278_1	BE019688 BE144460
413100	1349119_1	BE065208 BE065224 BE065168 BE065313
413158	1351251_1	BE068098 BE068119 BE068083 BE068088 BE068120 BE068155 BE068111
413316	1360169_1	W91931 W94979 BE081744
413671	1382504_1	Z43712 BE156729 BE156538 BE156731 BE156673 BE156539 BE156674 BE156430 BE156672 BE156675 BE156432 BE156541
414221	142696_1	AW450979 AA136653 AA136655 AW419381 AA984358 AA492073 BE158945 AA809054 AW238038 BE011212 BE011359 BE011367
		BE011368 BE011362 BE011215 BE011365 BE011363
414969	1510393_1	C16195 C16230 C16211 C16164 C16251
415204	1529407_1	T27434 Z25288 F00323 D82802 R86077
421934	209339_1	AA300525 R16859 R16860 AW898335 W24337
424040	234659_1	AA334400 AA334257 AW966124
428436	291472_1	BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131 AA528743
		AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906628 AA906582 AA758746 AA551717 AW063311 AA429538
431322	331543_1	AW970622 AA503009 AA502998 AA502805 T92188
432189	342819_1	AA527941 AI810608 AI620190 AA635266
433005	357346_1	AW939074 AW939073 BE160476 AW939938 AW939205 AW940012 AW939076 AA573577 AW750479 AA574383 AW970057
433108	35896_1	AB002446 TC3145
434414	38585_1	AI798376 S46400 AW811617 AW811516 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
		AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174
		T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705
		AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824
		AI829309 AW991957 N66951 AA527374 H56215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817652
		AW817705 AW817703 AW817659 BE081531 H59570
434572	38911_1	AF147340 T51948 T52029
436383	41888_1	BE065178 AJ227879
437240	435139_1	AA747537 BE089068 BE089070
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875
		AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493
		AA927794 AI560251 AW874068 AL134043 AW235353 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062
		AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI752688 AA988777 AA488892 AI356394 AW103813 AI539642
		AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499
		AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072529 AW513996

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		AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531
		H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
5	438990	46760_1 AF085890 H29949 H29856
	439780	47673_1 AL109688 R23665 R26578
	440012	483290_1 AA861072 H02819 R25946
	443309	55504_1 AI821874 AI821868 AA630932 AA653897 AA650103 AI821131 AI821124
	444163	593658_1 AI125098 AI184746 AI148521
	449325	80480_1 AA001162 AA018950 AA017505 R84446
10	451385	86787_1 AA017656 AA017374 AA019761
	453823	982526_1 AL137967 BE064160 BE064186
	453846	983043_1 AL157586 AL157590
	454789	1234742_1 BE156314 BE156316 AW820750
	455170	1256906_1 AW860972 AW862598 AW862599 AW860988 AW860983 AW860989 AW860925 AW860922 AW860986 AW860984 AW860989
15	455189	1259271_1 AW864176 AW864133 AW864185 AW864137
	455380	1287679_1 BE160188 AW935785 BE160401 BE160319 BE160313 BE160395
	455650	1348720_1 BE064655 BE153953
	455797	1366826_1 BE091833 BE091874 BE091871
	455807	1370914_1 BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
20	455831	1373969_1 BE144966 BE144957 BE144958
	458829	773443_1 AI557388 BE158936
	459169	920641_1 AI905517 AI905455 AI905452

25 TABLE 2C

30	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nl_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nl_position
35	401016	8117441	Plus	126234-126359,128050-128236
	401335	9884881	Plus	15736-16352
	401555	8099284	Minus	152520-162657
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401761	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
40	401961	4581193	Minus	124054-124209
	402239	7690131	Plus	38175-38304,42133-42266
	402305	7328724	Plus	40832-41362
	402424	9796344	Minus	64925-65073
	402777	9588235	Plus	126786-126948
	402778	9588235	Plus	128560-128702
45	402837	9369121	Minus	2013-2186,9570-9758,11136-11309,19429-19677,21210-21455,23368-23562,24342-24527,29132-29320
	402948	9368458	Minus	143456-143626,143808-143935
	402952	9408724	Minus	119452-119619
	403142	9444521	Plus	89286-90131
	403297	8096824	Minus	16584-17264
50	403637	8671936	Minus	142647-142771,145531-145762
	403657	8843996	Minus	156223-156370
	404136	6981900	Minus	42538-46428
	404249	8655533	Plus	64270-64633
	404875	9801324	Plus	96588-96732,97722-97831
55	404917	7341851	Plus	49330-49498
	404963	4432779	Minus	51178-51374,52000-52173
	405238	7249119	Minus	51728-51836
	405364	2281075	Minus	48325-48491,49136-49252
60	405531	9635194	Plus	35602-35803
	405601	5815493	Minus	147835-147935,149220-149299
	405621	5523811	Plus	59362-59607
	405932	7767812	Minus	123525-123713
	406117	9142932	Plus	54304-54584
65	406354	9256049	Minus	2095-2377
	406548	7711514	Minus	25138-26762
	406599	8248616	Plus	10933-11086

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Table 3A: Preferred therapeutic targets for bladder cancer

Pkey: Unique Eos probset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of bladder tumor Als divided by the 90th percentile of normal bladder sample Als
 R2: 90th percentile of bladder tumor Als divided by the 90th percentile of normal body sample Als

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
	421948	L42583	Hs.334309	keratin 6A	14.20	1.20
	439926	AW014875	Hs.137007	ESTs	11.31	21.34
5	413324	V00571	Hs.75294	corticotropin releasing hormone	9.15	45.75
	421110	AJ250717	Hs.1355	calthepsin E	9.07	45.35
15	417308	H60720	Hs.81892	KIAA0101 gene product	8.50	1.99
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	8.39	1.28
	418406	X73501	Hs.84905	cytokeratin 20	8.10	40.50
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.98	1.38
20	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	7.67	2.12
	408243	Y00787	Hs.624	interleukin 8	7.56	4.85
	417715	AW969587	Hs.86366	ESTs	7.45	4.70
	417720	AA205525	Hs.208067	ESTs	7.34	9.18
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	7.30	26.07
25	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.12	35.60
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	6.95	4.96
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	6.42	0.89
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	6.08	3.49
	407242	M18728		gb:Human nonspecific crossreacting antig	5.96	0.96
30	405033			C1002652*gi544327 sp Q04799 FMO5_RABIT	5.84	16.22
	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	5.82	2.28
	406685	M18728		gb:Human nonspecific crossreacting antig	5.80	0.89
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	5.77	28.85
	415511	AI732617	Hs.182362	ESTs	5.65	28.25
35	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	5.60	6.51
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.59	2.33
	428651	AF196478	Hs.188401	annexin A10	5.55	27.75
	400843			NM_003105*:Homo sapiens sortilin-related	5.51	4.92
	402230			Target: Exon	5.36	21.44
40	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	5.33	2.80
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	5.17	1.98
	428450	NM_014791	Hs.184339	KIAA0175 gene product	4.90	2.63
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.77	2.35
45	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	4.77	3.71
	418663	AK001100	Hs.41690	desmocollin 3	4.74	1.48
	414683	S78296	Hs.76888	hypothetical protein MGC12702	4.74	2.92
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	4.68	1.61
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	4.65	11.63
50	431958	XG3629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.63	2.06
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.55	3.35
	401780			NM_005557*:Homo sapiens keratin 16 (foca	4.49	1.62
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	4.43	2.39
	401093			C12000586*gi5330167 dicj BAA86477.1 (A	4.40	12.94
55	417933	X02308	Hs.82962	thymidylate synthetase	4.35	2.29
	418113	AI272141	Hs.83484	SRV (sex determining region Y)-box 4	4.32	2.82
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	4.24	8.15
	401781			Target: Exon	4.15	1.31
60	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	4.14	7.39
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	4.12	2.51
	408380	AF123050	Hs.44532	diubiquitin	4.11	3.26
	449722	BE280074	Hs.23960	cyclin B1	4.09	3.72
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	4.07	2.50
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.00	7.14
65	404977			Insulin-like growth factor 2 (somatomedi	3.89	5.17
	400409	AF153341		Homo sapiens winged helix/forkhead trans	3.88	7.29
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	3.87	1.61
	444371	BE540274	Hs.239	forkhead box M1	3.87	2.75
	443171	BE281128	Hs.9030	TONDU	3.83	9.48
70	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.82	2.98
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.77	3.83
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.73	4.91
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	3.68	7.08
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.68	2.29
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.67	3.06
75	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.67	1.18
	421508	NM_004833	Hs.105115	absent in melanoma 2	3.67	3.65
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.66	3.21

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5	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (ma	3.66	3.57
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.62	2.73
	441495	AW294603	Hs.127039	ESTs	3.60	2.71
	422282	AF019225	Hs.114309	apolipoprotein L	3.57	3.92
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.55	0.80
10	417275	X63578	Hs.295449	parvalbumin	3.54	4.60
	440005	AK000517	Hs.6844	hypothetical protein FLJ20510	3.52	2.59
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.50	3.61
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.50	17.50
	404875			NM_022819*:Homo sapiens phospholipase A2	3.46	3.24
15	420005	AW271106	Hs.133294	ESTs	3.40	2.22
	409757	NM_001898	Hs.123114	cystatin SN	3.39	2.93
	427719	AI393122	Hs.134726	ESTs	3.31	2.51
	408690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	3.28	0.42
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	3.28	2.52
20	406081			Target Exon	3.25	13.54
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.25	2.46
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	3.23	2.88
	429983	W92620	Hs.260855	ESTs	3.20	2.84
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.18	1.54
25	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	3.17	5.44
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	3.13	15.65
	415752	BE314524	Hs.78776	putative transmembrane protein	3.11	2.46
	408633	AW963372	Hs.46677	PRO2000 protein	3.11	3.30
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	3.09	1.52
30	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.08	2.22
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	3.05	12.49
	437931	AI249468	Hs.124434	ESTs	3.01	3.70
	421451	AA291377	Hs.50831	ESTs	2.99	14.95
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.97	2.10
35	402239			Target Exon	2.97	3.37
	429345	R11141	Hs.199695	hypothetical protein	2.96	2.61
	435904	AF261555	Hs.8910	1,2-alpha-mannosidase IC	2.93	2.13
	423961	D13665	Hs.136348	periostin (OSF-2os)	2.93	1.44
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	2.92	0.95
40	436608	AA628980		down syndrome critical region protein DS	2.92	4.86
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.88	2.93
	439223	AW238299	Hs.250618	UL16 binding protein 2	2.88	2.15
	401747			Homo sapiens keratin 17 (KRT17)	2.88	3.44
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	2.86	14.30
45	444444	AI149332	Hs.14855	ESTs	2.85	2.68
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	2.84	2.46
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.78	2.26
	417389	BE260954	Hs.82045	midkine (neurite growth-promoting factor	2.77	2.34
	442994	AI026718	Hs.16954	ESTs	2.75	2.82
50	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.74	2.44
	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	2.72	3.37
	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.69	2.70
	404440			NM_021048:Homo sapiens melanoma antigen,	2.69	13.45
	400844			NM_003105*:Homo sapiens soritin-related	2.69	13.45
55	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.69	1.36
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	2.69	12.08
	403381			ENSP00000231844*:Ecolotropic virus integra	2.68	13.40
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	2.68	2.43
	425205	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	2.67	2.68
60	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.67	1.79
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	2.65	0.73
	413281	AA861271	Hs.222024	transcription factor BMAL2	2.65	2.23
	446082	AI274139	Hs.156452	ESTs	2.65	2.65
	422424	AI186431	Hs.296638	prostate differentiation factor	2.64	2.68
65	407839	AA045144	Hs.161566	ESTs	2.64	1.08
	432441	AW292425	Hs.163484	ESTs	2.64	6.14
	417312	AW888411	Hs.250811	leukemia-associated phosphoprotein p18 (2.64	1.31
	430157	BE348705	Hs.278543	ESTs	2.63	2.58
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.61	1.93
70	418686	Z36830	Hs.87268	annexin A8	2.60	1.62
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.59	2.87
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	2.57	3.89
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	2.57	2.49
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	2.56	1.43
75	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.54	3.10
	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.51	3.60
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.50	2.91
	414416	AW409985	Hs.76064	hypothetical protein MGC2721	2.49	1.78
	426612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.49	1.80
	416658	U03272	Hs.79432	fibroillin 2 (congenital contractual ara	2.49	3.46
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	2.48	2.36

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5	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.46	2.33
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	2.44	2.49
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.43	1.42
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.41	2.05
	449019	AI949095	Hs.67775	ESTs, Weakly similar to T22341 hypotheti	2.40	1.90
10	417366	BE185289	Hs.1075	small proline-rich protein 1B (cornifin)	2.40	0.49
	420370	Y13645	Hs.97234	uroplakin 2	2.39	3.81
	408000	L11690	Hs.198589	bullous pemphigoid antigen 1 (230/240kD)	2.38	1.45
	406399			NM_003122*:Homo sapiens serine protease	2.36	4.20
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.31	4.05
15	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	2.31	1.17
	436246	AW450963	Hs.119991	ESTs	2.30	11.50
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	2.30	2.40
	424012	AW368377	Hs.137559	tumor protein 63 kDa with strong homolog	2.29	1.89
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.28	2.14
20	432829	W60377	Hs.57772	ESTs	2.28	4.85
	415025	AW207091	Hs.72307	ESTs	2.28	11.40
	436293	AI601188	Hs.120910	ESTs	2.27	3.80
	415989	AI267700		ESTs	2.27	11.35
	418067	AI127958	Hs.83393	cystatin E/M	2.25	1.54
25	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.25	2.45
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.25	1.55
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	2.22	11.10
	443247	BE614387	Hs.333893	c-Myc target JPO1	2.21	1.32
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	2.21	1.52
30	405932			C15000305:gi 3806122 gb AAC69198.1 (AF0	2.20	1.55
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.19	1.99
	423271	W47225	Hs.126255	interleukin 1, beta	2.19	2.01
	402305			C19000735*:gi 4508027 ref NP_003414.1 z	2.19	2.54
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	2.19	2.16
35	427747	AW411425	Hs.180655	serine/threonine kinase 12	2.18	1.80
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	2.17	10.85
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.17	2.14
	433437	U20535	Hs.3280	caspase 6, apoptosis-related cysteine pr	2.16	1.37
	407581	R48402	Hs.173508	P3ECSL	2.15	1.95
40	400845			NM_003105*:Homo sapiens sortilin-related	2.15	2.23
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.14	1.70
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.13	1.83
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.13	3.49
	453459	BE047032	Hs.257789	ESTs	2.13	2.30
45	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	2.12	10.60
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.11	1.89
	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	2.11	2.57
	420876	AA918425	Hs.177744	ESTs	2.09	2.30
	438817	AI023799	Hs.163242	ESTs	2.09	10.45
50	434293	NM_004445	Hs.3796	EphB6	2.08	2.42
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.08	2.10
	418216	AA662240	Hs.283099	AF15q14 protein	2.08	4.52
	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTERA2D1 teratoca	2.08	10.40
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	2.05	5.39
55	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.05	1.20
	400773			NM_003105*:Homo sapiens sortilin-related	2.05	1.78
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.04	2.06
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.04	1.70
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), solub	2.03	2.25
60	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	2.02	1.73
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	2.02	2.93
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	2.02	1.55
	441801	AW242799	Hs.86366	ESTs	2.01	10.05
	439780	AL109688		gb:Homo sapiens mRNA full length insert	2.00	10.00
65	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	2.00	1.53
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	2.00	1.91
	430152	AB001325	Hs.234642	aquaporin 3	1.99	1.74
	453134	AA032211	Hs.118493	ESTs	1.99	3.16
	412719	AW016610	Hs.816	ESTs	1.99	0.34
70	442577	AA292998	Hs.163900	ESTs	1.99	3.09
	409402	AF208234	Hs.695	cystatin B (stefin B)	1.98	1.50
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.97	1.84
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.95	1.42
	447334	AA515032	Hs.91109	ESTs	1.95	2.53
75	432015	AL157504	Hs.155115	Homo sapiens mRNA; cDNA DKFZp586C00724 (f	1.94	9.70
	429002	AW248439	Hs.2340	junction plakoglobin	1.94	1.57
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.94	2.02
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	1.93	0.56
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antago	1.92	1.01
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.92	1.47
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.92	1.59

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5	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	1.92	2.77
	424522	AL134847	Hs.149957	ribosomal protein S6 kinase, 90kD, polyp	1.92	1.21
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.92	1.72
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	1.91	1.41
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	1.90	1.61
10	400846			scorillin-related receptor, L(DLR class)	1.90	1.93
	417409	BE272506	Hs.82109	syndecan 1	1.89	1.75
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.88	1.16
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.88	3.09
	419092	J05581	Hs.89503	mucin 1, transmembrane	1.88	1.18
15	446673	NM_015361	Hs.15871	LPAP for lysophosphatidic acid phosphata	1.87	2.01
	431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	1.86	1.87
	430168	AW968343	Hs.24255	DKFZP434I1735 protein	1.86	2.11
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	1.85	1.77
	402901			NM_025206*:Homo sapiens hypothetical pro	1.85	2.35
20	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	1.85	1.59
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.84	1.90
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.84	1.03
	414732	AW410975	Hs.77152	minichromosome maintenance deficient (S.	1.84	1.54
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.83	1.74
25	452534	AA581322	Hs.4213	hypothetical protein MGC15207	1.82	1.84
	431630	NM_002204	Hs.255829	integrin, alpha 3 (antigen CD49C, alpha	1.82	1.83
	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.82	1.74
	402424			NM_024901:Homo sapiens hypothetical prot	1.81	1.61
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUS protein d	1.81	3.67
30	431846	BE019924	Hs.271580	uroplakin 1B	1.80	4.11
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.80	9.00
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.80	1.02
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.80	2.26
	451541	BE279383	Hs.26557	plakophilin 3	1.79	1.16
35	415786	AW419195	Hs.257924	hypothetical protein FLJ13782	1.79	5.59
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.79	8.95
	425852	AK001504	Hs.159551	death receptor 6, TNF superfamily member	1.79	2.08
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.77	2.96
	437044	AL035664	Hs.69517	differentially expressed in Fanconi's an	1.76	1.43
40	439606	W79123	Hs.58561	G protein-coupled receptor 87	1.76	8.80
	424098	AF077374	Hs.139322	small proline-rich protein 3	1.76	0.57
	430890	X54232	Hs.2699	glypican 1	1.73	1.39
	452862	AW378065	Hs.8687	ESTs	1.73	1.99
	427335	AA448542	Hs.251677	G antigen 7B	1.73	8.65
45	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFp434K0322 (f	1.72	2.07
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.72	1.65
	428484	AF104032	Hs.184501	solute carrier family 7 (cationic amino	1.72	1.03
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.71	1.66
	448993	AI471630	Hs.8127	KIAA0144 gene product	1.71	1.52
50	422406	AF025441	Hs.116206	Opa-interacting protein 5	1.71	5.52
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.71	8.55
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.71	8.55
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.71	8.55
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	1.71	13.98
55	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.70	1.84
	414053	BE391635	Hs.75725	transgelin 2	1.69	1.51
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	1.69	8.45
	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcript	1.69	1.60
	448262	AW880830	Hs.185273	ESTs	1.67	2.07
60	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.66	0.70
	452240	AI591147	Hs.61232	ESTs	1.66	1.23
	417151	AA194055	Hs.293858	ESTs	1.65	2.08
	452461	N78223	Hs.108106	transcription factor	1.65	8.25
	418462	BE001596	Hs.85286	integrin, beta 4	1.65	1.78
65	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.64	1.59
	436746	AI858515	Hs.184727	Human melanoma-associated antigen p97 (m	1.64	1.13
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	1.63	1.81
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	1.62	1.51
	402777			C1002652*:gij544327 sp QC4799 FMO5_RABIT	1.62	2.33
70	436569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)	1.62	2.18
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.62	1.27
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	1.61	2.05
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.60	1.78
	450635	AW403954	Hs.25237	mesenchymal stem cell protein DSCD75	1.60	1.63
75	437016	AU076916	Hs.5398	guanine monophosphate synthetase	1.59	1.50
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFp564O1763 (f	1.58	1.92
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	1.57	1.79
	408908	BE296227	Hs.250822	serine/threonine kinase 15	1.56	7.80
	433159	AB035898	Hs.150587	kinesin-like protein 2	1.56	7.80
	443211	AI128388	Hs.143655	ESTs	1.56	7.80
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.55	1.44

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5	426900	AW163564	Hs.142375	ESTs	1.54	1.93
	421066	AU076725	Hs.101408	branched chain aminotransferase 2, mitoc	1.54	1.71
	413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	1.53	1.55
	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.53	1.59
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	1.52	7.80
10	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	1.49	0.52
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.48	1.54
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.48	1.39
	402280			NM_001436*:Homo sapiens fibrillarin (FBL	1.47	1.48
	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	1.47	7.35
15	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.47	1.37
	422164	NM_014312	Hs.112377	cortic al thymocyte receptor (X. laevis	1.46	1.80
	444163	AH126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	1.45	1.58
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.45	1.58
	445182	AW189787		ESTs	1.43	7.15
20	408930	AA146721	Hs.334686	hypothetical protein FLJ21588	1.43	1.53
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.43	1.34
	406467			Target Exon	1.42	7.10
	424244	AV647184	Hs.143601	hypothetical protein hCLA-iso	1.42	1.32
	422094	AF129535	Hs.272027	F-box only protein 5	1.41	4.55
25	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	1.39	10.36
	401760			Target Exon	1.37	1.16
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.36	1.39
	424420	BE614743	Hs.146688	prostaglandin E synthase	1.33	1.49
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.31	1.44
30	422119	AI277829	Hs.111862	KIAA0590 gene product	1.31	1.22
	418729	AB028449	Hs.87889	helicase-moi	1.30	0.84
	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	1.30	1.32
	453028	AB006532	Hs.31442	RecQ protein-like 4	1.29	1.42
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (1.29	0.61
35	453321	AI984381	Hs.232521	ESTs	1.27	6.35
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.26	6.30
	425726	AF085808	Hs.159330	uroplakin 3	1.26	2.26
	406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.26	1.11
	429413	NM_014058	Hs.201877	DESC1 protein	1.25	1.01
40	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	1.23	1.17
	431840	AA534808	Hs.2860	POU domain, class 5, transcription facto	1.22	1.59
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.20	1.38
	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22496 fis, clone H	1.19	1.23
	403903			C5001632*:gil10645308jgb AAG21430.1 AC00	1.19	1.98
45	425721	AC002115	Hs.159309	uroplakin 1A	1.17	2.30
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	1.17	5.85
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.17	1.39
	443859	NM_013409	Hs.9914	collistatin	1.17	1.17
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	1.13	2.83
50	422330	D30763	Hs.115263	epiregulin	1.13	5.65
	420261	AI623693	Hs.323494	Predicted cation efflux pump	1.11	5.55
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	1.08	5.40
	440304	BE159984	Hs.125395	ESTs	1.06	5.30
	422170	AI791949	Hs.112432	anti-Mullerian hormone	1.06	1.55
55	417599	AA204688	Hs.62954	ESTs	1.05	1.02
	411874	AA096106	Hs.20403	ESTs	1.04	7.20
	449961	AW285634	Hs.133100	ESTs	1.03	0.65
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.03	0.92
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	1.02	5.10
60	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	1.02	0.60
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	1.00	0.05
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	1.00	0.25
	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	1.00	0.25
	439239	AI031540	Hs.235331	ESTs	1.00	0.27
65	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.00	0.45
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	1.00	0.72
	404403			Target Exon	1.00	1.00
	406974	M57293		gb:Human parathyroid hormone-related pep	1.00	1.00
	410348	AW182663	Hs.95469	ESTs	1.00	1.00
70	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	1.00	1.00
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
	426320	W47595	Hs.169300	transforming growth factor, beta 2	1.00	1.00
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	1.00	1.00
	432097	X51730	Hs.2905	progesterone receptor	1.00	1.00
75	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1.00	1.00
	453369	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal ki	1.00	1.00
	419078	M93119	Hs.89564	insulinoma-associated 1	1.00	1.25
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	1.00	1.35
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.75
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	1.00	1.80
	415178	D80503	Hs.322850	ESTs	1.00	2.20

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5	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	2.25
	425048	H05468	Hs.164502	ESTs	1.00	2.25
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	1.00	2.60
	449448	D60730	Hs.57471	ESTs	1.00	2.70
	417791	AW965339	Hs.111471	ESTs	1.00	2.95
	421373	AA808229	Hs.167771	ESTs	1.00	3.00
	427356	AW023482	Hs.97849	ESTs	1.00	3.15
	421070	AA283185	Hs.19327	ESTs	1.00	3.25
10	415542	R13474	Hs.290263	ESTs, Weakly similar to I38022 hypotheti	1.00	3.35
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	1.00	3.55
	402075			ENSP00000251056*:Plasma membrane calcium	1.00	3.95
	419559	Y07828	Hs.91096	ring finger protein	1.00	4.00
	418661	AA634543	Hs.79440	ICF-II mRNA-binding protein 3	1.00	4.00
15	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	1.00	4.35
	412723	AA648459	Hs.335951	hypothetical protein AF301222	1.00	4.40
	404877			NM_005365:Homo sapiens melanoma antigen,	1.00	4.45
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	1.00	4.45
	403047			NM_005556*:Homo sapiens transmembrane pr	1.00	4.50
20	408434			NM_030579*:Homo sapiens cytochrome b5 ou	1.00	4.65
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	1.00	4.65
	433365	AF026944	Hs.293797	ESTs	1.00	10.05
	427656	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	0.99	0.60
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.99	1.00
	431474	AL133990	Hs.190642	CEGP1 protein	0.94	9.14
25	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	0.93	21.15
	414221	AW450979		gb:LI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	0.91	2.60
	444649	AW207523	Hs.197628	ESTs	0.89	11.15
	458034	AW450979		gb:LI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	0.89	5.13
30	414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigeni	0.84	0.85
	439559	AW602166	Hs.222399	CEGP1 protein	0.84	2.42
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	0.81	6.75
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	0.80	0.57
	457292	AI921270	Hs.281462	hypothetical protein FLJ14251	0.77	1.40
35	431089	BE041395		ESTs, Weakly similar to unknown protein	0.76	14.88
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	0.74	11.03
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	0.56	0.80
	408964	M21305		gb:Human alpha satellite and satellite 3	0.53	11.16
	418225	AA577730	Hs.168684	ESTs, Weakly similar to PC4259 ferritin	0.48	3.01
40	400288	X06255	Hs.149609	integrin, alpha 5 (fibronectin receptor,	0.40	0.70
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.40	0.51

TABLE 3B

45	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

50	Pkey	CAT Number	Accession
	411880	1263110_1	AW872477 BE088101 T05990
	413804	1390710_1	T54682 BE168190 BE168255
	414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW236038 BE011212 BE011359 BE011367
55	415989	156454_1	BE011368 BE011362 BE011215 BE011365 BE011363
	431089	327825_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
	431322	331543_1	BE041395 AA491826 AA621946 AA715980 AA666102
	432222	343347_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
60	436808	42381_3	AI204995 AW827539 AW969908 AW440776 AA528756
	439780	47673_1	AA628990 AI126603 BE504035
	444163	593658_1	AL109688 R23655 R26578
	445182	632151_1	AI126098 AI184746 AI148521
	451844	888230_1	AW189787 AI215430 AW268499 AW205930 AI392907 BE093017 BE093019 BE093010
65	458034	142696_1	T51430 AI820546 AI821336
			AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW236038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 3C

70	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NL_position:	Indicates nucleotide positions of predicted exons.

75	Pkey	Ref	Strand	NL_position
	400773	8131629	Minus	44116-44238,46208-48321

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5	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
	400844	9188605	Plus	24746-24872,25035-25204
	400845	9188605	Plus	34428-34612
	400846	9188605	Plus	39310-39474
	401093	8516137	Minus	22335-23166
10	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
15	402230	9666312	Minus	29782-29932
	402239	7690131	Plus	38175-38304,42133-42266
	402260	3399665	Minus	113765-113910,115653-115765,116806-116940
	402305	7328724	Plus	40832-41362
	402424	9796344	Minus	64925-65073
20	402777	9568235	Plus	126786-126948
	402901	8894222	Minus	175426-175667
	403047	3540153	Minus	59793-59968
	403381	9438267	Minus	26009-26178
	403903	7710671	Minus	101165-102597
25	404403	7272157	Minus	72053-72238
	404440	7528051	Plus	80430-81581
	404875	9801324	Plus	96588-96732,97722-97831
	404877	1519284	Plus	1095-2107
	404977	3738341	Minus	43081-43229
30	405033	7107731	Minus	142358-142546
	405932	7767812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
	406399	9256288	Minus	63448-63554
	406434	9256651	Minus	17803-17931
	406487	9795551	Plus	182212-182958

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TABLE 4A: Preferred diagnostics for bladder cancer

5	Pkey:	Unique Eos probeset identifier number					
	ExAccn:	Exemplar Accession number, Genbank accession number					
	UnigenelD:	Unigene number					
	Unigene Title:	Unigene gene title					
	R1:	80th percentile of muscle-invasive bladder tumor (stage T2-T4) AIs divided by the 80th percentile of exophytic non-invasive carcinoma (stage Ta) AIs					
	R2	90th percentile of bladder tumor AIs minus background divided by 90th percentile of normal body sample AIs minus background, where background equals the 15th percentile of all sample AIs					
10	R3	90th percentile of bladder tumor AIs divided by the 90th percentile of normal body sample AIs					
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3
15	423961	D13665	Hs.136348	perostin (OSF-2os)	11.22	1.40	1.44
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	8.40	1.31	1.38
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	7.88	2.06	2.44
	408243	Y00787	Hs.624	interleukin 8	7.54	2.66	4.85
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.14	1.18	1.18
20	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	5.32	1.34	1.36
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	5.27	0.61	0.57
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.17	7.47	35.60
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.30	1.75	1.54
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	4.29	1.35	1.60
25	413324	V00571	Hs.75294	corticotropin releasing hormone	4.20	6.27	45.75
	412429	AV650262	Hs.75765	GRO2 oncogene	4.00	0.94	0.93
	406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	3.66	1.25	1.25
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.58	2.07	2.26
	406687	M31126		matrix metalloproteinase 11 (stromelysin	3.41	4.37	3.37
30	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	3.09	0.39	0.40
	410867	X63556	Hs.750	fibrillin 1 (Marfan syndrome)	2.96	0.44	0.45
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	2.90	1.94	3.46
	414812	X72755	Hs.77387	monokine induced by gamma interferon	2.80	1.67	3.10
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.77	5.62	26.07
35	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.71	2.26	2.91
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	2.40	0.47	0.37
	417849	AW291587	Hs.82733	nidogen 2	2.34	0.86	0.86
	400419	AF084545		Target	2.33	1.54	2.12
	407811	AW190902	Hs.40088	cysteine knot superfamily 1, BMP antagon	2.10	1.01	1.01
40	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	1.99	3.19	17.50
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.94	2.49	1.84
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalini	1.94	2.02	5.39
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.84	1.99	8.55
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	1.76	0.33	0.31
45	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	1.76	1.13	1.16
	421958	AA357185	Hs.109918	ras homolog gene family, member H	1.75	1.33	1.27
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.58	2.42	1.39
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.57	2.02	8.55
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BT3-like	1.55	1.57	1.55
	407939	W05608	Hs.312579	ESTs, Weakly similar to A49019 dynein he	1.41	0.79	0.67
50	429344	R94038	Hs.199538	inhibin, beta C	1.36	1.39	1.34
	402727			NM_025065:Homo sapiens hypothetical prot	1.34	1.34	1.56
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.31	1.63	2.22
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.27	2.00	1.67
55	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	1.25	0.16	0.30
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.23	1.70	4.34
	424479	AF064238	Hs.149098	smoothelin	1.19	0.27	0.47
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.17	1.59	2.93
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	1.16	0.82	0.80
60	421634	AA437414	Hs.106283	hypothetical protein FLJ10262	1.16	1.05	1.05
	439569	AW602166	Hs.222399	CEGP1 protein	1.15	2.01	2.42
	431346	AA371059	Hs.251636	ubiquitin specific protease 3	1.10	1.64	1.52
	448901	AK001021	Hs.22505	hypothetical protein FLJ10159	1.10	0.31	0.31
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	1.03	1.51	1.42
	422424	AI186431	Hs.296638	prostate differentiation factor	1.02	2.77	2.68
65	458781	AI444821	Hs.63085	ESTs, Weakly similar to MPP3_HUMAN MAGUK	1.00	1.64	5.45
	445413	AA151342	Hs.12677	CGI-147 protein	1.00	1.51	5.20
	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	1.00	1.55	4.30
	403106			C800064*:gi110432393 emb CAC10283.1 (A	1.00	1.48	4.24
70	402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.67	3.95
	404860			C1003394*:gi12314272 emb CAC00591.1 (A	1.00	1.40	3.90
	434037	AF116601		VW domain-containing oxidoreductase	1.00	1.56	3.70
	405738			CX000390*:gi6014646 gb AAAF01438.1 AF187	1.00	1.36	2.95
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.00	1.45	1.60
75	439898	AW505514	Hs.209561	KIAA1715 protein	1.00	1.28	1.59
	452567	D87120	Hs.29882	predicted osteoblast protein	1.00	1.10	1.31
	401271			C9000559*:gi12314195 emb CAB99338.1 (A	1.00	2.12	1.00
	411339	BE164598	Hs.274251	hypothetical protein FLJ20375; KIAA1797	1.00	2.05	1.00

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	403005		C21000027*:gij1817556 dbj BAA13672.1 (D	1.00	1.89	1.00
	431146	Z83850	Human DNA sequence from PAC B2J11 and co	1.00	1.89	1.00
	434939	AF161422	Hs.308567 Homo sapiens HSPC304 mRNA, partial cds	1.00	1.86	1.00
5	431753	X76029	Hs.2841 neuromedin U	1.00	1.82	1.00
	419121	AA374372	Hs.89626 parathyroid hormone-like hormone	1.00	1.89	1.00
	435505	AF200492	Hs.211238 interleukin-1 homolog 1	1.00	1.67	1.00
	452401	NM_007115	Hs.29352 tumor necrosis factor, alpha-induced pro	1.00	1.67	1.00
	406397		C16001447*:gij12053709 emb CAC20419.1 (1.00	1.66	1.00
	404488		NM_030958*:Homo sapiens organic anion tr	1.00	1.56	1.00
10	441206	BE552314	Hs.131823 ESTs, Weakly similar to TERA HUMAN [H.sa	1.00	1.49	1.00
	407853	AA336797	Hs.40499 dickkopf (Xenopus laevis) homolog 1	1.00	1.47	1.00
	446119	D29527	Hs.290931 ESTs	1.00	1.47	1.00
	406471		Target Exon	1.00	1.44	1.00
	402110		C18000178:gij11990779 emb CAC19649.1 (A	1.00	1.42	1.00
15	407911	AF104922	Hs.41565 growth differentiation factor 8	1.00	1.40	1.00
	404829		C1002937*:gij7499208 pir T20993 hypothe	1.00	1.37	1.00
	421925	S80310	Hs.109620 acidic epididymal glycoprotein-like 1	1.00	1.26	1.00
	406076	AL390179	Hs.334873 Homo sapiens mRNA; cDNA DKFZp547P134 (fr	1.00	1.19	1.00
20	458522	AA972412	Hs.13755 f-box and WD-40 domain protein 2	1.00	1.09	1.00
	416018	AW138239	Hs.78977 proprotein convertase subtilisin/kexin 1	1.00	1.04	1.00
	409357	M73628	Hs.54415 casein, kappa	1.00	1.03	1.00
	436684	AW976319	Hs.94806 ATP-binding cassette, sub-family A (ABC1	1.00	0.84	0.84
	436178	BE152396	Hs.21590 hypothetical protein DKFZp564O0523	1.00	0.91	0.80
25	402522		C1000568*:gij12697965 dbj BAB21801.1 (A	1.00	0.80	0.67
	405735		ENSP00000252164*:K1AA1578 protein (Fragm	1.00	0.86	0.56
	401905		ENSP00000252232*:Sterol regulatory eleme	1.00	0.65	0.52
	404152		C6000931*:gij9558454 dbj BAB03398.1 (AB	1.00	0.58	0.51
	418693	AI750878	Hs.87409 thrombospondin 1	1.00	0.85	0.51
30	451375	AI792066	Hs.283902 Homo sapiens BAC clone RP11-481J13 from	1.00	0.46	0.38
	430132	AA204686	Hs.234149 hypothetical protein FLJ20647	1.00	0.84	0.33
	458983	AI081687	Hs.11355 thymopoietin	1.00	0.61	0.29
	438681	AW384815	Hs.149208 KIAA1555 protein	1.00	0.60	0.28
	409038	T97490	Hs.50002 small inducible cytokine subfamily A (Cy	1.00	0.39	0.19
35	409196	NM_001874	Hs.334873 carboxypeptidase M	1.00	0.43	0.13
	410023	AB017169	Hs.57929 slit (Drosophila) homolog 3	1.00	0.30	0.12
	420674	NM_000055	Hs.1327 butyrylcholinesterase	1.00	0.30	0.08
	415165	AW887604	Hs.78065 complement component 7	1.00	0.08	0.06
	425545	N98529	Hs.158295 Homo sapiens, clone MGC:12401, mRNA, com	1.00	0.10	0.01
40	448256	BE614149	Hs.20814 CGI-27 protein	0.96	1.32	1.55
	417389	BE260964	Hs.82045 midkine (neurite growth-promoting factor	0.95	3.15	2.34
	403214		NM_016232*:Homo sapiens interleukin 1 re	0.94	1.63	2.51
	414799	AI752416	Hs.77326 insulin-like growth factor binding prote	0.92	1.87	1.60
	405665	U22961	Hs.184411 albumin	0.92	1.09	1.03
45	401519		C15000476*:gij12737279 ref XP_012163.1	0.88	1.46	3.44
	417501	AL041219	Hs.82222 sema domain, immunoglobulin domain (Ig),	0.87	0.41	0.50
	409632	W74001	Hs.55279 serine (or cysteine) proteinase inhibito	0.85	1.38	1.43
	405494		C2001837*:gij12697903 dbj BAB21770.1 (A	0.83	1.46	4.65
	444171	AB016249	Hs.10458 small inducible cytokine subfamily A (Cy	0.80	0.91	0.91
50	439706	AW872527	Hs.59761 ESTs, Weakly similar to DAP1_HUMAN DEATH	0.79	0.58	0.43
	436396	AI683487	Hs.152213 wingless-type MMTV integration site fami	0.77	1.47	2.37
	426716	NM_006379	Hs.171921 sema domain, immunoglobulin domain (Ig),	0.75	1.13	1.18
	431347	AI133461	Hs.251664 insulin-like growth factor 2 (somatomedi	0.68	2.61	1.87
	413753	U17760	Hs.75517 laminin, beta 3 (nicotin (125kD), kalinin	0.68	2.70	4.96
55	426322	J05068	Hs.2012 transcobalamin 1 (vitamin B12 binding pr	0.67	1.50	1.36
	426514	BE616633	Hs.170195 bone morphogenetic protein 7 (osteogenic	0.56	2.05	2.46
	422282	AF019225	Hs.114309 apolipoprotein L	0.55	3.91	3.92
	409757	NM_001898	Hs.123114 cystatin SN	0.53	2.72	2.93
	427450	AB014526	Hs.178121 KIAA0626 gene product	0.52	1.34	1.97
60	414555	N98569	Hs.76422 phospholipase A2, group IIA (platelets,	0.50	1.04	1.05
	423774	L39064	Hs.1702 interleukin 9 receptor	0.49	2.81	6.46
	404977		Insulin-like growth factor 2 (somatomedi	0.28	5.78	5.17
	428336	AA503115	Hs.183752 microseminoprotein, beta-	0.21	1.47	1.56
	451668	Z43948	Hs.326444 cartilage acidic protein 1	0.18	4.05	3.60
65	428651	AF196478	Hs.188401 annexin A10	0.17	5.14	27.75
	421110	AJ250717	Hs.1355 cathepsin E	0.12	5.49	45.35

TABLE 4B

70 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

75 Pkey CAT Number Accession
431146 32854_1 ZB3850 AA459717 AW965384 AA333635
434037 37918_1 AF116601 AI110691 AF063566

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TABLE 4C

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
10	Pkey	Ref	Strand	Nt_position
	401271	9797373	Minus	61292-61911
15	401519	6649315	Plus	157315-157950
	401905	8671966	Plus	153965-154441,156599-156819
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
	402110	8131678	Minus	173689-174062
20	402522	9796493	Plus	20605-20731
	402727	9211324	Plus	54596-54777
	403005	5791501	Minus	16945-17053,20018-20403
	403106	7331404	Plus	77162-77350,81338-81511
25	403214	7630945	Minus	76723-77027,79317-79484
	404152	9884757	Plus	41111-41281,45495-45716,47801-47910
	404488	8113286	Minus	64835-64994
	404829	6624702	Minus	4913-5093,7310-7468,9472-9521,9951-10082
30	404860	8979555	Plus	65852-66081
	404977	3738341	Minus	43081-43229
	405494	8050952	Minus	70284-70518
	405735	9931101	Minus	29854-29976
	405738	9943998	Plus	44370-45410
	406076	9123123	Plus	89972-90319
	406397	9256243	Minus	127317-127454
	406471	9795566	Plus	87363-87589

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TABLE 5A: Genes upregulated in bladder cancer

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1	90th percentile of bladder tumor Als divided by the 90th percentile of normal body sample Als			
10	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	459702	AI204995		gb:an03c03.x1 Stralagene schizo brain S1	11.03
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	10.40
	404917			Target Exon	9.65
	401066			C11000517*:gij1293105[gb]AAF48490.1 (AE	9.00
15	447475	AI380797	Hs.158992	ESTs	8.92
	427335	AA448542	Hs.251677	G antigen 7B	8.66
	450061	AI797034	Hs.346238	ESTs	8.35
	401335			Target Exon	7.95
	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	7.35
20	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	7.20
	436608	AA628980		down syndrome critical region protein DS	4.86
	451950	AW292317	Hs.213307	ESTs	4.45
	406542			C19000728*:gij12585552[sp]Q9Y2Q1 Z257_HU	3.73
	437931	AI249468	Hs.124434	ESTs	3.70
25	443133	AI033878	Hs.41379	ESTs	3.60
	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	3.37
	402239			Target Exon	3.37
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.21
	403383			Target Exon	3.13
30	438315	R56795	Hs.82419	ESTs	3.04
	452827	AI571835	Hs.55468	ESTs	3.01
	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	3.01
	402948			NM_025206:Homo sapiens hypothetical prot	2.91
	429983	W92620	Hs.260855	ESTs	2.84
35	429238	NM_002849	Hs.198288	protein tyrosine phosphatase, receptor t	2.78
	444371	BE540274	Hs.239	forkhead box M1	2.75
	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.70
	414906	AA157911	Hs.72200	ESTs	2.70
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	2.68
40	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.62
	429345	R11141	Hs.199695	hypothetical protein	2.61
	414221	AW450979		gb:U1-H-B13-ala-a-12-O-ULs1 NCL_CGAP_Su	2.60
	402305			C19000735*:gij4508027[ref]NP_003414.1 z	2.54
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	2.51
45	427719	AI393122	Hs.134726	ESTs	2.51
	455797	BE091833		gb:LL2-BT0731-260400-076-F04 BT0731 Homo	2.50
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	2.49
	456967	AW004056	Hs.168357	T-box 2	2.49
	406387			Target Exon	2.48
50	417997	AA418189	Hs.23017	Homo sapiens cDNA: FLJ22747 fls, clone K	2.48
	415752	BE314524	Hs.78776	putative transmembrane protein	2.46
	411248	AA551536	Hs.334605	Homo sapiens cDNA FLJ14408 fls, clone HE	2.43
	434293	NM_004445	Hs.3796	EphB6	2.42
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fls, clone MA	2.40
55	425997	AK000086	Hs.165948	hypothetical protein FLJ20079	2.38
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.35
	452012	AA307703	Hs.279766	kinesin family member 4A	2.34
	445600	AF034803	Hs.12953	PTPRF interacting protein, binding prote	2.33
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.33
60	454609	AW810204		gb:MR4-ST0125-021199-017-008 ST0125 Homo	2.28
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), solub	2.26
	420005	AW271106	Hs.133294	ESTs	2.22
	439826	NM_014965	Hs.6705	KIAA1042 protein	2.22
	405531			Target Exon	2.21
65	436569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)	2.16
	404394			ENSP00000241075:TRRAP PROTEIN.	2.17
	427479	BE410092	Hs.178471	KIAA0798 gene product	2.17
	435904	AF261655	Hs.8910	1,2-alpha-mannosidase 1C	2.13
	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	2.12
70	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.10
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.10
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4:HR Homo	2.09
	403477			C3002160*:gij7662420[ref]NP_055738.1 Ki	2.09
	417151	AA194055	Hs.293858	ESTs	2.08
75	448262	AW880830	Hs.186273	ESTs	2.07
	415192	D17793	Hs.78183	aldo-keto reductase family 1, member C3	2.04
	402994			NM_002463*:Homo sapiens myxovirus (influ	2.04

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5	426053	U68105	Hs.172182	poly(A)-binding protein, cytoplasmic 1	2.02
	423271	W47225	Hs.126256	interleukin 1, beta	2.01
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.99
	407581	R48402	Hs.173508	P3ECSL	1.95
	410197	NM_005518	Hs.59989	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.95
10	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	1.93
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.93
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	1.89
	401961			NM_021626:Homo sapiens serine carboxypep	1.86
	434042	A1589941	Hs.8254	Homo sapiens, Similar to tumor different	1.85
15	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.84
	418526	BE018020	Hs.85838	solute carrier family 16 (monocarboxylic	1.83
	428612	AF062649	Hs.252587	pituitary tumor-transforming 1	1.80
	422164	NM_014312	Hs.112377	cortic al thymocyte receptor (X. laevis	1.80
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	1.79
20	410407	X66839	Hs.63287	carbonic anhydrase IX	1.78
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	1.77
	414809	A1434699	Hs.77356	transferrin receptor (p90, CD71)	1.75
	432210	A1567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.74
	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.74
25	459198	A1086347	Hs.151138	ESTs	1.74
	421066	AU076725	Hs.101408	branched chain aminotransferase 2, mitoc	1.71
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.70
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	1.70
	417324	AW265494		ESTs	1.67
30	453883	A1638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.66
	428000	R35145	Hs.291904	accessory proteins BAP31/BAP29	1.65
	450635	AW403954	Hs.25237	mesenchymal stem cell protein DSCD75	1.63
	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	1.62
	415440	D83782	Hs.78442	SREBP CLEAVAGE-ACTIVATING PROTEIN	1.62
35	428028	U52112	Hs.182018	interleukin-1 receptor-associated kinase	1.62
	426783	Z19084	Hs.172210	MUF1 protein	1.62
	445937	A1452943	Hs.321231	UDP-Gal:betaGlcNAc beta 1,4-galactosylt	1.61
	445462	AA378776	Hs.289649	hypothetical protein MGC3077	1.60
	400965			C11002190*.gil12737279[ref:XP_012163.1]	1.59
40	432269	NM_002447	Hs.2942	macrophage stimulating 1 receptor (c-met	1.59
	429578	A1969028	Hs.99389	ESTs	1.59
	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	1.59
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	1.59
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.59
45	429002	AW248439	Hs.2340	junction plakoglobin	1.57
	442410	AW996503	Hs.197680	ESTs	1.56
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	1.55
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.54
	424611	NM_001421	Hs.151139	E74-like factor 4 (ets domain transcript	1.54
50	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.54
	406930	AA146721	Hs.334686	hypothetical protein FLJ21588	1.53
	448993	A1471630	Hs.8127	KIAA0144 gene product	1.52
	414053	BE391635	Hs.75725	transgelin 2	1.51
	433662	W07162	Hs.150826	CATX-8 protein	1.50
55	432562	BE531048	Hs.278422	DKFZP586G1122 protein	1.50
	402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.48
	426127	L36983	Hs.167013	dynamitin 2	1.48
	427567	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	1.48
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	1.47
60	418960	NM_004494	Hs.89525	hepatoma-derived growth factor (high-mob	1.46
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	1.46
	432344	A1476474	Hs.248156	ESTs	1.46
	453449	W16752	Hs.32981	sema domain, immunoglobulin domain (Ig),	1.46
	450690	AA296696	Hs.333418	FX1D domain-containing ion transport reg	1.46
65	441940	AW298115	Hs.128152	ESTs	1.45
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.44
	436318	AW837046	Hs.6527	G protein-coupled receptor 56	1.42
	422665	BE269035	Hs.118400	singed (Drosophila)-like (sea urchin fas	1.41
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	1.41
70	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	1.39
	441565	AW953675	Hs.303125	p53-induced protein PIGPC1	1.37
	439180	A1393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.35
	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	1.32
	432636	AA340864	Hs.278562	claudin 7	1.32
75	439053	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	1.32
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	1.31
	453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	1.26
	430056	X97548	Hs.229059	KRAB-associated protein 1	1.24
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.23
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	1.20
	439863	BE547830	Hs.9408	paired immunoglobulin-like receptor beta	1.19

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5	461541	BE279383	Hs.26557	plakophilin 3	1.16
	406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.11
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	1.00
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	0.86
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (0.61

TABLE 5B

10 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

15	Pkey	CAT Number	Accession
	414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW236038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
20	417324	166714_1	AW265494 AA455904 AA195677 AW265432 AW991605 AA456370
	436608	42361_3	AA628980 A1126603 BE604035
	451365	86787_1	AA017656 AA017374 AA019761
	454609	1226517_1	AW810204 AW810555 AW810196 AW810619 AW810507
	455797	1366826_1	BE091833 BE091874 BE091871

TABLE 5C

25 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

35	Pkey	Ref	Strand	Nt_position
	400965	7770576	Minus	173043-173564
40	401066	8217436	Plus	71448-71574
	401335	9884881	Plus	15736-16352
45	401961	4581193	Minus	124054-124209
	402239	7690131	Plus	38175-38304,42133-42266
50	402260	3399665	Minus	113765-113910,115653-115765,116808-116940
	402305	7328724	Plus	40832-41362
40	402948	9368458	Minus	143456-143626,143808-143935
	402994	2996643	Minus	4727-4969
45	403363	9438267	Minus	119837-121197
	403477	9958251	Plus	111834-112008
50	404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
	404917	7341851	Plus	49330-49498
45	405531	9665194	Plus	35602-35803
	406387	9256180	Plus	116229-116371,117512-117651
50	406542	7711499	Plus	117335-118473

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TABLE 6A: Genes upregulated in bladder cancer

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1	90th percentile of bladder tumor Als divided by the 90th percentile of normal urothelium biopsy Als			
10	R2	90th percentile of bladder tumor Als divided by the 90th percentile of normal urothelium biopsy and normal bladder Als			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
	439926	AW014875	Hs.137007	ESTs	11.31 11.31
	413324	V00571	Hs.75294	corticotropin releasing hormone	9.15 9.15
	421110	AJ250717	Hs.1355	cathepsin E	9.07 9.07
15	417308	H60720	Hs.81892	KIAA0101 gene product	8.50 8.50
	418406	X73501	Hs.84905	cytokeratin 20	8.10 8.10
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.98 7.98
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	7.67 7.67
	408243	Y00787	Hs.624	interleukin 8	7.56 7.56
20	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	7.17 5.17
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	7.17 8.24
	414183	AW957446	Hs.301711	ESTs	7.14 4.62
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.12 7.12
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	6.90 3.38
25	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	6.85 4.98
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	6.42 6.42
	438091	AW373062		nuclear receptor subfamily 1, group I, m	6.32 6.32
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.09 3.67
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	5.93 4.68
30	405033			C1002652*gi544327[sp]C04799[FMO5_RABIT	5.84 5.84
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	5.79 5.68
	428336	AA503115	Hs.183752	microseminoprotein, beta-	5.78 4.57
	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	5.69 5.82
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	5.69 7.30
35	415511	A1732617	Hs.182362	ESTs	5.65 5.65
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	5.60 5.60
	421948	L42583	Hs.334309	keratin 6A	5.59 14.20
	428651	AF196478	Hs.188401	annexin A10	5.55 5.55
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.38 5.59
40	406687	M31126		matrix metalloproteinase 11 (stromelysin	5.36 5.34
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	5.35 5.35
	408246	N56669	Hs.333823	mitochondrial ribosomal protein L13	5.20 3.50
	427678	BE267766	Hs.180312	mitochondrial ribosomal protein S16	5.13 4.10
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	4.97 3.71
45	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	4.90 4.90
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.90 4.77
	417720	AA206625	Hs.209067	ESTs	4.84 7.34
	423979	AF229181	Hs.136644	CS box-containing WD protein	4.81 4.81
	420981	L40904	Hs.100724	peroxisome proliferative activated recep	4.81 4.43
50	433470	AW960564		transmembrane 4 superfamily member 1	4.72 4.72
	429138	AB020657	Hs.197298	NS1-binding protein	4.71 4.71
	408063	BE086548	Hs.42346	calcineurin-binding protein calcarsin-1	4.71 4.71
	452714	AW770994	Hs.30340	hypothetical protein KIAA1165	4.69 4.69
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	4.68 4.68
55	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	4.65 4.65
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	4.64 4.64
	427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	4.63 5.12
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.61 4.61
	418030	BE207573	Hs.83321	neuromedin B	4.60 4.60
60	401192			Target Exon	4.60 4.29
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFp58612022 (f	4.59 3.51
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	4.58 5.33
	449618	AI076459	Hs.15978	KIAA1272 protein	4.58 4.58
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.55 4.55
65	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	4.52 4.70
	446742	AA232119	Hs.16085	putative G-protein coupled receptor	4.49 4.11
	419433	AA814807	Hs.7395	hypothetical protein FLJ23182	4.48 4.48
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	4.47 4.47
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.45 4.45
70	444371	BE540274	Hs.239	forkhead box M1	4.44 3.87
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	4.43 3.63
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	4.43 4.43
	401093			C1200586*gi6330167[pt]BAA86477.1[(A	4.40 4.40
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.39 4.39
75	417933	X02308	Hs.82962	thymidylate synthetase	4.38 4.35
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.36 3.68
	401451			NM_004496*Homo sapiens hepatocyte nucle	4.35 4.35
	450746	D82673	Hs.278589	general transcription factor II, i	4.35 3.36

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5	414663	S78296	Hs.76888	hypothetical protein MGC12702	4.34	4.74
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.31	4.31
	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	4.30	4.30
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.30	4.30
	440066	NM_005402	Hs.288757	v-rai simian leukemia viral oncogene hom	4.29	4.29
10	417715	AW969587	Hs.86366	ESTs	4.27	7.45
	409757	NM_001898	Hs.123114	cystatin SN	4.24	3.39
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	4.24	4.24
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	4.21	4.12
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	4.20	4.20
15	436856	AI469355	Hs.127310	ESTs	4.19	4.19
	428450	NM_014791	Hs.184339	KIAA0175 gene product	4.16	4.90
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.14	4.14
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.14	5.99
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	4.12	4.12
20	446649	AU076617	Hs.16251	cleavage and polyadenylation specific fa	4.12	3.43
	400843			NM_003105*:Homo sapiens sortilin-related	4.11	5.51
	449722	BE280074	Hs.23960	cyclin B1	4.09	4.09
	405506			Target Exon	4.09	3.75
	420344	BE483721	Hs.97101	putative G protein-coupled receptor	4.07	4.07
25	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	4.05	4.80
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.03	7.64
	437150	R51407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.02	4.02
	413794	AF234532	Hs.61638	myosin X	4.02	4.02
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	4.02	4.72
30	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.01	3.99
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	4.01	4.01
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.00	4.00
	400277			Eos Control	4.00	3.47
	415791	H09366	Hs.78853	uracil-DNA glycosylase	3.99	3.37
35	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.98	4.77
	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	3.98	3.95
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	3.96	6.95
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.92	5.04
	400409	AF153341		Homo sapiens winged helix/forkhead trans	3.91	3.88
40	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	3.90	3.90
	411676	AI907114	Hs.71465	squalene epoxidase	3.89	3.89
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	3.87	3.87
	428426	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	3.87	3.87
	442932	AA457211	Hs.8958	bromodomain adjacent to zinc finger doma	3.85	4.50
45	429083	Y09397	Hs.227817	BCL2-related protein A1	3.85	3.85
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.82	3.77
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.82	3.82
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.81	3.81
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.81	3.62
50	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	3.80	3.80
	447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.77	3.77
	404875			NM_022819*:Homo sapiens phospholipase A2	3.77	3.46
	411299	BE409857	Hs.69499	hypothetical protein	3.76	3.76
	418827	BE327311	Hs.47166	HT021	3.76	3.76
55	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.75	3.75
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.73	3.73
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.71	3.71
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	3.70	3.45
	409518	BE384836	Hs.3454	KIAA1821 protein	3.69	3.69
60	430024	AI808780	Hs.227730	integrin, alpha 6	3.69	3.69
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	3.68	3.68
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.68	3.68
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.67	3.67
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	3.67	3.41
65	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	3.67	3.88
	434263	N34895	Hs.44648	ESTs	3.65	3.65
	438280	AW015534	Hs.217493	annexin A2	3.63	3.36
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.63	3.68
	408989	AW361666	Hs.49500	KIAA0746 protein	3.61	3.66
70	416640	BE262478	Hs.79404	neuron-specific protein	3.60	4.22
	416926	H03109	Hs.108920	HT018 protein	3.59	3.59
	414368	W70171	Hs.75939	uridine monophosphate kinase	3.59	3.53
	402727			NM_025065:Homo sapiens hypothetical prot	3.58	3.58
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.56	3.77
75	416114	AI695549	Hs.183868	glucuronidase, beta	3.55	3.55
	424941	AA128376	Hs.153884	ATP binding protein associated with cell	3.55	3.55
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	3.54	4.63
	429238	NM_002849	Hs.198288	protein tyrosine phosphatase, receptor t	3.53	3.92
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	3.51	5.77
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.50	3.50
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.50	3.50

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	415220	AA431860	Hs.181174	ESTs, Weakly similar to T19201 hypotheti	3.50	3.50
	428371	AB012193	Hs.183874	culin 4A	3.46	3.46
	418663	AK001100	Hs.41690	desmocollin 3	3.45	4.74
	404977			Insulin-like growth factor 2 (somatomedi	3.45	3.89
5	422663	AW500087	Hs.119014	zinc finger protein 175	3.44	3.44
	434061	AW024973	Hs.283675	NPD009 protein	3.41	5.64
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.41	4.32
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.40	3.40
10	411943	BE502436	Hs.7962	ESTs, Weakly similar to S44608 C02F5.6 p	3.39	4.27
	420005	AW271106	Hs.133294	ESTs	3.38	3.40
	453450	AW797627	Hs.347459	ADP-ribosylation factor 6	3.38	3.87
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	3.36	3.36
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.35	3.35
15	437469	AW753112	Hs.15514	hypothetical protein MGC3260	3.35	3.35
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.34	3.34
	428157	AI738719	Hs.198427	hexokinase 2	3.33	3.73
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	3.33	3.33
	400750			Target Exon	3.33	3.33
20	450139	AK001838	Hs.296323	serum/glucocorticoid regulated kinase	3.33	3.33
	412636	NM_004415		desmoplakin (DPI, DPL)	3.30	4.81
	447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314 CDC28/cdc	3.27	3.38
	430315	NM_004293	Hs.239147	guanine deaminase	3.26	4.30
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	3.26	3.34
25	443030	R68048	Hs.9238	hypothetical protein FLJ23516	3.19	3.41
	438911	AA142984	Hs.5344	adaptor-related protein complex 1, gamma	3.17	3.40
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	3.06	3.52
	443171	BE281128	Hs.9030	TONDU	3.05	3.83
30	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, c'one	3.01	3.53
	408380	AF123060	Hs.44532	diubiquitin	2.99	4.11
	421508	NM_004833	Hs.105115	absent in melanoma 2	2.99	3.67
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.97	4.55
	452046	AB018345	Hs.27657	KIAA0802 protein	2.95	3.39
	451940	AI735759	Hs.52620	integrin, beta 8	2.93	3.58
35	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	2.90	3.68
	422282	AF019225	Hs.114309	apolipoprotein L	2.89	3.57
	402230			Target Exon	2.88	5.36
	406685	M18728		gb:Human nonspecific crossreacting antig	2.80	5.80
40	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	2.79	3.89
	447957	NM_014821	Hs.20126	KIAA0317 gene product	2.75	3.45
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.75	3.46
	417275	X63578	Hs.295449	parvalbumin	2.73	3.54
	431211	M96849	Hs.323733	gap junction protein, beta 2, 26kD (conn	2.72	8.39
	401781			Target Exon	2.62	4.15
45	407242	M18728		gb:Human nonspecific crossreacting antig	2.54	5.96
	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	2.52	4.27
	430200	BE613337	Hs.234896	geminin	2.52	4.19
	451035	AU076785	Hs.430	plastin 1 (i isoform)	2.51	4.15
	443162	T49951	Hs.9029	DKFZP434G032 protein	2.48	3.66
50	441495	AW294603	Hs.127039	ESTs	2.45	3.60
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	2.45	3.52
	401780			NM_005557*:Homo sapiens keratin 16 (foca	2.22	4.49
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.20	3.55
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	2.15	6.08
55	439394	AA149250	Hs.56105	ESTs	2.05	3.95
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.79	3.88

TABLE B3

60	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

65	Pkey	CAT Number	Accession
	412636	13165_1	NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376762 AW848769 AW361413 AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 AW990985 BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584 BE004047 AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AI805935 AW747877 AW748114 BE148516 AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157 AW365154 AW068840 BE005272 AW365145 BE001925 BE182166 BE144243 BE001923 AI951766 AI434518 BE184920 BE184933 AI284090 BE184941 AW804674 BE184924 C04715 W39488 AW995615 BE184948 BE159646 AW606653 AA099891 AA131128 AA337270 AA340777 AW384371 AA852212 R58704 AW366566 AW364859 AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW830264 AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090 AA066401 H91011 AW368529 AW390272 C13467 AW874920 N57176 AAC26480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784 AI022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95046 W25453 AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470 AI392926 AF139065 AW370813 AW370827 AW798417 AW798780 AW798883 AW798569 R33557 AA149190 C03029

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AW177783 AA088866 AW370829 AA247685 BE002273 A1760816 A1439101 AW879451 A1700963 AA451923 A1340326 A1590975 T48793
A1568096 A1142882 AA039975 A1470146 AA945936 BE067737 BE067786 W19287 AA644381 AA702424 A1417612 A1306554 A1686869
A1568892 AW190555 A1571075 A1220573 AA056527 A1471874 A1304772 AW517828 A1915596 A1627383 A1270345 AW021347 AW166807
AW105614 A1346078 AA552300 W95070 A1494069 A1911702 AA149191 AA026864 A1830049 A1887258 AW780436 A1910434 A1819984
A1658282 A1078449 A1025932 A1860584 A1635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514557 AW591892 T87181
AA782066 AW243815 AW150038 AW268383 AW004633 A1927207 AA782109 AW473233 A1804485 AW169216 A1572669 AA602182
AW015480 AW771865 A1270027 AA961816 AA263207 A1076962 A1498487 A1348053 A1783914 H44405 AW799118 AA128330 AA515500
AA918281 W02156 A1905927 AA022701 W38382 R20795 T77661 AW660878
AW960564 AA092457 T55890 D56120 T92525 A1815987 BE182608 BE182595 AW080238 M90657 AA347236 AW961666 AW176446
AA304671 AW583735 T61714 AA316968 A1446616 AA343532 AAC83489 AA488005 W52095 W39480 N57402 D82638 W25540 W52847
D82729 D58990 BE619182 AA315188 AA308636 AA112474 W76162 AAC88544 H52265 AA301631 H80982 AA113786 BE620997 AW651691
AA343799 BE613669 BE547180 BE546656 F11933 AA376800 AW239185 AA376086 BE544387 BE619041 AA452515 AA001806 AA190873
AA180483 AA158546 F00242 A1940609 A1940602 A189753 T97663 T66110 AW062896 AW062910 AW062902 A1051622 A1828930 AA102452
A1685095 A1819390 AA557597 AA383220 A1804422 A1633575 AW336147 AW603423 AW060600 AW750567 AW510672 A1250777 AA063510
AW629109 AW513200 AA921353 A1677934 A1148698 A1955858 AA173625 AA453027 A1027865 AW375542 AA454099 AA733014 A1591384
R79300 R80023 AA843108 AA626058 AA844898 AW375550 AA889018 A1474275 AW206937 A1052270 AW388117 AW388111 AA699452
A1242230 N47476 H38178 AA366621 AA113196 AA130023 H39740 T61629 A1885973 AW083671 AA179730 AA305757 A1285455 N83956
AA216013 AA336155 AW999959 T97525 AA345349 T91762 AA771981 A1285092 A1591386 BE392486 BE385852 AA682601 A1682684
AA345840 T85477 AA292949 AA932079 AA098791 D82607 T48574 AW752038 C06300
AW373062 T55662 A1299190 BE174210 AW579001 H01811 W40186 R67100 A1923886 AW952164 AA628440 AW898607 AW898616
AA709126 AW898628 AW898544 AA947932 AW898625 AW898622 A1276125 A1185720 AW510698 AA987230 T52522 BE467708 AW243400
AW043642 A1288245 A1186932 D52654 D55017 D52715 D52477 D53933 D54679 A1298739 A1146984 A1922204 N98343 BE174213 AA845571
A1813854 A1214518 A1635262 A1139455 A1707807 A1698085 AW884528 A1024768 A1004723 AW067420 A1565133 N94964 A1268939
AW513280 A1061126 A1435818 A1855106 A1360506 A1024767 AA513019 AA757598 X56196 AA902959 A1334784 A1860794 AA010207
AW890081 AW513771 A1951391 A1337671 T52499 AA890205 A1640908 H75966 AA463487 AA356868 A1961767 A1866295 AA780994
A1985913 BE174196 AA029094 AW592159 T55581 N79072 A1611201 AA910812 A1220713 AW149306 A1758412 AA045713 R79750 N76096

TABLE 6C

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Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400750	8119067	Plus	198991-199168,199316-199548
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
401093	8516137	Minus	22335-23166
401192	9719502	Minus	69559-70101
401451	6634068	Minus	119926-121272
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
402230	9966312	Minus	29782-29932
402727	9211324	Plus	54596-54777
404875	9801324	Plus	96588-96732,97722-97831
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
50 405506	6466489	Plus	80014-80401,80593-81125

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TABLE 7A: Genes downregulated in bladder cancer

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1 90th percentile of normal urothelium biopsy AIs divided by 75th percentile of bladder tumor AIs
 R2 90th percentile of normal urothelium biopsy and normal bladder AIs divided by the 90th percentile bladder tumor AIs

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
403010			C21000152:gl[6226483]spjQ52118 YMO3_ERWS	4.86	2.49
426796	S78234	Hs.172405	cell division cycle 27	4.28	2.48
416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	4.04	2.07
459006	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-like	3.82	2.66
404917			Target Exon	3.78	2.00
426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	2.64	1.79
419543	AA244170		gb:nc05h02.s1 NCL_CGAP_Pr1 Homo sapiens	2.63	3.42
453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	2.32	3.24
428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	2.20	3.80
451529	AI917901	Hs.208641	ESTs	2.18	3.69
417076	AW973454	Hs.238442	ESTs, Moderately similar to ALU7_HUMAN A	2.03	3.03
425438	T62216	Hs.270840	ESTs	2.00	5.17
450515	AW304225		biphenyl hydrolase-like (serine hydrolas	1.89	2.46
432873	AW837268	Hs.279639	Homo sapiens mRNA: cDNA DKFZp586M2022 (f	1.70	2.79
452123	AI267615	Hs.38022	ESTs	1.69	2.46
424378	W28020	Hs.167988	neural cell adhesion molecule 1	1.65	4.67
437601	AA761546	Hs.248844	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.50	3.34
402096			ENSP00000217725*:Laminin alpha-1 chain p	1.48	3.02
435563	AI018768	Hs.12482	glyceronephosphate O-acyltransferase	1.47	3.22
412810	M21574	Hs.74615	platelet-derived growth factor receptor,	1.46	2.30
458651	AW612481	Hs.104105	ESTs	1.39	2.89
414033	AL079707	Hs.207443	hypothetical protein MGC10848	1.36	2.80
433572	AL046859	Hs.3407	protein kinase (cAMP-dependent, catalyti	1.35	3.49
413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	1.34	2.93
420412	AW976674	Hs.125103	ESTs	1.32	5.13
421406	AF179897	Hs.104105	Meis (mouse) homolog 2	1.31	4.07
417446	AL118671	Hs.82163	monoamine oxidase B	1.27	2.86
452886	AI478250	Hs.13751	ESTs	1.26	1.95
446808	AA703226	Hs.16193	Homo sapiens mRNA: cDNA DKFZp586B211 (fr	1.25	3.44
443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	1.24	2.07
421348	M94048	Hs.103724	peripheral myelin protein 22	1.24	2.63
433070	N75346	Hs.306121	CDC20 (cell division cycle 20, S. cerevi	1.23	2.80
420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	1.22	3.43
408491	AI088063	Hs.7882	ESTs	1.20	6.01
447384	AI377221	Hs.40528	ESTs	1.00	7.92
421998	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	1.00	7.38
409619	AK001015	Hs.55220	BCL2-associated athanogene 2	1.00	6.40
444795	AI193356	Hs.160316	ESTs	1.00	5.53
406495	W68796	Hs.237731	ESTs	1.00	5.05
417124	BE122762	Hs.25338	ESTs	1.00	4.73
443998	AI620661	Hs.296276	ESTs	1.00	4.39
406303			C16000922:gl[7499103]pir T20903 hypothe	1.00	4.37
422994	AW891802	Hs.296276	ESTs	1.00	4.37
422195	AB007903	Hs.113082	KIAA0443 gene product	1.00	4.35
452877	AI250789	Hs.32478	ESTs	1.00	3.90
452487	AW207659	Hs.5630	Homo sapiens cDNA FLJ13329 fis, clone OV	1.00	3.90
417159	R01761		gb:ye81f10.s1 Soares fetal liver spleen	1.00	3.82
445607	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	1.00	3.62
406274			Target Exon	1.00	3.59
410611	AW954134	Hs.20924	KIAA1628 protein	1.00	3.06
426495	NM_001151	Hs.2043	solute carrier family 25 (mitochondrial	1.00	2.89
422292	AI815733	Hs.114360	transforming growth factor beta-stimulat	1.00	2.61
413040	AA193338	Hs.12321	sodium calcium exchanger	1.00	2.51
429623	NM_005308	Hs.211569	G protein-coupled receptor kinase 5	1.00	2.05
456607	AI660190	Hs.106070	cyclin-dependent kinase inhibitor 1C (p5	1.00	2.01
429143	AA333327	Hs.197335	plasma glutamate carboxypeptidase	0.97	2.45
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	0.90	2.47
442498	U54517	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	0.88	5.08
414449	AA557660	Hs.75152	decorin	0.88	3.13
412014	AI620650	Hs.43761	ESTs, Weakly similar to A46010 X-linked	0.76	1.88
425100	AF051850	Hs.154567	supervillin	0.70	3.90
432094	AI658580	Hs.61426	Homo sapiens mesenchymal stem cell prote	0.68	3.41
427818	AW511222	Hs.193765	ESTs	0.63	3.75

TABLE 7B

Pkey: Unique Eos probeset identifier number

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CAT number: Gene cluster number
Accession: Genbank accession numbers

5 Pkey CAT Number Accession
417159 1653899_1 R01761 R01760 N49787
419543 185745_1 AA244170 AI018087 AA244355
450515 83710_1 AW304226 AW008420 AA349212 H15015 AA317021 AI829484 H25661 H61744 AI906147 AA837938 AW167766 AW603578 AW842369
10 BE439926 AA902417 AW235409 AA010062 AW069319 AI280242 AW672925 H06848 H05808 R51905 R45023 AW675471 H28475 AI086597
AI197815 AI825355 N89134 AI075956 AI470122 AA449985 AW662833 AA850423 AA913342 T23825 AI394207 AI310319 T32467 AI589870
AI682293 AI810633 BE223045 H14620 AA626645 AA876023 T33571 AA953962 AI138631 H15016 AI304356 AA983631 AI350990 AI143993
AI708171 AA526961 H26247 W36486 AA847598 H81745 AW855486 BE299605 AI079409 AI278050 AI223158 AI860904 AW025415 AI339003
AA393692 AI354302 AI492838 N80194 AI015651 N34543 BE295397 AI085154 W24135

15 TABLE 7C

20 Pkey: Unique number corresponding to an Eos probeset.
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

25 Pkey Ref Strand Nt_position
402096 8117697 Minus 24993-25186
403010 3132346 Plus 78385-79062
404917 7341851 Plus 49330-49498
406274 7543787 Plus 932-1123
30 406303 8575868 Plus 173622-173786

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TABLE 8A: Genes predictive of bladder cancer progression

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1	80th percentile of Ta or T1 tumor Als from patients who upstaged divided by 80th percentile of Ta or T1 tumor Als from patients who did not upstage			
10	R2	median of Ta or T1 tumor Als from patients who upstaged divided by the median of Ta or T1 tumor Als from patients who did not upstage			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
	413324	V00571	Hs.75294	corticotropin releasing hormone	8.30 4.18
	437802	AI475995	Hs.122910	ESTs	7.51 2.50
	444444	AI149332	Hs.14855	ESTs	2.58 1.38
15	445033	AV652402	Hs.72901	mucin 13, epithelial transmembrane	2.26 1.13
	417771	AA804698	Hs.82547	retinoic acid receptor responder (Iazaro	3.27 5.33
	449618	AI076459	Hs.15978	KIAA1272 protein	2.70 3.33
	407242	M18728		gb:Human nonspecific crossreacting anti	3.58 1.90
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	3.32 1.00
20	423441	R68649	Hs.278359	absent in melanoma 1 like	2.44 2.40
	406033			C1002652*gi544327 sp Q04799 FMO5_RABIT	1.75 3.48
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	3.72 1.28
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	2.40 2.78
	437928	NM_005476	Hs.5920	UDP-N-acetylglucosamine-2-epimerase/N-ac	2.20 1.53
25	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	1.38 2.33
	436608	AA628980		down syndrome critical region protein DS	3.32 4.53
	404440			NM_021048:Homo sapiens melanoma antigen,	2.84 1.00
	436602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.06 1.09
	424098	AF077374	Hs.139322	small proline-rich protein 3	2.47 3.64
30	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	2.09 0.91
	428036	AW068302		Homo sapiens mRNA for caldesmon, 3' UTR	2.71 4.58
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.18 2.33
	448479	H96115	Hs.21293	UDP-N-acetylglucosamine pyrophosphorylas	2.81 1.81
	412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferri	1.90 2.02
35	401241	AB028969		mitogen-activated protein kinase 8 inter	1.26 2.55
	406741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.12 1.23
	415989	AI267700		ESTs	1.60 1.00
	431070	AW408184	Hs.249184	transcription factor 19 (SC1)	1.73 1.50
	452140	AB007928	Hs.28169	KIAA0459 protein	2.44 2.95
40	443162	T49951	Hs.9029	DKFZP434G032 protein	2.98 1.00
	435904	AF261655	Hs.8910	1,2-alpha-mannosidase 1C	2.56 1.20
	407379	AA332127	Hs.325804	transcription factor 17	2.10 1.72
	442712	BE465168	Hs.131011	ESTs	2.54 2.72
	411678	AI907114	Hs.71465	squalene epoxidase	1.12 3.11
45	406791	AI220684	Hs.347939	hemoglobin, alpha 2	1.69 1.38
	431805	NM_014053	Hs.270594	FLVCR protein	1.92 2.05
	438414	AA806794	Hs.131511	ESTs	1.04 2.15
	413924	AL119964	Hs.75616	seleadin-1	1.69 2.05
	437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	2.27 2.26
50	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	1.42 2.74
	408349	BE546947	Hs.44276	homeo box C10	1.60 2.05
	422545	X02761	Hs.287820	fibronectin 1	1.77 3.02
	406643	N77976	Hs.347939	hemoglobin, alpha 2	1.57 1.35
	407228	M25079	Hs.155376	hemoglobin, beta	1.81 1.50
55	449644	AW960707	Hs.148324	ESTs	1.90 3.19
	402305			C19000735*gi4508027 ref NP_003414.1 z	2.25 1.49
	427683	BE545490	Hs.15053	Homo sapiens HCMOGT-1 mRNA for sperm ant	1.08 2.25
	441690	R81733	Hs.33106	ESTs	1.80 2.65
	434467	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	2.13 1.63
60	403362			NM_001615*:Homo sapiens actin, gamma 2,	2.33 2.22
	445496	AB007860	Hs.12802	development and differentiation enhancin	1.12 2.60
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	1.83 3.05
	402366	AV648601		apolipoprotein B (including Ag(x) antige	1.32 2.05
	427254	AL121523	Hs.97774	ESTs	2.44 1.00
65	414533	AA149060	Hs.296100	ESTs	1.70 2.06
	430157	BE348706	Hs.278543	ESTs	2.54 3.00
	413433	NM_003199	Hs.326198	transcription factor 4	2.26 1.41
	410532	T53088	Hs.155376	hemoglobin, beta	1.52 1.56
	405779			NM_005367:Homo sapiens melanoma antigen,	2.42 1.22
70	450455	AL117424	Hs.25035	chloride intracellular channel 4	2.48 2.13
	414081	AW969976	Hs.279009	matrix Gla protein	1.81 1.53
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	1.65 2.08
	415062	H45100	Hs.49753	uveal autoantigen with coiled coil domai	1.62 3.75
	406317			C2002658*gi6625694 gb AA19354.1 AF185	1.68 2.11
75	453259	R93125	Hs.124187	ESTs	1.08 2.25
	445937	AI452943	Hs.321231	UDP-Gal:betaGlcNAc beta 1,4- galactosyl	1.76 1.01
	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	1.12 2.08
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.02 2.40

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5	432331	W37862	Hs.274368	MSTP032 protein	4.36	2.18
	451735	AW080356	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.51	3.45
	413109	AW389845	Hs.110855	ESTs	4.34	5.98
	413643	AA130987	Hs.188727	ESTs	1.30	2.42
	433217	AB040914	Hs.278628	KIAA1481 protein	1.70	2.49
10	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	1.79	1.66
	438006	BE148799	Hs.127951	hypothetical protein FLJ14503	1.76	2.04
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	2.32	2.45
	433656	AW974941	Hs.292385	ESTs, Weakly similar to I78835 serine/th	1.14	2.50
	415714	NM_002290	Hs.78672	laminin, alpha 4	2.52	1.13
15	450282	AA007655	Hs.93523	ESTs	1.40	2.58
	442855	AI074465	Hs.133469	ESTs	1.54	2.20
	432917	NM_014125	Hs.241517	PRO0327 protein	2.24	3.03
	429041	AJ132820	Hs.194768	a disintegrin and metalloproteinase doma	1.61	2.60
	442807	AL049274	Hs.8736	Homo sapiens mRNA; cDNA DKFZp564H203 (fr	1.73	1.19
20	427719	AI393122	Hs.134726	ESTs	1.46	2.00
	408778	AI500519	Hs.63382	hypothetical protein PRO2714	1.46	2.58
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.40	2.03
	424425	AB031480	Hs.146824	SPR1 protein	1.60	1.11
	445391	T92576	Hs.191168	ESTs	1.69	2.40
25	446899	NM_005397	Hs.16426	podocalyxin-like	1.22	2.42
	420996	AK001927	Hs.100895	hypothetical protein FLJ10462	2.68	2.98
	424909	S78187	Hs.153752	cell division cycle 25B	2.18	1.33
	413593	AA205248		gb:zq78c12.r1 Stratagene hNT neuron (937	1.69	2.00
	408734	AW264996	Hs.254299	ESTs	2.06	2.94
30	413880	AI660842	Hs.110915	interleukin 22 receptor	1.24	2.20
	437063	AA351109	Hs.5437	Tax1 (human T-cell leukemia virus type I	1.78	2.60
	418044	AI640532	Hs.119830	ESTs, Weakly similar to ALUF_HUMAN IIII	1.54	2.53
	441971	W27060	Hs.265855	ESTs	1.62	2.13
	450401	AW959281	Hs.8184	ESTs	1.42	2.30
35	440157	AA868350	Hs.343636	ESTs	1.38	2.60
	457587	AA992841	Hs.27263	KIAA1458 protein	1.47	2.42
	440707	BE256751	Hs.22867	Homo sapiens cDNA: FLJ22073 fis, clone H	1.18	2.10
	402241			Target: Exon	2.58	2.52
	413428	AA430155	Hs.151343	KIAA1524 protein	1.22	2.45
40	416735	R11275	Hs.194485	ESTs	1.14	2.14
	421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.25	1.03
	431031	AA830335	Hs.105273	ESTs	2.35	2.95
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	3.72	1.00
	420786	AW296466	Hs.43628	deleted in lymphocytic leukemia, 2	1.23	2.60
45	401335			Target: Exon	1.18	1.68
	417670	R07785		gb:yf15c06.r1 Soares fetal liver spleen	1.56	2.00
	406314			C14001020:gil12597441[gb]AAG60049.1[AF31	1.60	3.08
	458981	AW968318	Hs.285996	hypothetical protein FLJ23375	1.70	2.50
	417509	AA203414	Hs.42009	ESTs	1.82	2.05
50	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	1.34	1.37
	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	1.37	1.02
	457871	AI168278		ESTs	1.20	2.19
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	1.43	1.22
	413276	Z24725	Hs.75260	mitogen inducible 2	1.78	2.28
55	421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	2.55	2.60
	417151	AA194055	Hs.293858	ESTs	1.68	1.67
	453556	AA425414	Hs.33287	nuclear factor I/B	2.06	2.40
	440859	AW070865	Hs.346390	ESTs	1.12	1.70
	420629	AW204343	Hs.156823	ESTs, Weakly similar to T30868 RhoA-bind	1.21	2.38
60	422363	T55979	Hs.115474	replication factor C (activator 1) 3 [38	1.58	2.15
	434831	AA248060	Hs.273397	KIAA0710 gene product	1.69	1.78
	412055	AA099907	Hs.271806	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.36	2.65
	445468	AW450439		ESTs	1.52	2.50
	444550	BE250716	Hs.87614	ESTs	1.30	2.28
65	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	1.50	3.02
	430233	AW367902	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (f	1.24	2.95
	413444	BE141019		gb:MR0-HT0067-201099-002-b10 HT0067 Homo	1.68	2.80
	433844	AA610175	Hs.179647	Homo sapiens cDNA FLJ12195 fis, clone MA	1.49	2.01
	427055	AI301740	Hs.173381	dihydropyrimidinase-like 2	1.11	2.58
70	454244	R51604	Hs.300842	KIAA1608 protein	1.00	2.02
	429503	AA394183	Hs.26873	ESTs	2.58	4.08
	422940	BE077458		gb:RC1-BT0606-090500-015-b04 BT0606 Homo	3.48	2.46
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.13	1.48
	437312	AA809350	Hs.246180	ESTs	1.10	2.05
75	449426	T92251	Hs.198882	ESTs	1.22	2.08
	447620	AW290951	Hs.224865	ESTs	1.80	2.18
	444700	NM_003645	Hs.11729	fatty-acid-Coenzyme A ligase, very long-	1.72	2.81
	436258	AW867491	Hs.107125	plasmalemma vesicle associated protein	1.99	1.80
	415712	AW249188	Hs.169577	Homo sapiens cDNA FLJ14743 fis, clone NT	1.66	2.98
	432677	AW974111	Hs.292477	ESTs	1.63	2.79
	412085	AW891667		gb:CM3-NT0089-110500-179-h09 NT0089 Homo	1.40	2.08

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5	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	1.96	3.58
	409714	AW367812	Hs.199961	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.24	2.10
	423013	AW875443	Hs.22209	secreted modular calcium-binding protein	1.49	2.09
	422663	AW500087	Hs.119014	zinc finger protein 175	1.01	2.78
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	1.54	2.57
10	413196	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma	1.04	2.18
	439349	AI660898	Hs.195602	ESTs	2.03	2.43
	443005	AI027184	Hs.200918	ESTs	1.42	2.10
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.58	3.43
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	2.08	1.70
15	413916	N49813	Hs.75615	apolipoprotein C-II	0.70	0.42
	418332	R34976	Hs.78293	ESTs	2.74	2.43
	426552	BE297660	Hs.170328	moesin	1.28	1.52
	456583	AF179897	Hs.104105	Meis (mouse) homolog 2	1.42	2.02
	447214	AI367288	Hs.273621	Homo sapiens cDNA: FLJ21350 fis, clone C	1.14	2.10
20	449254	W26908	Hs.172762	ESTs	2.04	2.50
	443651	W22152	Hs.282929	ESTs	2.94	3.08
	421021	AA808018	Hs.109302	ESTs	1.41	2.04
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.61	1.21
	432027	AL096678	Hs.272353	KIAA0957 protein	1.70	2.76
25	452688	AA721140	Hs.49930	ESTs, Weakly similar to putative p150 [H	1.80	2.95
	417042	C75563	Hs.113029	ribosomal protein S25	2.22	3.20
	443574	U83993	Hs.321709	purinergic receptor P2X, ligand-gated io	1.21	2.51
	429372	AA451859	Hs.99253	ESTs	1.28	2.43
	424290	AA338396		gb:EST43386 Fetal brain Homo sapiens c	1.82	2.03
30	428518	AW969656		gb:EST381733 MAGE resequences, MAGK Homo	1.72	2.52
	455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	1.65	3.03
	414665	AA160873	Hs.332053	serum amyloid A1	1.36	1.08
	418298	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	1.04	2.03
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	4.94	4.34
35	433924	AA618304	Hs.258785	ESTs	1.44	2.40
	452683	AI089575	Hs.9071	progesterone membrane binding protein	1.48	2.48
	439437	AI207788	Hs.343628	sialyltransferase 4B (beta-galactosidase	1.36	2.33
	432314	AA533447	Hs.312989	ESTs	0.96	2.78
	400881			NM_025080:Homo sapiens hypothetical prot	1.70	3.15
40	426477	AA379464		gb:EST92386 Skin tumor Homo sapiens cD	2.01	2.37
	454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	2.12	3.44
	423977	AA333232		gb:EST37283 Embryo, 8 week Homo sapien	1.38	2.13
	450396	AU077002	Hs.24950	regulator of G-protein signalling 5	2.13	3.28
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	1.90	2.23
45	415157	D63257		gb:HUM514B08B Clontech human: placenta po	1.29	2.90
	418236	AW994005	Hs.337534	ESTs	1.74	2.37
	454390	AB020713	Hs.56966	KIAA0908 protein	1.47	1.38
	436143	AA705245	Hs.192189	ESTs	1.46	2.45
	436251	BE515065	Hs.296585	nucleolar protein [KKE/D repeat]	1.43	2.07
50	450735	AI732321		SRY (sex determining region Y)-box 4	1.36	2.02
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	2.70	1.68
	447100	AI361801	Hs.167130	hypothetical protein	1.66	2.03
	453577	AL043049		gb:DKFP434A1523_r1 434 (synonym: htes3)	1.41	2.75
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.59	1.38
55	412632	AL120379	Hs.74284	aldehyde dehydrogenase 7 family, member	1.81	2.51
	423291	NM_004129	Hs.126590	guanylate cyclase 1, soluble, beta 2	1.54	2.83
	456172	R99050		gb:yq65c02.r1 Soares fetal liver spleen	1.46	2.68
	452123	AI267615	Hs.38022	ESTs	1.24	1.93
	433900	AA721668	Hs.257761	ESTs	1.78	2.66
60	408436	R31954	Hs.7885	phosphatidylinositol binding clathrin as	1.21	2.35
	417123	BE326521	Hs.159450	ESTs	1.46	2.09
	436023	T81819	Hs.302251	ESTs	2.68	2.70
	454150	AA131893	Hs.154088	hypothetical protein FLJ22756	1.40	2.50
	444094	AI695764	Hs.202394	ESTs	1.28	4.03
65	429176	AW975021	Hs.193800	ESTs	1.08	2.53
	422259	AA307584		gb:EST1178498 Colon carcinoma (HCC) cell	1.80	3.03
	451164	AA015912	Hs.60659	ESTs, Weakly similar to T46471 hypotheti	1.47	1.17
	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (Ig),	2.92	2.70
	455642	BE063965		gb:QV3-BT0296-140200-085-h01 BT0296 Homo	1.70	2.70
70	443387	BE139135	Hs.254629	ESTs	1.48	2.32
	420995	AA282495	Hs.89014	ESTs	1.45	1.51
	407329	AA576061	Hs.269834	ESTs, Weakly similar to ALUD_HUMAN IIII	1.13	2.38
	438797	C16161	Hs.283040	hypothetical protein PRO2543	0.99	2.75
	443357	AW016773		low molecular mass ubiquinone-binding pr	1.60	2.08
75	412656	AF006011	Hs.74375	dishevelled 1 (homologous to Drosophila	1.32	1.13
	427377	AU077029	Hs.177543	antigen identified by monoclonal antibod	1.24	0.79
	412200	R08110	Hs.187462	ESTs, Weakly similar to I38022 hypotheti	1.35	1.54
	432586	AA568548		ESTs	1.50	2.25
	411590	T96183		gb:ye09f07.s1 Stratagene lung (937210) H	1.22	2.53
	422672	X12784	Hs.119129	collagen, type IV, alpha 1	2.27	2.20
	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	1.59	2.11

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	419900	AI469960	Hs.170698	ESTs	1.30	2.68
	410805	AW804742	Hs.84264	acidic protein rich in leucines	1.16	2.28
	452560	BE077084	Hs.99969	ESTs	1.44	2.58
5	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	4.02	1.00
	424436	AW818428	Hs.4953	golgi autoantigen, golgin subfamily a, 3	1.10	2.00
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	1.45	1.28
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	1.82	2.10
	443696	AW607444	Hs.134622	ESTs	1.98	2.01
10	436094	AI798701	Hs.222222	ESTs	1.34	2.40
	420168	AF217508	Hs.95594	serine carboxypeptidase vitellogenic-like	1.58	2.45
	430325	AF004562	Hs.239356	syntactin binding protein 1	1.34	2.43
	439022	AA356599	Hs.173904	ESTs	2.76	2.40
	420563	AA278327	Hs.136237	ESTs, Moderately similar to Y140_HUMAN H	1.78	2.65
15	429494	AA769365	Hs.126058	ESTs	1.50	2.40
	420689	H79979	Hs.88678	ESTs	1.26	2.28
	448988	Y08763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.72	1.29
	439943	AW083789	Hs.124620	ESTs	1.45	2.84
	442300	AI765908	Hs.129166	ESTs	1.24	2.35
20	449614	AI989490	Hs.197703	ESTs	1.12	2.22
	444363	AI142827	Hs.143656	ESTs	1.32	2.08
	424479	AF064238	Hs.149098	smoothelin	1.59	1.10
	437321	AA768966	Hs.292026	ESTs, Weakly similar to 2109260A B cell	1.28	2.07
	431926	AW972724		gb:EST384816 MAGE resequences, MAGL Homo	1.52	2.63
25	433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ23538 fis, clone L	1.69	1.30
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.71	2.19
	437199	AL110175	Hs.306337	Homo sapiens mRNA; cDNA DKFZp564H0616 (f	1.48	2.50
	457450	AW294163	Hs.146127	ESTs	1.07	2.60
	456678	AF141305	Hs.173736	ancient ubiquitous protein 1	1.44	2.35
30	451079	AI827988	Hs.240728	ESTs, Moderately similar to PC4259 ferri	0.95	3.00
	405944			Target Exon	1.48	2.45
	408877	AA479033	Hs.130315	ESTs, Weakly similar to A47582 B-cell gr	1.38	2.20
	446682	AW205632	Hs.211198	ESTs	1.38	3.00
	431380	AW610282	Hs.291003	ESTs	1.43	2.64
35	442027	AI652926	Hs.128395	ESTs	1.18	2.43
	423578	AW960454	Hs.222830	ESTs	1.56	2.18
	441495	AW294603	Hs.127039	ESTs	2.80	1.73
	417900	BE250127	Hs.82906	ODC20 (cell division cycle 20, S. cerevi	1.36	1.18
	443949	AW827419	Hs.235070	ESTs	1.30	2.28
40	440495	AA887212	Hs.14161	hypothetical protein DKFZp434I1930	1.74	2.78
	449948	R19156	Hs.20798	ESTs	1.12	2.23
	439564	W77911	Hs.110006	ESTs	1.34	2.85
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	1.24	1.09
	436139	AA765786	Hs.120336	ESTs	1.30	2.10
45	456968	AI174861	Hs.190623	ESTs	1.14	2.15
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	1.21	2.18
	411652	AW855393		gb:CM3-CT0275-191099-024-f10 CT0275 Homo	1.85	1.94
	420732	AA789133	Hs.88650	ESTs	1.66	2.71
	409291	AW373472		gb:RC3-BT0523-181299-011-d12 BT0523 Homo	1.56	2.30
50	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	1.56	1.39
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	1.58	1.24
	450946	AA374569	Hs.127698	ESTs, Moderately similar to 2109260A B c	1.02	2.25
	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	1.70	2.39
	415361	F06724		gb:HSC1IG021 normalized infant brain cDN	1.34	2.40
55	406490			C5001926:gi 7511572 pir T42245 probable	1.28	2.40
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	1.52	2.00
	440010	AA534930	Hs.127236	hypothetical protein FLJ12879	1.12	2.20
	429508	AW369620	Hs.33944	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.33	2.28
	426340	Z97989	Hs.169370	FYN oncogene related to SRC, FGR, YES	1.88	2.18
60	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	1.65	1.16
	451870	AI820991	Hs.8377	ESTs	1.24	2.03
	444091	AV647924	Hs.282376	ESTs	1.05	2.13
	410793	AW581906	Hs.66392	intersectin 1 (SH3 domain protein)	2.00	3.13
	452222	AW806287	Hs.21432	SEX gene	1.25	1.10
65	433010	AW970018		gb:EST382097 MAGE resequences, MAGK Homo	1.36	2.41
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	1.14	2.03
	438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	2.24	1.77
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	1.52	2.65
	402685			Target Exon	2.04	2.46
70	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.66	2.05
	422058	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	1.89	4.98
	451225	AI433694	Hs.283608	ESTs	1.79	2.70
	441078	AI453268	Hs.323409	Homo sapiens cDNA FLJ14113 fis, clone MA	1.44	2.58
	409406	H83092	Hs.49605	ESTs	1.38	2.05
75	422297	AW961290		p30 DBC protein	1.20	2.73
	408711	AW376061	Hs.63335	ESTs, Moderately similar to A46010 X-lin	1.20	2.08
	426696	AW363332	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H	1.35	2.68
	417324	AW265494		ESTs	1.66	1.25

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	408283	BE141579		gb:QV2-HT0083-071299-018-b05 HT0083 Homo	1.25	2.65
	415166	NM_003652	Hs.78068	carboxypeptidase Z	1.34	1.09
	406300			Target Exon	1.61	2.47
5	411880	AW872477		gb:hm3003.x1 NCI_CGAP_Thy4 Homo sapiens	3.60	4.03
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIa polype	2.16	1.44
	422567	AF111178	Hs.118407	glypican 6	1.57	2.03
	436855	AA732624	Hs.165952	ESTs	1.08	2.75
	403536			Target Exon	0.93	2.13
10	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.18	1.07
	417117	N46778		gb:yy52b02.r1 Soares_multiple_sclerosis_	1.70	2.85
	411690	AA669253	Hs.136075	RNA, U2 small nuclear	2.12	2.78
	443243	AI452496	Hs.132056	ESTs	1.15	2.83
	423074	AL109963		FSH primary response (LRPR1, rat) homolo	1.37	1.43
15	408916	AW295232	Hs.429	ATP synthase, H transporting, mitochondr	1.63	2.23
	449799	AI143466	Hs.125060	ESTs	1.40	2.08
	415378	T16964		gb:NIB2079-5R Normalized infant brain, B	1.88	1.85
	431089	BE041395		ESTs, Weakly similar to unknown protein	1.57	2.57
	434959	AW974949	Hs.186564	ESTs, Weakly similar to I38022 hypotheti	1.30	2.30
20	416311	D80529		gb:HUM081H05B Human fetal brain (TFujiwa	1.58	4.35
	444614	R44284	Hs.2730	heterogeneous nuclear ribonucleoprotein	1.88	2.98
	456206	NM_006895	Hs.81182	histamine N-methyltransferase	1.24	2.08
	410583	AW770280	Hs.36258	ESTs, Moderately similar to JC5238 galac	1.56	4.33
	430410	AF099144	Hs.334455	trypsin beta 1	1.91	1.58
25	408139	AA451966		RAB9-like protein	1.42	2.14
	432621	AI298501	Hs.12807	ESTs, Weakly similar to T46428 hypotheti	2.08	1.94
	441584	AW148329	Hs.175208	ESTs	1.12	2.05
	445940	D60438	Hs.34779	ESTs	1.86	2.70
	453022	AA031499	Hs.118489	ESTs	2.02	1.75
30	444008	BE544855	Hs.236572	ESTs, Weakly similar to SFR4_HUMAN SPLIC	1.54	1.29
	442994	AI026718	Hs.16954	ESTs	3.60	3.78
	402085			C18000504*gi 2627436 gb AA886683.1 (AF	1.36	2.53
	411918	AW876354		gb:PM4-PT0019-141299-009-F08 PT0019 Homo	2.00	2.63
	455508	AW976165		gb:EST388274 MAGE resequences, MAGN Homo	1.70	3.04
35	426106	AI678765	Hs.21812	ESTs	1.49	2.11
	425131	BE252230	Hs.99163	ESTs	2.04	2.65
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	1.17	2.55
	420447	AA687306	Hs.88448	ESTs	1.66	2.58
	428055	AA420564	Hs.101760	ESTs	1.08	2.15
40	422110	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	1.76	1.82
	438581	AW977766	Hs.292133	ESTs, Moderately similar to I78885 serin	1.08	2.10
	403290			C10001011*gi 4758212 ref NP_004411.1 d	0.97	2.48
	408175	W29089	Hs.19066	hypothetical protein DKFZp667O2416	1.42	1.41
	432390	AA936177	Hs.274460	olfactory receptor, family 5, subfamily	1.26	2.05
45	443441	AW291196	Hs.92195	ESTs	1.52	2.13
	419925	AA159850	Hs.93765	lipoma HMGIC fusion partner	1.72	2.80
	445256	AI658635	Hs.144763	ESTs	1.97	3.33
	456381	AA236606		gb:zr9b10.r1 NCI_CGAP_GCB1 Homo sapiens	1.16	1.95
	422433	AA310560	Hs.153746	hypothetical protein FLJ22490	1.06	2.20
50	432529	AI989607	Hs.162245	ESTs	1.36	2.25
	424951	AW964082		gb:EST376155 MAGE resequences, MAGH Homo	2.22	2.58
	420785	H89633	Hs.191346	ESTs	1.26	2.15
	411347	AW636126		gb:QV2-LT0051-240300-097-f01 LT0051 Homo	1.38	2.38
	438742	AW204126	Hs.196543	ESTs	1.10	2.30
55	414900	AW452420	Hs.248678	ESTs	2.01	3.08
	443284	AI369813	Hs.64783	ESTs, Weakly similar to T42705 hypotheti	0.66	0.43
	402049			Target Exon	2.28	2.00
	429400	AW604940	Hs.201668	transcription factor 20 (AR1)	1.16	2.00
	423916	AW993496	Hs.17235	Homo sapiens clone TCCCIA00176 mRNA sequ	1.59	1.05
60	432495	AW973537	Hs.186734	ESTs, Weakly similar to I61746 pheromone	1.50	2.05
	414840	R27319	Hs.23823	hair/enhancer-of-split related with YRP	1.89	2.09
	428711	R46414	Hs.56828	trinucleotide repeat containing 5	1.77	1.83
	448609	AW139420	Hs.7972	KIAA0671 protein	1.14	2.26
	443859	NM_013409	Hs.9914	folistatin	1.17	1.05
65	411141	AW819561		gb:RC5-ST0293-140200-013-G04 ST0293 Homo	1.44	2.40
	440116	AI798851	Hs.266959	hemoglobin, gamma G	1.18	2.08
	417944	AJ077196	Hs.82985	collagen, type V, alpha 2	2.10	1.37
	429640	U83508	Hs.2463	angiotensin 1	1.92	2.98
	410064	X53416	Hs.195464	filamin A, alpha (actin-binding protein-	1.51	1.29
70	458218	AI435179	Hs.126820	ESTs	1.49	1.15
	443114	AI033377	Hs.153298	ESTs	1.38	2.05
	427788	AA412397	Hs.116858	ESTs	1.45	1.85
	435913	W95006	Hs.269559	ESTs, Weakly similar to S65657 alpha-1C-	1.63	3.90
	457949	W69171	Hs.71741	ESTs, Highly similar to I38945 melanoma	1.01	2.00
75	419203	AA488719	Hs.190151	ESTs	1.94	2.45
	412510	AI056689	Hs.133538	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.91	2.20
	413885	BE177442		gb:RC1-HT0595-200400-012-f01 HT0595 Homo	1.48	2.80
	426239	AA669615	Hs.214226	ESTs	1.36	2.50

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	408866	AW292096	Hs.255036	ESTs	1.93	2.92
	412857	AI703484	Hs.128052	ESTs	1.72	1.60
	427340	BE167242	Hs.47099	hypothetical protein FLJ21212	1.46	2.13
	412902	BE008018		gb:QV0-BN0147-290490-214-c01 BN0147 Homo	0.90	2.05
5	451141	AW772713	Hs.247186	ESTs	2.38	3.95
	412626	AA114945	Hs.151839	ESTs	1.75	2.15
	406667			Target Exon	2.62	3.79
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	1.24	2.08
	401400			Target Exon	1.16	1.90
10	426796	S78234	Hs.172405	cell division cycle 27	2.14	1.63
	435046	AA662772	Hs.174330	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.14	2.28
	448401	AI498509	Hs.346254	ESTs	2.50	2.83
	450832	AW970602	Hs.105421	ESTs	0.55	0.39
	441057	AL043897	Hs.126483	ESTs	1.08	2.13
15	438725	AA815163	Hs.127307	ESTs	1.31	2.65
	450062	AW001043	Hs.200854	ESTs	1.30	2.48
	441214	AI820648	Hs.129136	ESTs	1.43	1.71
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.22	2.30
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.35	1.49
20	423622	BE154847		gb:PM1-HT0345-121199-001-d05 HT0345 Homo	1.57	2.30
	450835	BE262773	Hs.25584	hypothetical protein FLJ10767	1.40	1.12
	444014	AI095718	Hs.135015	ESTs	2.30	1.78
	431603	AA807955	Hs.325984	EST	1.26	2.03
	406697	AW419069	Hs.209670	ESTs	1.35	2.60
25	444312	R44007		ESTs	1.95	2.07
	404286			C6001909.gii704441[dbj]BAA18909.1 (D298	2.29	2.22
	438613	M27346		gb:Homo sapiens (clone HGP09/HGF32) T ce	1.03	2.43
	445534	AL036823	Hs.12840	Homo sapiens germline mRNA sequence	1.00	2.16
30	426046	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	1.59	2.73
	451907	AI822065	Hs.50749	ESTs, Moderately similar to ALU7_HUMAN A	1.74	2.65
	416796	AA228351	Hs.34060	ESTs	1.28	2.12
	422431	AI769410	Hs.221461	ESTs	1.80	3.58
	417557	AA225622	Hs.293589	ESTs	1.32	2.14
	455313	AW894409	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	1.48	2.57
35	415479	F10042	Hs.4840	ESTs	1.83	2.01
	450433	AW444538	Hs.231863	ESTs	1.31	2.58
	410581	AA018982	Hs.125036	tumor endothelial marker 7 precursor	1.54	1.62
	455407	AW936813		gb:PM2-DT0023-050400-003-b10 DT0023 Homo	1.32	2.15
40	417552	R00916	Hs.166510	ESTs	1.50	2.63
	428290	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	1.94	2.70
	432391	AI732374	Hs.339827	Human DNA sequence from clone RP5-881L22	0.96	2.38
	456283	U68162	Hs.84171	myeloproliferative leukemia virus oncoge	1.22	2.13
	436535	L09078		gb:Homo sapiens mRNA fragment	2.14	1.95
	416564	AW795793	Hs.2575	Homo sapiens cDNA FLJ12257 fis, clone MA	2.28	1.93
45	435200	AA670310	Hs.145903	ESTs	1.16	2.13
	457635	AV660976	Hs.3569	hypothetical protein	1.37	3.10
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	0.99	2.45
	449319	AA373630	Hs.188750	ESTs	1.56	3.28
	416992	AW074143	Hs.87134	ESTs	1.88	2.20
50	408367	AW382767		gb:PM0-HT0339-081199-001-h05 HT0339 Homo	1.30	2.50
	434973	AW449285	Hs.313636	EST	1.11	2.65
	408363	BE466959	Hs.144153	ESTs	1.30	2.44
	440100	BE382685	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.23	2.71
	431996	AL122087	Hs.272304	Homo sapiens mRNA; cDNA DKFZp564C0371 (f	1.24	2.27
55	427681	AB018263	Hs.180338	tumor necrosis factor receptor superfam	1.70	1.68
	405146			C6001690.gii6754446[ref]NP_034760.1 [k	2.00	0.68
	436154	AA764950	Hs.119898	ESTs	1.43	3.00
	451233	AA047221	Hs.59752	ESTs	1.38	2.20
	446856	AI814373	Hs.164175	ESTs	1.33	3.93
60	448211	BE384592	Hs.6451	PRO0659 protein	1.48	2.73
	418283	S79895	Hs.83942	cathepsin K (pseudocystosis)	1.33	2.68
	409609	AW444670	Hs.335685	ESTs	1.27	1.51
	450414	AI907735	Hs.21446	KIAA1716 protein	1.60	1.24
	452929	AW954938	Hs.172816	neuregulin 1	2.01	3.70
65	435112	AW976145	Hs.143198	inhibitor of growth family, member 3	1.22	1.30
	439806	AA846824	Hs.180908	ESTs	0.80	2.04
	439910	H66765	Hs.339397	ESTs	1.28	2.16
	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	1.06	2.82
	441354	AA931221	Hs.126813	ESTs	1.20	2.28
70	428951	AL138153	Hs.300410	ESTs, Moderately similar to A47582 B-cl	1.50	1.83
	438272	AI167963	Hs.143700	ESTs, Weakly similar to S65824 reverse t	1.34	2.51
	429642	X68264	Hs.211579	melanoma cell adhesion molecule	1.18	1.18
	422121	AI767949	Hs.179833	ESTs	1.18	2.26
75	411184	AW821117		gb:PM2-ST0303-170100-003-g03 ST0303 Homo	1.18	2.21
	435871	AF257077	Hs.283627	eukaryotic translation initiation factor	1.17	1.57
	430570	AI417881	Hs.292464	ESTs	1.49	3.17
	431995	AL080197	Hs.272302	hypothetical protein	1.52	2.11

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	451326	AW296946	Hs.256078	ESTs	1.19	2.18
	437046	BE149154		gb:RC2-HT0252-271099-017-c11 HT0252 Homo	1.18	2.25
	410154	F06959		gb:HSC1QD011 normalized infant brain cDN	1.41	2.05
5	434373	AI565566	Hs.168587	ESTs	1.39	1.33
	444552	AW295211	Hs.230777	ESTs	1.36	2.20
	411608	AW853441		gb:RC1-CT0252-030100-023-g09 CT0252 Homo	2.12	1.80
	440573	BE550891	Hs.270624	ESTs	2.19	2.17
	443047	AW157377	Hs.132910	ESTs	1.81	2.28
10	451473	AW298047	Hs.346198	ESTs	1.18	2.30
	416265	AA177088	Hs.190065	ESTs	2.37	3.38
	435375	AI733610	Hs.187832	ESTs	1.12	2.18
	401469			NM_022137*:Homo sapiens secreted modular	1.32	1.61
	456152	AA174126	Hs.332163	ESTs	1.26	2.50
15	415808	R21439	Hs.334578	Homo sapiens, clone IMAGE:3929520, mRNA	1.39	2.43
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-ph	0.92	2.20
	435127	AI217926	Hs.179863	EST	1.36	2.65
	420772	AW752658	Hs.222707	KIAA1718 protein	1.19	1.50
	456332	AA228357		gb:nc39d05.r1 NCL_CGAP_Pr2 Homo sapiens	1.45	3.57
20	444678	AI741513	Hs.143739	ESTs	1.43	1.62
	416475	AL036568	Hs.291	glutamyl aminopeptidase (aminopeptidase	1.00	1.53
	416463	H59241		Homo sapiens cDNA FLJ11095 fis, clone PL	1.44	2.13
	405158			ENSP00000243337:CDNA FLJ13984 fis, clone	1.38	2.68
	403903			C5001632*:gii10645308[gb]AAG21430.1JAC00	1.32	1.43
25	407271	X98937		gb:H.sapiens rearranged Ig heavy chain (1.40	2.68
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	1.59	1.33
	450778	U81375	Hs.25450	solute carrier family 29 (nucleoside tra	1.17	1.10
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	1.92	2.80
	400075			Eos Control	1.76	2.60
30	433694	AI208611	Hs.12066	Homo sapiens cDNA FLJ11720 fis, clone HE	1.48	2.33
	454826	AW833676		gb:QV4-TT0008-181199-038-h04 TT0008 Homo	1.57	2.89
	415158	AA160805	Hs.199832	ESTs, Weakly similar to I76885 serine/th	2.08	1.76
	439486	AF086303	Hs.103185	ESTs	1.49	2.19
	403291			Target Exon	1.36	2.28
35	438618	AA897673	Hs.123457	ESTs	0.75	0.79
	455087	AW855389		gb:CM3-CT0275-191099-024-e06 CT0275 Homo	0.91	2.63
	408075	AA382881	Hs.42409	CGI-146 protein	1.46	2.15
	436826	AA731863	Hs.120276	ESTs	1.04	3.11
	408961	AW297475	Hs.323180	ESTs	1.25	1.39
40	424408	AI754813	Hs.146428	collagen, type V, alpha 1	1.64	2.05
	423300	AK000742	Hs.126774	L2DTL protein	1.47	3.44
	403217	AL134878		ribosomal protein, large P2	1.70	2.22
	437990	AI686579	Hs.121784	ESTs	2.14	1.69
	419155	AC002366	Hs.45329	amelogenin (X chromosome, amelogenesis i	1.40	1.45
45	411817	BE302900	Hs.72241	mitogen-activated protein kinase kinase	1.18	1.12
	425701	AA361850	Hs.322149	Human clone 137308 mRNA, partial cds	1.60	2.15
	418757	AI864193	Hs.169728	hypothetical protein FLJ13150	1.57	2.23
	415184	AA380436	Hs.211973	homolog of Yeast RRP4 (ribosomal RNA pro	1.32	2.09
	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	1.61	1.50
	401723			Target Exon	1.01	2.68
50	439010	AW170332	Hs.75216	Homo sapiens cDNA FLJ13713 fis, clone PL	1.28	1.65
	449166	BE168981	Hs.23131	kinesin family member C3	1.64	2.58
	410842	AW792784		gb:CM0-UM0001-010300-258-h11 UM0001 Homo	1.54	1.90
	409556	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	1.63	1.21
55	439894	AA853077	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.76	0.51
	401913			ENSP00000249159*:CDNA	0.97	2.59
	406097			Target Exon	1.11	1.23
	414745	AA160511	Hs.5326	amino acid system N transporter 2; porcu	1.29	1.12
60	445752	AI733942	Hs.344887	ESTs	2.03	1.68
	408052	AW501117	Hs.283585	ESTs	1.32	1.72
	407256	AA204763	Hs.298036	tRNA isopentenylpyrophosphate transferas	1.01	2.09
	423264	AJ133439	Hs.126076	Glutamate receptor interacting protein	1.51	2.39
	418859	AA229558		gb:nc15d10.s1 NCL_CGAP_Pr1 Homo sapiens	1.40	2.35
	410370	AB037753	Hs.62767	KIAA1332 protein	1.34	2.00
65	417254	AA195100	Hs.188695	ESTs	1.09	2.51
	444909	AI933051	Hs.192280	ESTs	1.56	2.92
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	1.14	2.28
	439212	AF087995	Hs.134877	ESTs	1.06	2.90
	437766	W69171	Hs.71741	ESTs, Highly similar to I38945 melanoma	1.25	2.28
70	448951	AI611221	Hs.334802	hypothetical protein FLJ10101	1.88	2.17
	401659			Target Exon	1.63	2.05
	419145	N99638		gb:za39g11.r1 Soares fetal liver spleen	2.63	3.85
	444813	AW054834	Hs.210356	ESTs	1.73	2.14
	433902	AW292820	Hs.144906	ESTs	1.88	2.46
75	403072			NM_003319*:Homo sapiens titin (TTN), mRN	1.32	2.91
	452484	AB033042	Hs.29679	cofactor required for Sp1 transcriptiona	0.72	0.70
	456788	AA724612	Hs.133130	Homo sapiens mRNA; cDNA DKFZp566H0124 (f	1.90	3.40
	403315			Target Exon	1.22	2.00

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	406432	AJ289116		CD1E antigen, e polypeptide	2.31	2.63
	457785	AA682670	Hs.160884	ESTs	0.96	2.38
	433259	AA580665	Hs.326082	ESTs	1.46	1.07
5	436882	AW016722	Hs.194976	SH2 domain-containing phosphatase anchor	1.38	2.13
	401473			Target Exon	1.47	2.04
	444816	Z48633	Hs.283742	H.sapiens mRNA for retroltransposon	1.64	2.15
	438029	H61502	Hs.10235	chromosome 5 open reading frame 4	1.44	2.25
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	1.26	2.21
10	450817	N71597	Hs.29698	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.20	2.90
	404427			C8000068*:gij5453579[ref]NP_006120.1] bo	0.74	0.81
	430658	AW970093	Hs.24453	ESTs	1.45	2.55
	405723			Target Exon	1.60	2.28
	436896	AW977385	Hs.278615	ESTs	1.17	1.64
15	411974	AW880414	Hs.84264	acidic protein rich in leucines	1.54	2.08
	412528	AI123478	Hs.32112	ESTs	1.72	2.85
	446425	AW295364	Hs.255418	ESTs	1.25	1.31
	424991	AA775471	Hs.241467	ESTs	0.62	0.37
	443100	AI033188		gb:ow94e08.s1 Soares_fetal_liver_spleen_	1.15	2.34
20	445332	AI220225	Hs.321057	ESTs	1.07	2.00
	414781	D50917	Hs.77293	KIAA0127 gene product	1.04	3.43
	421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	1.15	2.53
	424265	AF173901	Hs.144287	hairly/enhancer-of-split related with YRP	1.26	2.00
	446667	BE161878	Hs.224805	ESTs	1.12	2.13
25	426399	AA652588	Hs.301348	Homo sapiens cDNA FLJ13271 fis, clone OV	2.26	1.29
	438190	AA780020	Hs.136798	ESTs, Moderately similar to KBF3_HUMAN N	1.44	2.07
	406972	M32053		gb:Human H19 RNA gene, complete cds.	1.38	2.11
	417086	AA194446		ESTs, Weakly similar to S55024 nebulin,	2.12	3.30
	446410	AI361109	Hs.151721	ESTs, Weakly similar to I38022 hypothe	1.14	2.33
30	427674	NM_003528	Hs.2178	H2B histone family, member Q	1.24	1.00
	422526	AA311763	Hs.131056	ESTs	1.29	2.04
	439317	AF086127	Hs.50600	ESTs, Weakly similar to T47156 hypothe	1.26	2.12
	409126	AA063426		gb:zf70c08.s1 Soares_pineal_gland_N3HPG	1.28	2.20
	412093	BE242691	Hs.14947	ESTs	0.87	2.58
	420169	AA256126	Hs.16179	hypothetical protein FLJ23467	1.38	2.07
35	426096	D87436	Hs.166318	lipin 2	2.00	2.25
	402551			NM_005012*:Homo sapiens receptor tyrosin	0.80	0.82
	405760			Target Exon	1.44	2.85
	402901			NM_025206*:Homo sapiens hypothetical pro	1.63	1.27
40	453982	AW014252	Hs.252837	ESTs	1.44	2.03
	424244	AV647184	Hs.143601	hypothetical protein hCLA-iso	1.40	1.18
	439984	BE559514	Hs.275425	hypothetical protein	1.30	2.15
	457297	AW968188		gb:EST380383 MAGE resequences, MAGJ Homo	1.64	3.17
	415054	AI733907		gb:zo86h09.y5 Stratagene ovarian cancer	1.00	2.20
45	426273	AI174861	Hs.190623	ESTs	1.19	1.16
	405187			NM_014272:Homo sapiens a disintegrin-lik	1.31	1.35
	413939	AL047051	Hs.199961	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.44	1.88
	427596	AA449506	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.06	1.50
	408049	AW076098	Hs.345588	desmoplakin (DPI, DPII)	2.01	3.90
50	406002			Target Exon	1.73	2.08
	408284	AW248254	Hs.44101	protein kinase PKNbeta	1.28	1.31
	431377	AW178807	Hs.246182	ESTs	1.40	2.70
	451456	AW386183	Hs.210305	ESTs	1.44	2.08
	427530	AA405093	Hs.126519	ESTs	1.07	1.12
55	431957	AK002104	Hs.272246	hypothetical protein FLJ11292	1.27	2.89
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.74	1.28
	419600	AA448958	Hs.91481	NEU1 protein	1.13	1.15
	423314	AI400661	Hs.127811	disintegrin metalloproteinase with throm	1.44	2.53
	451690	AW451469	Hs.209990	ESTs	1.41	2.49
60	454662	AW812715		gb:RC4-ST0185-271099-011-g01 ST0185 Homo	1.35	2.86
	454413	AI653672	Hs.40092	PNAS-123	1.79	2.03
	416861	AW977206	Hs.151858	ESTs	1.52	2.10
	415908	H08623	Hs.22833	ESTs	1.37	2.13
	438942	AW875398	Hs.6451	PRO0659 protein	1.80	1.55
65	407618	AW054922	Hs.53478	Homo sapiens cDNA FLJ12366 fis, clone MA	2.16	3.18
	429177	AA447527	Hs.207429	ESTs	1.74	3.19
	448357	N20169	Hs.108923	RAB38, member RAS oncogene family	0.77	0.73
	422008	AJ000534	Hs.110708	sarcoglycan, epsilon	1.52	4.08
	434461	AA744046	Hs.133350	ESTs, Weakly similar to I78885 serine/th	1.66	2.16
70	413489	BE144228		gb:MRO-HT0165-140200-009-d04 HT0165 Homo	1.28	2.23
	405551			Target Exon	1.11	1.19
	441183	BE562910	Hs.92679	Homo sapiens clone CDABP0014 mRNA sequen	1.20	1.20
	450334	AW450979		gb:U1-H-BI3-ala-a-12-Q-U1.s1 NCI_CGAP_Su	1.98	2.53
	420611	AA994635	Hs.129929	ESTs	1.46	2.15
	422061	BE178434	Hs.267995	ESTs, Moderately similar to G02654 ribos	1.42	2.30
75	437908	AI082424		ESTs	1.38	2.21
	423052	M28214	Hs.123072	RAB3B, member RAS oncogene family	0.74	0.43
	401927			C17C00914*:gij8394367[ref]NP_058549.1] s	2.26	2.14

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	432967	AA572049	Hs.207566	ESTs	1.52	2.28
	439159	AF067972	Hs.120938	ESTs	2.03	2.08
	415357	H22757	Hs.13471	ESTs	1.82	2.07
	442327	AA991745	Hs.42522	ESTs	1.48	2.88
5	430186	AB020696	Hs.234791	KIAA0889 protein	1.46	2.23
	426971	AI809984	Hs.243209	ESTs, Weakly similar to NPA1_HUMAN NEURO	1.06	2.13
	422687	AW069823	Hs.119206	insulin-like growth factor binding prote	1.61	1.37
	432954	AI076345	Hs.214199	ESTs	1.19	2.84
10	429040	AL035542	Hs.248169	olfactory receptor, family 2, subfamily	1.25	1.44
	414169	AA136169	Hs.149335	ESTs	1.59	2.51
	419882	AA687313	Hs.190043	ESTs	1.20	2.50
	426900	AW163564	Hs.142375	ESTs	1.87	1.77
	418773	T39748	Hs.325474	Target CAT	1.35	2.02
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	1.32	2.10
15	428712	AW085131	Hs.190452	KIAA0365 gene product	1.41	1.52
	408839	AW277084		gb:xp61h09.x1 NCL_CGAP_Ov39 Homo sapiens	1.14	2.03
	450492	AW290961	Hs.201815	ESTs	1.17	2.21
	434654	AI825942	Hs.139366	Homo sapiens clone L5 polyadenylated HER	1.62	2.31
20	457567	AW939074		gb:QV1-DT0069-010200-057-c12 DT0069 Homo	1.80	3.73
	452426	AI904823	Hs.31297	duodenal cytochrome b	2.15	1.84
	418559	AA225048	Hs.104207	ESTs	1.84	2.33
	439099	AB037800	Hs.6462	protein kinase C and casein kinase subst	1.07	1.15
	451984	R60571	Hs.27406	Homo sapiens mRNA; cDNA DKFZp566F1946 (f	1.18	1.22
	420789	AI670057	Hs.199882	ESTs	2.24	2.55
25	456396	AA236663	Hs.188894	ESTs, Weakly similar to APXL_HUMAN APICA	1.07	1.14
	402948			NM_025206:Homo sapiens hypothetical prot	2.41	1.83
	426405	AW296631	Hs.283403	ESTs	1.28	1.07
	439732	AW629604	Hs.167641	hypothetical protein from EUROIMAGE 1703	0.85	0.77
30	416784	AA334552	Hs.79914	lumican	1.88	1.27
	422531	AW967280	Hs.293894	ESTs, Weakly similar to HERC2 [H.sapiens	1.20	1.25
	415608	F12755	Hs.12286	ESTs, Moderately similar to ALU1_HUMAN A	1.03	2.31
	428671	BE297851	Hs.185482	zinc finger protein 179	1.26	2.20
	420007	H13700	Hs.31235	ESTs, Weakly similar to Y934_HUMAN HYPOT	1.60	2.25
35	400850			Target Exon	1.22	1.03
	404580			trichorhinophalangeal syndrome 1 gene (T	1.00	1.00
	407680	AW064284	Hs.279153	ESTs	1.02	2.28
	410420	AA224053	Hs.172405	cell division cycle 27	1.64	1.00
	421234	AA907153	Hs.190060	ESTs	1.76	1.45
40	426791	AA384910	Hs.46519	ESTs	1.12	2.15
	430439	AL133561		DKFZP434B061 protein	1.00	1.00
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	1.00	1.00
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.40	1.00
	440304	BE159984	Hs.125395	ESTs	1.00	1.00
45	441699	AW511126	Hs.127572	ESTs	1.00	1.73
	443383	AI792453	Hs.166507	ESTs	2.04	1.00
	445660	AI702668	Hs.201955	ESTs	1.00	1.00
	453160	AI263307	Hs.239884	H2B histone family, member L	1.00	1.00
	456513	AA279143	Hs.88561	ESTs	1.00	1.40
50	457231	AI472022	Hs.301959	proline synthetase co-transcribed (bacte	0.98	0.63
	459585	W27086	Hs.209694	ESTs	1.00	1.00
	429317	AA831552	Hs.268016	Homo sapiens cDNA: FLJ21243 fis, clone C	1.00	1.00
	430971	M25150	Hs.248177	H3 histone family, member L	1.14	1.40
	408376	AW971303	Hs.292601	ESTs	1.08	1.60
55	411920	AW876263		gb:PM4-PT0019-131299-006-E09 PT0019 Homo	0.82	0.45
	457389	AW970939		gb:EST383074 MAGE resequences, MAGK Homo	0.92	0.71
	408565	BE502544	Hs.282244	ESTs, Weakly similar to peptidoglycan re	1.00	2.10
	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group 1, m	1.00	1.00
	446779	AI341135	Hs.156064	ESTs	1.06	2.02
60	441691	AI015418	Hs.127556	ESTs	1.13	2.03
	402039			Target Exon	0.44	0.36
	437133	AB018319	Hs.5460	KIAA0776 protein	0.95	0.63
	438089	W05391		nuclear receptor subfamily 1, group 1, m	3.12	1.00
	409582	R27430	Hs.271565	ESTs	1.00	1.00
65	428769	AW207175	Hs.106771	ESTs	1.00	1.48
	442868	AI022701	Hs.336984	ESTs	1.27	1.62
	439559	AW364675	Hs.173921	ESTs, Weakly similar to 2109260A B cell	1.00	1.33
	426958	R18845	Hs.172979	zinc finger protein 177	1.24	2.25
	419015	T79262	Hs.14463	ESTs	1.16	2.03
70	415806	AA169560		gb:zo89x08.r1 Stratagene ovarian cancer	1.00	1.33
	436110	AA704899	Hs.291651	ESTs, Weakly similar to i38022 hypotheri	1.60	2.21
	458760	AI498631	Hs.111334	ferritin, light polypeptide	1.10	1.43
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	1.28	1.00
	438182	AW342140	Hs.182545	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.90	2.31
	438091	AW373062		nuclear receptor subfamily 1, group 1, m	4.70	1.00
75	441633	AW588544	Hs.112242	normal mucosa of esophagus specific 1	2.48	1.00
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.96	2.84
	416055	Z45423	Hs.13349	Homo sapiens cDNA FLJ14547 fis, clone NT	1.52	1.46

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	417895	AA838392	Hs.56237	hypothetical protein FLJ20495	1.05	1.18
	422959	AV647015		paired immunoglobulin-like receptor beta	1.33	1.25
	408969	AW297929	Hs.328317	EST	1.88	2.07
5	409536	H59024	Hs.14485	Homo sapiens cDNA: FLJ23220 fis, clone A	1.18	2.38
	447449	AW137091	Hs.18624	KIAA1052 protein	1.07	1.13
	437315	AW976247	Hs.153248	ESTs	1.16	2.53
	459317	BRCA1b		Eos Control	1.36	1.32
	405137			Target: Exon	1.11	1.18
	400366	M22333		Target	1.55	1.42
10	423413	AA325560	Hs.346401	ESTs	1.78	1.57
	433972	AI878910	Hs.278670	cisplatin resistance-associated overexpr	1.62	2.98
	440748	AW451780	Hs.130363	ESTs	1.42	2.14
	422637	AA399024	Hs.118836	myoglobin	1.46	2.38
	432342	AL036128	Hs.274404	plasminogen activator, tissue	1.67	1.10
15	442820	AW293459	Hs.172681	ESTs	1.02	1.13
	436573	AA723297	Hs.127138	ESTs	1.18	1.15
	403779			Target: Exon	1.13	1.15
	447686	AI939440	Hs.345192	ESTs	1.66	2.78
20	447506	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	1.44	2.48
	425853	BE348404	Hs.24740	ESTs	1.40	2.75
	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	1.52	2.00
	424132	AA335715	Hs.200299	ESTs	1.34	1.32
	421707	NM_014921	Hs.107054	lectomedin-2	1.09	1.14
25	442871	AI290691	Hs.131393	ESTs	1.40	2.50
	448489	AI523875		gb:ig97d04.x1 NCL_CGAP_CLL1 Homo sapiens	1.31	2.20
	436365	AW444548	Hs.163118	ESTs	1.07	1.12
	415733	AI052628	Hs.271570	ESTs, Weakly similar to 2109260A B cell	1.91	2.01
	413888	AA580288		gb:nnt12d01.s1 NCL_CGAP_Co12 Homo sapiens	1.75	1.93
30	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	1.92	1.73
	442959	AI025248	Hs.6927	ESTs	1.05	1.12
	409610	AW444736	Hs.27864	ESTs	1.62	2.45
	424793	AI559696	Hs.298885	ESTs	1.37	2.78
	449977	C16939	Hs.297848	ESTs	1.52	4.57
35	414051	BE244127		gb:TCBAP1E0661 Pediatric pre-B cell acut	1.68	2.84
	422400	AA974434	Hs.128353	ESTs	1.04	2.20
	443908	AW295791	Hs.13040	G protein-coupled receptor 86	1.47	2.10
	439316	AF086126	Hs.118208	Homo sapiens cDNA FLJ11727 fis, clone HE	2.08	0.59
	438605	AA808948	Hs.173776	ESTs, Moderately similar to ALU1_HUMAN A	1.44	2.73
40	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.17	1.00
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	1.88	2.58
	431756	R69465	Hs.255889	ESTs	1.12	1.30
	424487	T08754	Hs.6259	KIAA1698 protein	1.15	1.15
	435392	R07195	Hs.19918	ESTs	1.38	2.64
45	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	0.92	2.12
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	1.44	2.51
	411664	BE065069	Hs.270833	amphiregulin (schwannoma-derived growth	1.94	2.33
	416586	D44643	Hs.14144	secreted modular calcium-binding protein	1.72	2.68
	419612	AI486267	Hs.110613	KIAA0421 protein	2.28	2.46
50	435800	AI248285	Hs.118348	ESTs	1.42	2.45
	433363	AA584829	Hs.275163	non-metastatic cells 2, protein (NM23B)	2.07	2.53
	422936	AA319278		gb:EST21478 Adrenal gland tumor Homo sap	1.46	1.22
	413358	BE259180	Hs.75313	aldo-keto reductase family 1, member B1	1.43	1.43
	435357	N71820	Hs.118173	ESTs	1.44	2.93
55	441063	AA913819	Hs.188025	ESTs	1.20	2.80
	450724	R55428		gb:yj79b05.r1 Soares breast 2NbH8st Homo	1.44	4.18
	430446	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	1.03	2.34
	401677			NM_000761: Homo sapiens cytochrome P450,	1.13	1.22
	403978			C5000010* g 10440464 dbj BAB15785.1 (A	1.22	1.66
60	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.72	4.60
	416708	H78836	Hs.181900	ESTs, Moderately similar to ALU1_HUMAN A	1.36	2.03
	451410	AL110235	Hs.26358	DKFZP566K1924 protein	1.51	2.28
	451159	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	1.33	1.09
	448455	AI252625	Hs.269860	ESTs, Moderately similar to S65657 alpha	0.83	0.40
65	444020	R92962	Hs.35052	ESTs	1.66	2.50
	414623	BE391050		gb:601285674F1 NIH_MGC_44 Homo sapiens c	1.84	3.88
	454915	AW841619		gb:RC1-CN0017-120200-012-b09 CN0017 Homo	1.14	2.10
	444064	W85970	Hs.16292	ESTs	0.80	0.63
	454353	AW389693	Hs.300700	hypothetical protein FLJ20727	1.30	2.10
70	447794	AI424999	Hs.161445	EST	1.26	2.05
	426686	AI362802	Hs.171814	parathymosin	1.16	1.11
	435815	AA700482	Hs.113157	ESTs	1.66	2.73
	432482	L19267	Hs.275924	dystrophin myotonic-containing WD repea	1.10	1.15
	431062	AA491270	Hs.187946	ESTs	1.44	2.60
75	429191	AF065215	Hs.198161	phospholipase A2, group IVB (cytosolic)	1.35	1.06
	424456	AA341017	Hs.25549	hypothetical protein FLJ20898	1.21	3.45
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	1.23	2.10
	432828	AB042326	Hs.267402	chondroitin 4-sulfotransferase	1.11	2.71

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	431866	BE246400	Hs.285176	acetyl-Coenzyme A transporter	1.03	3.10
	429321	AA449921		gb:zx37g07.r1 Soares_tetal_fetus_Nb2HF8_	1.68	2.93
	417890	R79048		gb:y187g02.r1 Soares_placenta_Nb2HP Homo	1.32	1.80
	439590	AF086410		gb:Homo sapiens full length insert cDNA	1.32	2.43
5	420232	AW450051	Hs.256295	ESTs	1.28	2.26
	418927	BE349635	Hs.190284	ESTs	1.46	1.23
	441940	AW298115	Hs.128152	ESTs	1.34	1.34
	401090			C9000193*g j6330729 dbj BAA86547.1 (AB	1.50	1.40
	409136	AW206670	Hs.50748	chromosome 21 open reading frame 18	1.02	2.38
10	438267	AW205708	Hs.292725	ESTs, Weakly similar to T18818 hypotheti	1.28	2.25
	422482	AI439905	Hs.344476	gb:li57g08.x1 NCI_CGAP_Lym12 Homo sapien	1.05	2.81
	420067	T52431	Hs.94795	Homo sapiens mRNA; cDNA DKFZp564O222 (fr	1.77	2.40
	442160	AA983913	Hs.128929	ESTs	1.76	2.38
	434256	AI378817	Hs.191847	ESTs	1.05	2.06
15	444519	AI160304	Hs.28313	ESTs	0.55	0.63
	454459	AW855738	Hs.17767	KIAA1554 protein	1.10	2.05
	455988	BE177983		gb:RC3-HT0600-230300-021-g10 HT0600 Homo	1.70	2.64
	444510	AI367823	Hs.146872	ESTs	1.44	2.08
	456210	N49729	Hs.156875	ESTs	1.64	2.65
20	450569	AW192334	Hs.38218	ESTs	1.78	2.71
	414921	BE390551	Hs.77628	steroidogenic acute regulatory protein r	1.05	1.12
	401381			C14000165:gil12698069 dbj BAB21853.1 (A	0.63	0.85
	439998	BE559554	Hs.61790	hypothetical protein FLJ23338	1.06	1.14
	453762	AW977286	Hs.17428	RBP1-like protein	1.42	2.68
25	419403	AA744520	Hs.87734	ESTs, Weakly similar to nonsyndromic hea	0.99	2.17
	423736	AW936874		gb:RC1-DT0029-120100-011-407 DT0029 Homo	2.05	1.56
	421186	AI798039	Hs.270563	ESTs, Moderately similar to T12512 hypot	1.29	1.31
	426435	AI827946	Hs.124854	hypothetical brain protein my040	1.36	1.59
	439312	AA833902	Hs.270745	ESTs	1.60	2.50
30	407924	BE537128	Hs.299797	ESTs	1.51	1.15
	409692	AI500724		KIAA1550 protein	1.72	2.21
	415449	H15034		gb:ym20a03.s1 Soares infant brain 1N1B H	1.50	2.13
	423436	R21176	Hs.100926	ESTs	1.18	2.60
	458697	AI797713	Hs.156471	ESTs	1.54	2.20
35	415770	M79237		gb:EST01385 Subtracted Hippocampus, Stra	1.49	1.55
	449279	AI962312	Hs.224976	ESTs, Weakly similar to CRX_HUMAN CONE-R	2.50	3.60
	429735	AA458759	Hs.188794	ESTs	1.84	2.31
	442124	R66412	Hs.129013	Homo sapiens cDNA FLJ14309 fis, clone PL	1.10	1.19
	412557	AA761612	Hs.291557	ESTs	1.10	1.18
40	409335	NM_001502	Hs.53985	glycoprotein 2 (zymogen granule membrane	1.18	1.12
	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	1.35	2.39
	420855	AA281092	Hs.33417	Homo sapiens cDNA: FLJ22806 fis, clone K	1.22	2.09
	450567	AA033904	Hs.269235	ESTs	1.60	2.20
	414197	W44877	Hs.55501	ESTs	1.06	2.08
45	448800	AI571294	Hs.298889	ESTs, Moderately similar to ALU1_HUMAN A	1.65	2.79
	421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	1.47	2.90
	412679	BE144762		gb:CMC-HT0180-041099-065-b04 HT0180 Homo	1.32	2.53
	417882	R22311		gb:yh26c09.r1 Soares placenta Nb2HP Homo	1.58	2.43
	425112	AW953291	Hs.64211	hypothetical protein MGC5601	0.70	0.63
50	401658			C16000210:gil12585542 sp O14771 Z213_HUM	1.68	2.04
	409325	AW377549	Hs.17865	ESTs	1.68	2.21
	437402	AI553976	Hs.121191	ESTs	1.20	2.35
	433455	AA360439	Hs.89319	ESTs	0.98	2.53
	457329	AI634860	Hs.247043	type 1 tumor necrosis factor receptor sh	0.59	0.43
55	434830	AW852235		gb:QV0-CT0225-230300-169-e11 CT0225 Homo	1.24	1.12
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	1.44	2.53
	446098	AW072215	Hs.208470	ESTs	1.38	2.93
	443310	BE552018	Hs.133152	ESTs	0.85	0.83
	424015	N95696	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.42	2.25
60	420229	AA256675	Hs.194058	ESTs, Weakly similar to AF252293 1 PAR3	1.70	2.39
	403371			Target Exon	1.50	3.43
	410744	H86002		gb:ys92b01.r1 Soares retina N2b5HR Homo	1.32	2.13
	424160	T74062		gb:yc81f01.r1 Soares infant brain 1N1B H	1.30	2.17
	438818	AW979008	Hs.222487	ESTs	1.98	2.43
65	438791	AA825750	Hs.129983	ESTs	1.12	2.15
	411206	AW827390	Hs.16899	ESTs	1.17	2.58
	432211	BE274530	Hs.273333	hypothetical protein FLJ10986	0.42	0.30
	448518	AB011152	Hs.22572	KIAA0580 protein	1.54	2.63
	424496	AI733451	Hs.167165	hypothetical protein FLJ12975	1.39	2.25
70	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	1.84	3.23
	457681	AA578512		gb:nh22e11.s1 NCI_CGAP_Pr1 Homo sapiens	1.21	1.09
	435353	AW243062	Hs.190348	ESTs	1.90	2.98
	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G pr	1.21	1.24
	433682	AA642418	Hs.17381	ESTs	1.18	2.23
75	424915	R42755	Hs.23096	ESTs	1.60	2.73
	442201	AW516704	Hs.208726	ESTs	1.74	3.20
	429111	AI870811	Hs.7579	KIAA1151 protein	1.27	1.40

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	429282	N27596	Hs.21342	ESTs	1.84	3.73
	436604	AW105129	Hs.242158	ESTs	1.27	2.70
	448712	W01046	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	0.79	2.70
5	412274	AA101443		gb:zn74a07.r1 Stratagene NT2 neuronal pr	1.40	2.53
	403859			C5001408*:gil12621134[ref NP_075244.1] M	1.76	2.00
	451521	AA018237	Hs.128189	gb:ze53a02.r1 Soares retina N2b4HR Homo	1.48	2.51
	443210	AI692649	Hs.9451	hypothetical protein MGC13168	1.44	2.60
	442722	AL048889	Hs.131029	ESTs, Weakly similar to B28096 line-1 pr	1.20	2.25
10	400840			Target Exon	0.66	0.60
	454639	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo	1.23	1.41
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	1.77	2.12
	410725	AW799279		gb:RC0-UM0051-210300-012-h06 UM0051 Homo	1.08	2.55
	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	1.94	2.29
15	450717	T94709		gb:ye35d09.r1 Stratagene lung (937210) H	1.56	2.64
	400314	NM_018949	Hs.192720	G protein-coupled receptor 14	0.89	0.87
	434947	AA654320	Hs.183819	Homo sapiens cDNA FLJ12304 fis, clone MA	1.19	2.14
	453582	AW854339	Hs.33476	hypothetical protein FLJ11937	1.24	2.19
	409005	AW299806	Hs.297256	ESTs	1.24	2.03
20	406584			Target Exon	1.52	2.37
	420203	AA256374	Hs.191069	ESTs	1.16	1.37
	406156			Target Exon	1.18	1.17
	422132	AB002337	Hs.112078	KIAA0339 gene product	1.08	1.16
	441371	AW452292	Hs.197354	ESTs	1.19	2.00
25	434607	AA364183	Hs.323443	hypothetical protein FLJ11806	1.30	2.76
	424542	AI860558	Hs.272009	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.48	2.48
	450893	AK002185	Hs.25625	hypothetical protein FLJ11323	1.15	1.57
	418481	M81945	Hs.85289	CD34 antigen	2.16	1.76
	443077	AI459490	Hs.60090	Homo sapiens cDNA FLJ13595 fis, clone PL	1.36	2.41
30	437521	AA758756	Hs.121380	ESTs	1.07	2.05
	430265	L36033	Hs.237356	stromal cell-derived factor 1	2.34	1.35
	446698	AV660306	Hs.184411	albumin	1.52	1.33
	429725	AA457367	Hs.191638	ESTs	1.38	3.00
	425114	AW409763	Hs.50699	ESTs, Weakly similar to 2109260A B cell	1.13	2.34
35	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	1.62	1.71
	435284	AA879470	Hs.96849	Homo sapiens cDNA FLJ11492 fis, clone HE	1.20	2.50
	415634	F13165	Hs.12549	ESTs, Weakly similar to 2109260A B cell	1.46	2.35
	420565	AI806770	Hs.30258	ESTs	1.39	3.85
	419494	W01060	Hs.34382	ESTs	1.10	1.75
40	458183	AL031591	Hs.7370	phosphatidylinositol transfer protein, b	1.28	2.24
	416620	R93080	Hs.35035	ESTs	1.81	2.58
	431356	AW499632	Hs.288512	Homo sapiens cDNA FLJ11632 fis, clone HE	1.42	2.03
	433282	BE539101	Hs.5324	hypothetical protein	0.33	0.20
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	1.50	0.95
45	458126	AW979136	Hs.124629	ESTs	1.34	1.32
	414005	AA134489	Hs.269379	ESTs	1.52	2.07
	411496	AW849241		gb:IL3-CT0215-210200-088-E03 CT0215 Homo	1.10	2.21
	451147	AA016982	Hs.64341	ESTs	1.53	2.29
	450238	T89693	Hs.138777	ESTs	1.32	2.28
50	449284	BE502240	Hs.38592	hypothetical protein FLJ23342	1.46	1.40
	449479	AI797619	Hs.197659	ESTs	0.72	0.66
	403066			Target Exon	1.32	1.19
	410118	AW590680	Hs.110802	von Willebrand factor	1.72	2.54
	437674	AI749921	Hs.205377	ESTs	1.38	2.21
55	431065	AA491286	Hs.128792	ESTs	1.30	2.08
	416352	H78006	Hs.19553	ESTs	1.05	1.14
	452565	BE066552		gb:RC3-BT0333-300300-017-h08 BT0333 Homo	1.46	2.53
	418115	AW005376	Hs.173280	ESTs	1.20	0.98
	422031	R66895	Hs.28788	ESTs	1.37	1.37
60	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	1.64	2.20
	457683	AI821877	Hs.140002	ESTs, Moderately similar to ALU7_HUMAN A	1.03	2.35
	435521	W23814	Hs.6361	mitogen-activated protein kinase kinase	0.73	0.59
	438874	H02780	Hs.347520	gb:yj41a11.r1 Soares placenta Nb2HP Homo	1.56	2.73
	441167	AA921754	Hs.211781	ESTs	1.74	2.12
65	455917	BE156765		gb:RC1-HT0370-120100-012-c09 HT0370 Homo	1.29	1.35
	419058	AW675039	Hs.1227	aminolevulinic acid, delta-, dehydratase	2.04	1.83
	408651	BE266928	Hs.17126	hypothetical protein MGC15912	1.30	1.23
	442737	AB002319	Hs.8663	KIAAC321 protein	0.85	0.79
	407134	T51588		gb:yb27e06.s1 Stratagene fetal spleen [9	1.23	0.97
70	447492	AI381619	Hs.20188	ESTs	1.26	2.28
	437840	AA884836	Hs.292014	ESTs	2.05	2.29
	412294	AA689219	Hs.117176	poly(A)-binding protein, nuclear 1	1.47	3.55
	419909	AL136653	Hs.93675	decidual protein induced by progesterone	1.10	2.18
	432569	AI131140	Hs.152434	ESTs	1.34	1.83
75	412252	AW903782		gb:CM4-NN1032-190400-527-g09 NN1032 Homo	1.26	2.00
	444298	Z17370		gb:HSDH1020 Stratagene cDNA library Hum	1.36	2.68
	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypothi	0.95	2.23
	418315	T06475	Hs.124962	Homo sapiens, clone IMAGE:3510191, mRNA,	0.82	0.82

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5	440357	AA379353	Hs.20950	phospholysine phosphohistidine inorganic	0.83	0.68
	440867	AI417007	Hs.166338	ESTs	1.45	1.50
	410956	AW938322		gb:PM1-DT0054-231289-002-c02 DT0054 Homo	1.06	2.95
	446574	AI310135	Hs.335933	ESTs	1.54	2.45
	447912	AW576549	Hs.165728	ESTs, Weakly similar to I38022 hypothe	1.22	2.07
10	457741	BE044740		gb:hm55g10.x1 NCL_CGAP_RDF1 Homo sapiens	1.89	2.08
	433762	AA732484	Hs.169399	ESTs	1.24	2.58
	418156	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m	3.71	1.38
	409282	AW966480		gb:EST378554 MAGE resequences, MAGI Homo	1.70	1.70
	425169	AW292500	Hs.128514	ESTs	1.13	1.12
15	458497	AI161428	Hs.75916	splicing factor 3b, subunit 2, 145kD	1.26	2.28
	405673			NM_022775:Homo sapiens hypothetical prot	2.00	1.00
	442691	AW341438	Hs.278036	ESTs	1.38	2.28
	424316	AA676403	Hs.145078	regulator of differentiation (in S. pom	1.06	2.10
	444608	AI174683	Hs.329863	ESTs	1.95	1.82
20	447345	BE247787	Hs.18166	KIAA0870 protein	1.26	2.10
	439648	AW979249		gb:EST391359 MAGE resequences, MAGP Homo	1.68	2.63
	428546	D42046	Hs.194665	DNA2 (DNA replication helicase, yeast, h	1.32	2.33
	403214			NM_016232*:Homo sapiens interleukin 1 re	1.02	2.15
	404495			C8001441*:gij8923061[re]NP_060114.1] hy	2.20	2.49
25	443471	AW236939	Hs.172154	Homo sapiens clone FLB3442 PRO0872 mRNA,	1.58	1.74
	437116	AL049253	Hs.190162	ESTs	1.22	2.53
	451357	AB020640	Hs.26319	Human DNA sequence from clone RP3-467L1	0.94	2.35
	408255	AW807321		gb:MR4-ST0062-240300-003-g05 ST0062 Homo	1.12	1.39
	448931	AI597806	Hs.192671	ESTs	1.30	3.29
30	422343	AI628633	Hs.346823	gb:ly77d05.x1 NCL_CGAP_Kid11 Homo sapien	1.86	2.32
	407140	AA059106	Hs.271780	ESTs, Weakly similar to I38022 hypothe	1.37	1.01
	429187	AA447648	Hs.163872	ESTs, Weakly similar to S65657 alpha-1C-	1.74	1.55
	423614	AI457640	Hs.206632	ESTs	1.48	2.83
	429073	AA446187	Hs.47385	ESTs	1.24	2.00
35	415732	AA167566	Hs.271570	ESTs, Weakly similar to 2109260A B cell	1.31	2.34
	412634	U55984	Hs.289088	heat shock 90kD protein 1, alpha	0.42	0.22
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.94	1.27
	415007	BE244332	Hs.77770	adaptor-related protein complex 3, mu 2	0.78	0.71
	402654			Target Exon	0.90	0.85
40	457974	AW842353	Hs.321717	ESTs, Weakly similar to S22765 heterogen	0.86	0.90
	405340			C2002952:gij1345964[sp]P10079[FBP]_STRPU	1.46	2.33
	426259	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	1.63	2.75
	442237	AW905607	Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCLE	1.08	3.38
	456370	AA234938	Hs.87384	ESTs	0.77	2.83
45	407041	X15673		gb:Human pTR2 mRNA for repetitive sequen	2.00	1.84
	452001	AI827675	Hs.274281	fidgetin	1.38	2.03
	445137	AI733837	Hs.145661	ESTs	1.60	3.00
	440808	AK001339	Hs.7432	hypothetical protein FLJ10477	1.17	2.10
	404418			Target Exon	1.90	3.36
50	447658	AI916872	Hs.213424	ESTs	1.90	2.21
	434414	AI798376		gb:tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens	1.58	1.24
	400834			NM_002240*:Homo sapiens potassium inward	1.25	2.33
	449542	AW857362	Hs.268855	ESTs, Weakly similar to I38022 hypothe	1.46	1.28
	441043	AA913422	Hs.192104	ESTs	1.26	1.09
55	403391			C3001164*:gij1730196[sp]P50573[GAR3_RAT	1.46	2.55
	449129	AI631602	Hs.258949	ESTs	1.27	2.48
	418321	D63477	Hs.84087	KIAA0143 protein	0.56	0.52
	426789	F06596	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	1.31	2.06
	443679	AK001810	Hs.9670	hypothetical protein FLJ10948	1.34	1.22
60	428554	R46070	Hs.6407	ESTs	1.04	2.08
	401890			Target Exon	1.24	1.14
	419501	AW843822		gb:CM4-CN0045-010200-514-f08 CN0045 Homo	1.74	1.38
	457096	AI809202	Hs.208343	ESTs, Weakly similar to cerebroside sulf	0.82	0.87
	426123	AA370352		gb:EST82246 Prostate gland I Homo sapien	1.28	2.35
65	449445	AW197349	Hs.232197	ESTs	1.24	2.13
	430683	AC004862	Hs.247768	Homo sapiens PAC clone RP4-697H17 from 7	1.30	2.00
	440642	AI744995		ESTs, Moderately similar to ALU4_HUMAN A	1.29	2.44
	455236	AW875972		gb:CM3-PT0014-071299-051-b05 PT0014 Homo	1.78	2.95
	449622	AW013915	Hs.196578	ESTs	1.42	2.20
70	415116	AA160363	Hs.269956	ESTs	2.02	1.03
	457269	AI338993	Hs.134535	ESTs	1.93	1.35
	427877	AW138725	Hs.178067	ESTs	1.91	2.42
	454631	AW811324		gb:IL3-ST0141-131099-017-A02 ST0141 Homo	1.00	3.13
	456390	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN IIII	1.02	2.21
75	435844	AA700856	Hs.59651	ESTs, Weakly similar to I78885 serine/th	0.85	0.81
	427237	AA399964	Hs.97763	ESTs	1.57	1.44
	408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	1.20	3.13
	442151	AI733404	Hs.128865	ESTs	1.50	2.13
	412708	R26830	Hs.106137	ESTs, Weakly similar to CGHU7L collagen	1.16	3.00
	417262	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot	1.25	2.40
	419362	N64116	Hs.24624	hypothetical protein FLJ21945	1.38	2.48

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5	447248	AW295831	Hs.6496	ESTs	1.56	2.03
	415622	F13010	Hs.12400	ESTs	1.48	2.30
	414065	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 fis, clone PL	1.26	2.88
	414585	W46954	Hs.334716	hypothetical protein MGC16291	1.24	2.05
	443197	Z43613		gb:HSC1GD091 normalized infant brain cDN	1.11	2.04
10	428266	A1382001	Hs.43590	ESTs	1.09	2.03
	447083	A1472124	Hs.157757	ESTs	1.66	3.53
	412302	AW936334		gb:QV4-DT0021-281299-070-g05 DT0021 Homo	1.74	3.00
	445555	AW974013		ESTs	1.32	1.29
	453117	AW162044	Hs.104203	hypothetical protein MGC12981	0.73	0.81
15	436757	AW975663	Hs.293404	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.21	1.88
	431976	AA719001	Hs.291065	ESTs	1.23	2.01
	430657	AA482910	Hs.279664	ESTs	1.64	2.65
	438744	BE314727	Hs.75721	profilin 1	0.85	0.85
	439325	AF086139	Hs.150423	cyclin-dependent kinase 9 (CDC2-related	1.16	2.05
20	438117	AA328041	Hs.194329	hypothetical protein FLJ21174	0.79	0.76
	401686			NM_014587*:Homo sapiens SRY (sex determi	1.32	2.31
	420269	U72937	Hs.96264	alpha thalassemia/mental retardation syn	0.78	0.53
	434288	AW189075	Hs.116265	fibrillin3	2.42	4.23
	433215	AB040912	Hs.191098	hypothetical protein FLJ11598	1.36	1.36
25	413429	BE139117	Hs.278881	ESTs	1.30	2.98
	426417	AA377908	Hs.13254	ESTs	1.36	1.77
	413882	AA132973	Hs.184492	ESTs	1.55	2.10
	413346	AA128586		gb:z124h06.r1 Soares_pregnant_luterus_NbH	1.29	1.77
	445020	AI205655	Hs.147221	ESTs	1.90	2.00
30	418175	AW967054	Hs.206312	ESTs, Weakly similar to I38022 hypotheti	1.60	3.70
	429582	AI569068	Hs.22247	ESTs	1.06	2.38
	409134	AW340389	Hs.250585	ESTs	1.64	2.57
	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	0.73	2.33
	435667	F13625	Hs.124183	ESTs	1.10	2.33
35	440513	BE407106	Hs.65907	Homo sapiens, clone IMAGE:3959816, mRNA,	0.85	2.03
	419711	C02621	Hs.159282	ESTs	1.22	2.00
	434249	AA987537	Hs.129875	ESTs	1.29	2.48
	437355	AL359557	Hs.306508	Homo sapiens mRNA; cDNA DKFZp762O1415 (f	1.86	2.08
	428360	H10291	Hs.30974	ESTs	1.40	2.05
40	435339	AI358300	Hs.129827	ESTs	1.38	2.18
	435345	AW360966	Hs.6653	ESTs	1.49	2.27
	435105	AI878982	Hs.131859	Homo sapiens F-box protein FBX11 mRNA, p	1.78	2.33
	459645	AA074346	Hs.250715	ESTs	1.50	2.40
	449691	AA002143	Hs.21413	solute carrier family 12, (potassium-chil	0.74	0.69
45	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	1.42	2.76
	437272	AW975957		gb:EST388066 MAGE resequences, MAGN Homo	1.00	2.16
	456955	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5	0.84	0.81
	421362	AK003050	Hs.103853	hypothetical protein FLJ20043	1.30	2.21
	457926	AA452378	Hs.11637	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	1.27	2.12
50	444557	AI167637	Hs.146924	ESTs	1.83	2.35
	434476	AW858520	Hs.84264	acidic protein rich in leucines	1.43	3.80
	458059	AW015588	Hs.137232	ESTs, Weakly similar to S65657 alpha-1C-	1.30	2.23
	413595	AW235215	Hs.16145	ESTs	2.10	2.43
	417281	R98773	Hs.268883	ESTs	1.26	2.10
55	445689	BE158869		gb:QV0-HT0398-210100-096-f08 HT0398 Homo	1.15	2.15
	423249	AA323682	Hs.125374	ESTs, Weakly similar to S26689 hypotheti	1.76	1.50
	408366	AW511255	Hs.346442	ESTs	1.74	2.91
	441359	AI435179	Hs.126820	ESTs	2.43	1.59
	413068	BE063792		gb:QV3-BT0295-260100-066-d06 BT0295 Homo	1.52	2.09
60	441322	AW071851	Hs.130628	ESTs	1.42	2.10
	409124	AW292809	Hs.50727	N-acetylglucosaminidase, alpha- (Sanfil	1.11	2.20
	432413	AK000257	Hs.274505	Homo sapiens mRNA; cDNA DKFZp564A216 (fr	1.10	2.25
	425391	AI248252	Hs.160672	ESTs	1.17	2.38
	443861	AW449462	Hs.134743	ESTs	1.44	2.30
65	454609	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	2.30	1.33
	425893	AA629695		gb:ad43b07.s1 Stratagene lung carcinoma	1.76	2.51
	443611	NM_014397	Hs.9625	NIMA (never in mitosis gene a)-related k	1.81	2.90
	410359	R38624	Hs.106313	ESTs	1.78	2.05
	406308			NM_025192:Homo sapiens hypothetical prot	1.92	2.24
70	432476	T94344	Hs.326263	ESTs	1.40	2.45
	435073	AA664078		gb:ac04a05.s1 Stratagene lung (937210) H	1.66	2.26
	420581	AA278459	Hs.151940	ESTs	1.48	2.58
	435579	AI32373	Hs.156924	ESTs	1.46	2.68
	439633	AF086464	Hs.86248	ESTs	1.40	2.48
75	430551	AA481150	Hs.136343	ESTs	1.40	2.28
	450855	T97988	Hs.295605	mannosidase, alpha, class 2A, member 2	1.48	2.40
	444326	AI939357	Hs.270710	ESTs	0.88	2.28
	412149	R49355	Hs.273824	ESTs	1.58	2.19
	455116	AW857271		gb:CM0-CT0307-210100-158-g09 CT0307 Homo	1.56	2.50
	449626	AA774247	Hs.301637	zinc finger protein 258	0.60	0.53
	410047	AI167810	Hs.132390	zinc finger protein 36 (KOX 18)	0.66	0.58

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	418865	AW117500	Hs.104241	ESTs	1.58	2.63
	402762			ENSP00000235171*:GAP junction beta-4 pro	0.81	0.82
	436449	AI418027	Hs.120361	ESTs	1.46	1.46
5	403488			ENSP00000201948:KARYOPHERIN BETA2B HOMOL	1.38	2.23
	431235	AA318271	Hs.250905	hypothetical protein	1.14	2.55
	448576	AB026730	Hs.21495	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	0.70	0.78
	408100	AW205382	Hs.42676	KIAA0781 protein	1.36	2.66
	433436	AW162474		Bruno (Drosophila) -like 6, RNA binding	1.50	2.15
10	422337	R38572		gb:yc87c11.s1 Soares infant brain 1N1B H	2.23	1.71
	426160	AA206020	Hs.167460	splicing factor, arginine/serine-rich 3	1.08	2.09
	447008	BE010189		nuclear receptor subfamily 1, group I, m	1.26	1.27
	420141	AA702961	Hs.124103	ESTs, Weakly similar to I38344 titin, ca	1.46	2.60
	423840	AA332434	Hs.72465	ESTs, Weakly similar to non-lens beta ga	1.26	2.47
15	447793	AI424924	Hs.211203	ESTs	2.38	1.83
	407328	AA509857	Hs.187748	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.11	2.54
	432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.63	2.05
	421311	N71848	Hs.283609	hypothetical protein PRO2032	0.51	0.44
	444649	AW207523	Hs.197628	ESTs	1.21	2.24
20	448688	R94570	Hs.268869	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.91	3.25
	428847	AI954833	Hs.98881	ESTs	1.48	2.66
	413750	BE161453		gb:IL2-HT0437-290200-045-A06 HT0437 Homo	1.22	1.00
	429355	AW973253	Hs.292689	ESTs	1.86	2.35
25	427798	AA412499	Hs.104779	ESTs	1.82	2.33
	431179	AI338644	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	0.60	2.00
	451719	AI373532	Hs.157910	ESTs	1.29	3.85
	438094	AI821755	Hs.131805	ESTs, Weakly similar to A56194 thromboxa	1.74	2.54
	418504	BE159718	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (f	0.52	0.49
	407414	AF072164		gb:Homo sapiens HSFE-1 mRNA, partial cds	1.67	2.28
30	416410	H53777	Hs.36822	ESTs	1.85	2.28
	439141	AI241470	Hs.268982	ESTs	1.08	2.28
	441181	AA416925	Hs.121076	peptidylprolyl isomerase (cyclophilin)-I	1.81	2.02
	434482	AF143331	Hs.16073	ESTs	1.22	2.00
	455757	BE079531		gb:RC5-BT0624-240300-013-D08 BT0624 Homo	1.53	2.16
35	425787	AA363887	Hs.155029	ESTs	0.76	2.13
	405727			CX001244:gil11420428[ref]XP_004814.1] be	1.70	2.21
	441846	AW850960		gb:IL3-CT0220-150200-068-B03 CT0220 Homo	1.16	2.14
	451945	BE504055	Hs.211420	ESTs	0.84	2.73
40	438432	AW444990	Hs.258800	ESTs, Weakly similar to I38022 hypotheti	1.60	2.43
	451140	AW411354	Hs.26002	LIM domain binding 1	1.14	1.20
	407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.03	2.42
	453041	AI680737	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	1.69	3.43
	437613	R19892	Hs.10267	MIL1 protein	1.16	2.11
	451507	AW291109	Hs.208787	ESTs, Weakly similar to T31611 hypotheti	1.22	2.05
45	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	2.85	1.00
	453669	AL049029	Hs.7258	hypothetical protein FLJ22021	0.75	0.64
	455065	AW854352		gb:RC3-CT0255-200100-024-g10 CT0255 Homo	1.49	2.20
	442220	AL037800	Hs.8148	selenoprotein T	0.50	0.18
	437936	AW798475	Hs.288549	hypothetical protein FLJ14710	1.50	2.44
50	442556	AL137761	Hs.6379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	0.54	0.37
	405223			Target Exon	1.09	2.80
	437225	AW975962	Hs.252935	ESTs	1.03	2.47
	421101	AF010446	Hs.101840	major histocompatibility complex, class	0.72	0.57
55	436200	R51386	Hs.124881	ESTs	1.64	2.93
	402025			NM_021624:Homo sapiens histamine H4 rece	1.52	2.28
	407019	U49973		gb:Human Tigger1 transposable element, c	2.40	2.12
	451305	AW003571	Hs.211191	ESTs, Weakly similar to A46010 X-linked	1.24	3.23
	423450	AJ290445	Hs.128759	KIAA0524 protein	1.64	2.13
	423139	AW402725	Hs.288560	hypothetical protein FLJ21106	1.61	2.28
60	451763	AW294647	Hs.233634	hypothetical protein FLJ14220	1.39	2.08
	458915	AI915689	Hs.212781	EST	1.62	2.02
	452829	AI955579	Hs.63368	ESTs, Weakly similar to TRHY_HUMAN TRICH	0.60	0.41
	446383	T05816	Hs.92511	ESTs	2.08	1.48
	432576	AW157424	Hs.165954	ESTs, Weakly similar to I38022 hypotheti	1.86	2.49
65	433820	AI401627	Hs.174067	ESTs	1.30	2.00
	419719	AA844700	Hs.39297	ESTs, Moderately similar to ALU1_HUMAN A	1.33	2.00
	415868	H06728	Hs.21017	ESTs	1.34	2.08
	420738	NM_004185	Hs.258575	wingless-type MMTV integration site fami	1.42	2.29
	446614	AK001733	Hs.15562	hypothetical protein FLJ10871	0.79	0.78
70	404167			NM_021956*:Homo sapiens glutamate recept	1.62	2.55
	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	0.72	0.75
	401215			C12000457*:gil7512178[pir][T30337 polypr	1.14	2.08
	421600	AW893889	Hs.323231	Homo sapiens cDNA FLJ11946 fis, clone HE	1.88	2.66
	426248	T18988	Hs.293668	ESTs	1.17	3.44
	454523	AW803980		gb:PM0-UM0084-240300-001-G11 UM0084 Homo	1.34	2.40
75	420656	AA279098	Hs.187636	ESTs	1.22	2.43
	402833			C1002508:gil6691937[emb][CAB65797.1] (AL0	1.31	2.00
	438910	AA827921	Hs.291858	ESTs, Weakly similar to ALUC_HUMAN !!!	1.39	3.13

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	416170	H42454	Hs.220645	ESTs	0.99	2.18
	433598	AI762836	Hs.271433	ESTs, Moderately similar to ALU2_HUMAN A	2.04	1.28
	417699	T91491	Hs.119670	ESTs	1.36	2.50
5	459605	AL045773		gb:DKFZp434F246_r1 434 (synonym: htes3)	1.21	2.13
	453204	R10799	Hs.191990	ESTs	3.12	2.98
	458971	AL119206	Hs.126257	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.34	2.09
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	1.68	2.00
	400414	AF083118	Hs.283968	Homo sapiens CATX-2 mRNA, complete cds	1.70	2.54
10	426263	AI908774	Hs.259785	carnitine palmitoyltransferase 1, liver	0.96	2.14
	439334	AI148976	Hs.112062	ESTs	1.50	2.45
	455527	AW984479		gb:PM1-HN0012-220300-001-b12 HN0012 Homo	1.46	2.28
	408084	AL040832	Hs.160422	Homo sapiens clone PP502 unknown mRNA	1.61	2.23
	432059	AF227131	Hs.272387	taste receptor, type 2, member 4	1.66	2.15
15	429791	AW015667	Hs.119427	ESTs	1.51	2.83
	438695	AI885190	Hs.156089	ESTs, Weakly similar to repressor protel	1.19	2.03
	458139	AI525711	Hs.253147	ESTs	1.42	2.10
	413035	BE155563		gb:PM4-HT0352-171199-001-Q05 HT0352 Homo	1.62	2.30
	422444	AA310688		gb:EST181501 Jurkat T-cells V Homo sapie	1.38	2.05
20	409546	AW410190	Hs.250624	hypothetical protein MGC4473	1.87	2.18
	411432	AW846272		gb:QV0-CT0179-300999-024-d12 CT0179 Homo	1.04	2.03
	445327	AI220082	Hs.147722	ESTs	1.16	2.10
	424628	AB011136	Hs.151385	KIAA0564 protein	0.61	0.63
	440197	AW340708	Hs.317714	pallid (mouse) homolog, pallidin	0.56	0.39
25	409894	BE081731		gb:QV2-BT0635-220400-158-e04 BT0635 Homo	1.50	2.45
	422776	AA316987	Hs.129846	ESTs	1.36	2.20
	428255	AI627478	Hs.187670	ESTs	1.34	2.40
	412484	AA112090	Hs.269961	ESTs	0.97	2.00
	432789	D26361	Hs.3104	KIAA0042 gene product	1.44	2.73
30	430100	AA766178	Hs.291601	ESTs, Highly similar to T00350 hypothell	1.06	2.02
	419528	AA244000	Hs.222365	ESTs	1.34	2.06
	441793	AA968459	Hs.158785	ESTs	1.80	2.70
	429468	AF033579		T-box 10	0.71	0.61
	410248	AA166653	Hs.268171	ESTs	2.55	2.10
35	401818			NM_000664*:Homo sapiens acetyl-Coenzyme	1.76	2.58
	451724	AI903765		gb:UL-BT037-301298-102 BT037 Homo sapien	1.64	2.28
	431866	NM_012098	Hs.8025	angiotensin-like 2	1.56	2.36
	432719	AW935411	Hs.314460	ESTs	1.36	2.25
	418977	AA233094	Hs.191517	ESTs	2.06	3.60
40	404220			C5000989*:gij7573285[emb CAB87644.1 (AL	1.54	2.23
	446708	BE549905	Hs.231754	ESTs	1.35	2.16
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	1.42	2.38
	422050	AA302741	Hs.25796	ESTs, Moderately similar to J05238 galac	1.40	2.50
	400704			Target Exon	1.48	1.00
45	406104			Target Exon	1.22	2.03
	411008	AW813238		gb:MR3-ST0191-020200-207-d04 ST0191 Homo	1.00	2.13
	426582	AA381797	Hs.281121	ESTs	1.35	2.45
	430653	AI734179	Hs.105676	ESTs	1.43	2.23
	432420	AL044659	Hs.43791	ESTs	1.15	2.03
50	403197			C2002793*:gij1353148[splQ09568]YR86_CAEE	0.52	0.47
	432407	AA221036		gb:zr03f12.r1 Stratagene NT2 neuronal pr	1.93	2.23
	414996	AW747800	Hs.55016	hypothetical protein FLJ21935	1.66	2.72
	401016			ENSP00000227126:NAALADASE II PROTEIN.	1.25	2.45
	433335	AA584134	Hs.269454	ESTs	1.31	2.24
55	458668	BE244127		gb:TCBAP1E0661 Pediatric pre-B cell acut	1.16	2.03
	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypotheli	3.75	2.72
	452277	AL049013	Hs.28783	KIAA1223 protein	0.33	0.26
	425712	AA412548	Hs.21423	ESTs, Moderately similar to ALU1_HUMAN A	1.34	2.21
	427598	AA406057	Hs.97998	ESTs	1.06	2.05
60	412565	M85975	Hs.344069	gb:EST02500 Fetal brain, Stratagene (cat	1.24	2.59
	422043	AL133649	Hs.110953	retinoic acid induced 1	0.48	0.41
	421814	L12350	Hs.108623	thrombospondin 2	0.48	2.45
	413645	AA130992		gb:zo15e02.s1 Stratagene colon (937204)	1.32	2.45
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	0.39	0.28
65	452396	H10302	Hs.112577	ESTs	1.60	2.45
	440612	BE561384		gb:601344969F1 NIH_MGC_8 Homo sapiens cD	1.08	2.60
	454721	AW815588		gb:QV0-ST0216-061299-066-a09 ST0216 Homo	1.44	1.65
	417796	AA206141	Hs.6786	ESTs	1.68	3.85
	432864	D16217	Hs.279607	calpastatin	0.43	0.35
70	454480	AA088375	Hs.22612	hypothetical protein DKFZp666D1346	2.19	1.91
	434490	AF143870	Hs.15246	ESTs	2.26	2.07
	418797	AA515814		gb:ng64b03.s1 NCL_CGAP_Lip2 Homo sapiens	1.42	2.55
	403871			C5001783*:gij780367[gb AAB05844.1 (L416	1.60	2.63
	441263	AA927670	Hs.131704	ESTs	1.31	3.63
	442250	AW290871	Hs.129121	ESTs	1.14	2.38
75	456747	AL037357	Hs.125864	tropomodulin 2 (neuronal)	1.61	1.26
	425757	AA363171		gb:EST72986 Ovary II Homo sapiens cDNA 5	1.29	2.95
	405494			C2001837*:gij12697903[dbj BAB21770.1 (A	2.09	1.00

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	432250	AA452088	Hs.274170	Opa-interacting protein 2	1.26	2.71
	431911	AK000156	Hs.272193	Homo sapiens cDNA FLJ20149 fis, clone CO	1.46	2.60
	413923	AI733852	Hs.199957	ESTs	1.62	2.10
	449590	AA694070	Hs.268835	ESTs	1.20	2.53
5	438467	AA808027	Hs.123277	ESTs	1.48	2.10
	432121	AI824879	Hs.211286	ESTs, Weakly similar to 1207289A reverse	1.27	3.13
	412298	AW936300		gb:QV4-DT0021-281299-070-a04 DT0021 Homo	1.42	2.60
	408519	AA679082	Hs.43481	hypothetical protein DKFZp564K192	1.84	3.70
10	416067	T79732	Hs.14633	ESTs	1.11	3.08
	420497	AW206285	Hs.253548	ESTs	1.90	2.48
	405704			NM_001844*:Homo sapiens collagen, type I	1.42	2.90
	423443	AI432601	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	1.42	2.03
	415904	Z44679	Hs.336391	ESTs	1.62	2.94
15	413786	AW613780	Hs.13500	ESTs	0.33	0.17
	404031			C5001700*:gij9256616[ref]NP_061761.1] pr	1.94	2.29
	457412	N40711	Hs.333300	hypothetical protein FLJ14026	1.92	3.20
	439719	AF086554	Hs.326048	Homo sapiens mRNA; cDNA DKFZp434M0420 (f	1.62	2.30
	418161	AI950754	Hs.81716	ESTs	1.81	2.42
20	425894	AW954011	Hs.180711	ESTs	0.92	2.20
	419988	W39388	Hs.55335	Homo sapiens, clone MGC:17421, mRNA, com	1.34	2.57
	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	1.67	2.66
	450177	AI698091	Hs.107845	ESTs	1.50	2.25
	459704	AA719572	Hs.274441	Homo sapiens mRNA; cDNA DKFZp434N011 (fr	1.27	3.35
25	410357	AW653614		gb:hj22e04.x1 NCL_CGAP_L18 Homo sapiens	0.69	0.59
	459234	AI940425		gb:CM0-CT0052-150799-024-c04 CT0052 Homo	1.67	2.08
	421313	NM_014923	Hs.103329	KIAA0970 protein	0.57	0.26
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	1.80	2.73
	423086	AB028984	Hs.123420	KIAA1061 protein	0.40	0.56
30	425980	AA366951		gb:EST77963 Pancreas tumor III Homo sapi	1.33	2.50
	423185	BE295590	Hs.125079	ornithine decarboxylase antizyme 1	0.60	0.56
	410840	AW806924		gb:QV4-ST0023-160400-172-h10 ST0023 Homo	1.50	2.88
	403917			Target Exon	1.82	2.02
	437384	AI674710	Hs.174397	ESTs	1.26	2.05
35	444389	AW439340	Hs.189720	ESTs	1.26	2.13
	443318	AI051603	Hs.133141	ESTs	1.46	2.20
	441093	AI698138	Hs.126918	ESTs	1.40	2.35
	439432	AI984203	Hs.57874	ESTs	0.88	2.18
	454629	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	1.96	2.31
40	406207			Target Exon	2.77	2.55
	444872	AI936264		p30 DBC protein	1.48	2.45
	401908			C17000154:gij12003960[gb]AAG43830.1 AF21	1.15	2.28
	404730			Target Exon	1.84	2.78
	457498	AI732230	Hs.191737	ESTs	1.49	2.55
45	448471	AA158617	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	0.37	0.36
	438978	AI095207	Hs.307972	ESTs	1.57	2.39
	418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	2.86	3.34
	400416	AF083130		Homo sapiens CATX-14 mRNA, partial cds	2.03	1.55
	450446	AI696334	Hs.14450	ESTs	1.32	2.38
50	419791	AI579909	Hs.105104	ESTs	0.41	0.27
	449436	AA860329	Hs.279307	hypothetical protein DKFZp434I2117	2.01	1.50
	430808	L08603	Hs.247980	melanocortin 4 receptor	1.09	2.18
	443116	AI033397	Hs.132225	ESTs	1.30	2.25
	437923	BE088433	Hs.334696	hypothetical protein KIAA1335	1.40	2.50
55	403294			Target Exon	0.98	2.18
	436007	AI247716	Hs.232168	ESTs	1.38	1.00
	430649	AB040941	Hs.247713	KIAA1508 protein	1.52	2.85
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566C0134 (fr	1.29	2.59
	444500	AV651273	Hs.282966	ESTs, Moderately similar to 2109260A B c	1.22	2.05
60	447434	R16890	Hs.137135	ESTs	1.72	2.85
	400830			NM_025006:Homo sapiens hypothetical prot	2.04	2.68
	428114	AI821548	Hs.98363	ESTs, Weakly similar to I38022 hypotheti	1.09	2.74
	409688	AI150485		gb:qf36a10.x1 Soares_testis_NHT Homo sap	1.67	1.38
	440781	BE561823	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.28	2.50
65	442662	U78168	Hs.8578	Rap1 guanine-nucleotide-exchange factor	1.92	2.28
	443078	M78728	Hs.132694	Homo sapiens cDNA: FLJ23149 fis, clone L	1.42	2.03
	440179	AI990151	Hs.125904	ESTs	1.49	2.63
	446780	R31107		gb:yh61g01.s1 Soares placenta Nb2HP Homo	1.96	2.78
	444173	AI126432	Hs.149493	ESTs	1.50	2.10
70	417939	R53863	Hs.337512	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.60	2.03
	428490	BE301738	Hs.49806	ESTs, Weakly similar to A46010 X-linked	0.47	0.44
	443869	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	1.25	2.68
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.12	1.15
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	0.64	0.48
75	454701	AW854930		gb:PMO-CT0263-201099-003-f06 CT0263 Homo	1.30	2.33
	439795	N77294	Hs.194294	ESTs	1.17	2.33
	425546	BE409762	Hs.26118	hypothetical protein MGC13033	1.17	2.85
	411245	AW833441		gb:QV4-TT0008-271099-020-g01 TT0008 Homo	1.90	3.98

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	434957	AF283775	Hs.35380	x 001 protein	0.47	0.41
	425724	AA362525		gb:EST72223 Namalwa B cells l Homo sapie	1.38	2.63
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.34	0.28
5	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	1.28	2.19
	421718	AL117574		Homo sapiens mRNA; cDNA DKFZp434L2221 (f	2.04	1.79
	415924	H18047	Hs.335821	ESTs	2.02	3.17
	450850	AA648886	Hs.151999	ESTs	1.68	2.45
	443153	AI371823	Hs.34079	ESTs	1.13	2.41
10	434420	AA688278	Hs.194864	hypothetical protein FLJ22578	1.34	2.38
	426126	AL118747	Hs.26691	ESTs	1.31	2.25
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	1.48	2.40
	459663	AI590487	Hs.49760	gb:tt77d04.x1 NCLCGAP_HSC3 Homo sapiens	1.74	3.33
	453006	AI362575	Hs.303171	ESTs	1.17	2.24
15	437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	0.54	0.46
	417016	AA837098	Hs.269933	ESTs	1.04	2.18
	420223	N27807	Hs.286	ribosomal protein L4	2.08	3.10
	425303	AA354785		gb:EST63098 Jurkat T-cells V Homo sapien	2.18	2.85
	400375	NM_014115		NM_014115: Homo sapiens PRO0113 protein	1.83	2.14
20	456169	Y07909	Hs.79368	epithelial membrane protein 1	1.54	2.08
	409707	AA861773	Hs.313501	ESTs	0.79	0.84
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.46	2.06
	443152	AI803470	Hs.204529	KIAA1806 protein	1.07	2.43
	452714	AW770994	Hs.30340	hypothetical protein KIAA1165	0.45	0.34
25	415110	H04043		gb:yj45c03.r1 Soares placenta Nb2HP Homo	1.62	2.07
	443251	BE185436	Hs.278839	ESTs	1.34	2.05
	433441	R37094	Hs.13742	ESTs	1.76	2.05
	434612	R76513	Hs.301183	molecule possessing ankyrin repeats Indu	0.83	2.88
	417807	R17806	Hs.269452	gb:yj09b06.r1 Soares infant brain 1N1B H	1.30	2.23
	426902	AI125334	Hs.97408	ESTs	1.94	2.20
30	436028	AA731124	Hs.120931	ESTs	2.01	1.73
	428878	AA436884	Hs.48926	ESTs	1.22	2.17
	439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	1.32	2.75
	442435	AI986208	Hs.244760	ESTs, Highly similar to B34087 hypotheti	2.09	3.13
35	416527	T62507	Hs.11038	ESTs	1.66	2.12
	441808	AW118601	Hs.127887	ESTs, Moderately similar to 1609195B blo	1.22	2.58
	417054	AF017060	Hs.174151	aldehyde oxidase 1	2.57	1.48
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	1.16	2.23
	418442	AI873471	Hs.186898	ESTs	1.39	2.26
40	416640	BE262478	Hs.79404	neuron-specific protein	0.31	0.26
	403146			Target Exon	1.49	2.18
	457397	AW989025	Hs.109154	ESTs	1.32	2.26
	439189	AI951185	Hs.144630	nuclear receptor subfamily 2, group F, m	1.76	2.90
	423969	AI830571	Hs.34969	hypothetical protein DKFZp566N034	1.18	2.00
45	459683	AI674906	Hs.199460	gb:wc73f02.x1 NCLCGAP_Pan1 Homo sapiens	1.74	2.00
	426826	AK001890	Hs.172654	guanine nucleotide binding protein beta	2.04	1.60
	414462	BE622743	Hs.301064	arap1n.1	0.40	0.29
	438027	N93047	Hs.19131	transcription factor Dp-2 (E2F dimerizat	1.08	2.40
	408623	AW811978	Hs.254037	ESTs	1.64	3.08
	433765	AA909619	Hs.112668	ESTs	1.52	2.02
50	417132	N56605	Hs.269053	ESTs	1.64	2.51
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	0.28	0.16
	435186	AL119470	Hs.145631	ESTs	1.74	3.10
	411107	AW958042	Hs.95870	PTD015 protein	0.49	0.24
55	406930	U04691		gb:Human olfactory receptor (OR17-219) g	2.21	3.88
	411026	AW813786		gb:RC3-ST0197-120200-015-b05 ST0197 Homo	1.64	1.03
	415766	H01613	Hs.50628	adaptor-related protein complex 4, sigma	1.64	2.51
	446018	AW631111	Hs.249727	gb:hh92e12.y1 NCLCGAP_GU1 Homo sapiens	1.56	2.48
	440125	AW238410	Hs.253888	ESTs	1.46	2.25
60	449832	AA694284	Hs.60049	ESTs	1.27	2.33
	431899	AA521381	Hs.187726	ESTs	1.11	2.53
	431531	BE142052	Hs.62654	kringle-containing transmembrane protein	1.06	2.00
	441077	AI241273	Hs.15312	ESTs	1.12	2.13
	426799	H14843	Hs.303154	popeye protein 3	0.61	0.51
65	419480	BE536584	Hs.122546	hypothetical protein FLJ23017	1.88	2.38
	455908	BE156306		gb:QV0-HT0367-150200-114-h04 HT0367 Homo	1.77	2.55
	403332			Target Exon	1.46	2.60
	455753	BE075124		gb:PM1-BT0585-110200-003-h02 BT0585 Homo	1.40	2.43
	404429			Target Exon	1.31	2.01
70	438941	AF075047	Hs.31864	ESTs	1.34	2.21
	428745	AA433896	Hs.201634	ESTs	1.72	2.06
	411567	AW851630		gb:MR2-CT0222-211099-002-h06 CT0222 Homo	1.60	2.70
	458714	R20916	Hs.344777	ESTs	0.93	2.07
	426839	M74782	Hs.172689	interleukin 3 receptor, alpha (low affin	1.39	2.71
	444539	AI955765	Hs.146907	ESTs, Weakly similar to 2004399A chromos	1.66	2.18
75	407322	AA171892	Hs.324570	ESTs, Weakly similar to ALU3_HUMAN ALU S	1.30	2.65
	453826	AL138129		gb:DKFZp547F152_r1 547 (synonym: hibr1)	1.52	2.73
	435695	AA694324	Hs.257675	ESTs	1.24	2.00

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	402294		Target Exon	1.80	3.08
	417759	R13567	ESTs	1.63	2.58
	417527	AA203524	gb:zx56e10.r1 Soares_fetal_liver_spleen_	1.52	2.02
5	427526	AA405062	gb:zu12e04.r1 Soares_testis_NHT Homo sap	2.03	1.90
	455300	AW891707	gb:CM3-NT0090-040500-171-e02 NT0090 Homo	1.12	2.20
	448121	AL045714	hypothetical protein DKFZp564F013	0.93	2.28
	415855	Af921875	gb:wp07e04.x1 NCL_CGAP_Kid12 Homo sapien	1.43	2.08
	425702	N59555	gb:yv76f05.s1 Soares fetal liver spleen	1.61	2.80
10	441056	H37860	ESTs	1.11	2.10
	400311	AF072164	Homo sapiens HSFE-1 mRNA, partial cds	2.04	2.95
	451478	NM_012331	methionine sulfoxide reductase A	0.50	0.20
	425288	AA354502	gb:EST62799 Jurkat T-cells V Homo sapien	0.99	2.08
	456397	W28339	PTD010 protein	1.11	2.29
	405654		C12001521:gil7513934[pir][T31031 cca3 pr	2.30	1.00
15	450151	AI088196	Homo sapiens clone IMAGE:451939, mRNA se	1.21	2.60
	419851	AA287987	ESTs, Weakly similar to 1207289A reverse	1.26	2.60
	406016		Target Exon	0.57	0.48
	440903	AI468079	ESTs	2.02	1.61
20	445026	W90337	ESTs, Moderately similar to 2109260A B c	1.56	2.23
	414182	AA136301	KIAA1105 protein	1.32	2.55
	457048	AA400352	ESTs	1.54	2.05
	440542	AA889143	ESTs, Weakly similar to PC4259 ferritin	1.48	2.15
	422857	R71461	gb:yl51h07.r1 Soares placenta Nb2HP Homo	1.42	2.78
25	445948	AW444562	ESTs	1.50	2.48
	454002	BE299567	ESTs, Moderately similar to ALU8_HUMAN A	1.31	2.25
	413656	T91703	gb:ye20g09.s1 Stratagene lung (937210) H	2.10	1.69
	420441	AI986160	dual specificity phosphatase 6	0.99	2.33
	412062	H09124	Homo sapiens cDNA: FLJ23573 fls, clone L	2.14	1.61
30	408991	BE501816	ESTs	1.76	2.83
	432534	AW361625	hypothetical protein FLJ11240	0.41	0.28
	435136	R27299	ESTs	0.76	3.40
	451052	AA281504	Homo sapiens cDNA: FLJ22165 fls, clone H	2.16	1.85
	413928	AA442498	ESTs, Moderately similar to Z195_HUMAN Z	1.30	2.00
35	439448	AA970788	ESTs	1.87	2.23
	403344		NM_000341:Homo sapiens solute carrier fa	1.36	2.22
	418056	AA524886	gb:nh34f02.s1 NCL_CGAP_Pr3 Homo sapiens	1.42	2.85
	435428	AI791746	ESTs	2.44	1.32
	419964	AA811657	ESTs	1.32	2.08
40	440926	AW196772	ESTs	1.80	2.65
	452625	AA724771	ESTs	1.64	2.18
	452797	AI369787	ESTs	1.47	3.16
	436120	AI248193	ESTs	1.41	2.83
	449567	AI990790	ESTs	1.48	2.45
45	409628	AB021865	potassium voltage-gated channel, Shal-re	1.70	2.23
	416617	H69311	ESTs	1.83	2.04
	452266	AI767250	ESTs	0.58	0.43
	404606		Target Exon	1.47	3.75
	401814		Target Exon	2.00	1.91
50	428403	AI393048	leucine rich repeat (in FLJ1) Interactin	0.33	0.21
	433390	AA586950	Homo sapiens mRNA; cDNA DKFZp761G18121 (2.00	4.90
	451443	AW295527	ESTs	1.87	2.25
	411188	BE161168	gb:PM0-HT0425-170100-002-a10 HT0425 Homo	2.15	1.69
	452704	AA027823	Homo sapiens PNAS-130 mRNA, complete cds	2.64	1.65
55	424060	X92108	H.sapiens mRNA for subtelomeric repeat s	2.40	2.58
	433331	AI738815	ESTs	1.46	2.10
	428520	AA331901	hypothetical protein FLJ10067	0.44	0.19
	439492	AF086310	ESTs	0.42	0.26
	426736	AA431615	ESTs	1.90	2.45
60	416225	AA577730	ESTs, Weakly similar to PC4259 ferritin	2.72	6.25
	404917		Target Exon	1.60	2.15
	448955	AW207597	ESTs	2.08	1.75
	402797		Target Exon	2.12	1.37
	457951	U23860	gb:Human clone mcag19 chromosome 16 CTG	1.72	2.00
65	426982	AA149707	ubiquitin-like 3	0.36	0.17

TABLE 8B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

75	Pkey	CAT Number	Accession
	408139	10421_1	AA451966 NM_016370 AB036693 AL139228 R58124 AI634847 AL119333 W07356 AI334284 H29050 AI192685 AA652438 AW172843 W19794 N21460 AI743862 AW130622 AA991348 AI204553 AA992664 NC0848 AA699329 AI824676 R26624 R49653 AW807321 AW807262 AW177104 AW807319 AW807115 AW807344 AW807324 AW178116 BE141575 AW845849 AW807105 AW845868 BE140542 AW807178 AW807167 AW807398 AW807320 AW807306 AW845866
	408255	1049351_1	

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	408283	1050275_1	BE141579 AW807555 AW807502 BE141596 AW845845 AW807500 AW845864 AW807480 AW807486 AW807478 AW178109 AW807228 AW807374 AW807125 AW846124 AW807470 AW807477 AW807510 AW807208 BE141573 AW807465
	408839	1085657_1	AW277084 R27662 R26970 D79194
5	409126	110159_1	AA063426 AW962323 AW408063 AA063503 AA772927 AW753492 BE175371 AA311147
	409282	111512_1	AW966480 AA069840 AA384646
	409291	1115745_1	AW373472 AW373484 BE071899 BE071898
	409367	1123651_1	AW382767 BE153835 BE153702 BE153572
	409688	114831_3	AI150485 AW938392 AA076894 AW883422
10	409692	114869_1	AI500724 AA399661 AA397891 AI471084 AI423511 T07531 AI094336
	409894	1157906_1	BE081731 AW861738 AW503629 BE081969
	410154	117950_1	F06959 Z43559 AA082002
	410357	1197159_1	AW663614 BE045540 BE045760 AW627443 BE046544
	410642	1213736_1	AW792784 Z44444 H06639
15	410725	1218207_1	AW799279 AW799395 AW799392 AW799276 AW799479 H57895
	410730	121847_1	AW368660 AA457091 AI903441 AA088823 W88852 AW979154 AA826016 R94779
	410744	1219485_1	H86002 W92289 AW801558 AW801324 AW801270 AW801307 AW801351 AW801357 AW801299 AW801609 AW801356 AW801420 AW801425 AW801358 AW801429 AW801428 AW801427 AW801424 AW801306
	410840	1223800_1	AW806924 AW866537 AW866473 AW866298 AW866390 AW866478 AW866454 AW866309 AW866539 AW866521 AW866547 AW866517 AW866403 AW866369
20	410956	1227882_1	AW938322 AW938307 AW938320 AW938323 AW811840
	411008	1229027_1	AW813238 AW813474 AW813334 AW816081 AW813296 AW813363 AW813397 AW813327 AW813328 AW816031 AW816140
	411026	1229373_1	AW813786
	411141	1233793_1	AW819561 AW819682 AW819563 AW819688 AW819499 AW819458 AW819690 BE065081
25	411184	1234977_1	AW821117 AW855541 AW855405 AW855374
	411188	1235093_1	BE161168 BE162466 AW821260
	411245	1236412_1	AW833441 AW833552 AW833700 AW833610 AW833673 AW833675
	411347	1239834_1	AW838126 AW838294 AW838247 AW838251 AW838292 AW838299 AW838374
	411432	1245636_1	AW846272 AW846564 AW846545 AW846285 AW846135 AW846317 AW846200 AW846265 AW846326 AW846196 AW846357 AW846153 AW846286 AW846319 AW846277 AW846381 AW846438 AW846481 AW846352
30	411496	1248073_1	AW849241 AW849569 AW849243
	411567	1249774_1	AW851630 AW851703 AW851735 AW851723 AW851708 AW851712
	411590	125064_1	T96183 T64070 AA094134
	411608	1251259_1	AW853441 BE145228 BE145218 BE145162 BE145283
35	411652	1252836_1	AW855393 AW855560 AW855424
	411880	1263110_1	AW872477 BE088101 T05990
	411918	1265807_1	AW876354 AW876179 AW876318 AW876290 AW876234 AW876125 AW876199 AW876198
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35 TABLE 8C

40	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NI_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NI_position
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	400830	8570385	Plus	157683-163035
	400834	8705192	Plus	121963-122288
	400840	9188586	Plus	113882-114121
	400850	1927150	Minus	4506-4691
50	400881	2842777	Minus	91446-91803,92123-92265
	401016	8117441	Plus	126234-126359,128050-128236
	401090	8492704	Minus	201281-201460
	401215	9858408	Plus	103739-103919
55	401241	4827300	Minus	30503-30844,31056-31248
	401335	9884881	Plus	15736-16352
	401381	8570226	Minus	118629-119146,119392-119657
	401400	7708226	Minus	33028-33585
	401469	6682292	Minus	125521-125639
60	401473	7249001	Plus	115142-117305
	401577	9280797	Minus	139377-139674,141195-141261,142217-142340
	401658	9100654	Plus	89638-90028
	401659	7689875	Minus	183379-183521
	401686	6468551	Plus	5005-5426,6810-7042
65	401723	7656694	Plus	147273-147503
	401814	7408052	Plus	136003-136726
	401818	7467933	Minus	10964-11084,11674-11817
	401890	8516144	Plus	148955-149396,149569-150002
	401908	8698760	Minus	126888-127024
	401913	9369520	Minus	33753-33904
70	401927	3873185	Minus	112000-112137
	402025	7547159	Plus	173835-173998
	402039	7770432	Plus	560-1294
	402049	8072512	Plus	100065-100419
	402085	7249154	Plus	90533-90687,94949-95158
75	402241	7690131	Minus	125073-125206,130996-131125
	402294	2282012	Minus	2575-3000
	402305	7328724	Plus	40832-41362

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	402366	9454515	Plus	195808-196863
	402551	9856793	Minus	37346-37633
	402654	8076879	Plus	44058-44803
5	402685	8318556	Plus	58962-59294
	402762	9230904	Minus	123298-124035
	402797	3421043	Minus	15758-15930
	402833	8918545	Plus	26987-27778
	402901	8894222	Minus	175426-175667
10	402948	9368458	Minus	143456-143626,143808-143935
	403066	8954202	Plus	158189-158433
	403072	8954241	Plus	141829-142006
	403146	9799812	Plus	162877-163118
	403197	9930749	Plus	79990-80237
15	403214	7630945	Minus	76723-77027,79317-79484
	403217	7630969	Plus	54089-54163,55427-55623
	403290	8083176	Plus	19288-20076
	403291	7230870	Plus	95177-95435
	403294	8096496	Plus	41565-41881
20	403315	8247953	Minus	125117-125287
	403332	8568139	Minus	31409-31674
	403344	8569726	Plus	70823-70990
	403362	8571772	Plus	64099-64260
	403371	9087278	Plus	105655-106050
25	403391	9438337	Plus	42410-42544,83317-83540,86840-86922,87970-88110
	403488	9966515	Minus	12450-12753
	403536	8076924	Plus	34972-35182
	403779	8018040	Minus	95602-95969
	403859	7708954	Plus	113738-113858
30	403871	7709262	Plus	104545-104757
	403903	7710671	Minus	101165-102597
	403917	7710849	Plus	109718-109847,109927-110202
	403978	8578014	Plus	97326-97808
	404031	7671252	Plus	171477-172316
35	404167	9926594	Minus	77030-77280
	404220	6706820	Plus	48107-48439
	404286	2326514	Plus	51086-51301
	404418	7382420	Minus	153339-153481,155099-155294
	404427	7407959	Plus	127170-127358
40	404429	7407979	Plus	31352-31498
	404440	7528051	Plus	80430-81581
	404495	8151634	Minus	59449-60477
	404580	6539738	Minus	240588-241589
	404606	9212936	Minus	22310-23269
45	404730	8389582	Plus	119832-120016,124110-124275
	404917	7341851	Plus	49330-49498
	405033	7107731	Minus	142358-142546
	405137	8570507	Plus	158969-159423
	405146	9438278	Minus	102529-102633
50	405158	9966252	Plus	42873-43056,43815-43949
	405187	7229826	Plus	117025-117170,118567-118736
	405223	7239814	Plus	106184-106313
	405340	6094635	Plus	49644-49760
	405494	8050952	Minus	70284-70518
55	405551	1552506	Plus	12525-12997
	405654	4895155	Minus	53624-53759
	405667	4726099	Plus	5798-5914
	405673	4589984	Plus	50700-50842
	405704	4204244	Plus	138842-139051
60	405723	9801668	Plus	114896-115831
	405727	9838331	Minus	78865-79664
	405760	6066938	Minus	37424-38045
	405779	7280331	Minus	33048-33856
	405944	7883702	Minus	5143-5634
65	406002	8247797	Minus	154007-154579
	406016	8272661	Plus	41341-41940
	406097	7107918	Minus	36898-37269
	406104	9124028	Plus	35309-35977
	406156	7144867	Plus	379-597
70	406207	5923650	Minus	162607-162800
	406300	6479046	Minus	19234-19401
	406308	9211532	Plus	358408-358651
	406314	9211609	Minus	12899-13011,18022-18136
	406317	9211652	Plus	108018-108410
75	406432	9256504	Plus	3904-3930,4026-4120,4929-5109
	406490	7711309	Minus	80295-80480
	406584	3983530	Minus	3989-4497

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TABLE 9A: Genes predictive of no bladder cancer progression

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1	80th percentile of Ta or T1 tumor AIs from patients who did not upstage divided by the 80th percentile of Ta or T1 tumor AIs from patients who did upstage			
10	R2	median of Ta or T1 tumor AIs from patients who did not upstage divided by the median of Ta or T1 tumor AIs from patients who upstaged			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	4.64 5.88
	412129	M21984	Hs.73454	troponin T3, skeletal, fast	4.54 5.10
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	4.37 1.63
15	400844			NM_003105*:Homo sapiens sortilin-related	3.69 5.90
	419555	AA244416		gb:nc07d11.s1 NCL_CGAP_Pr1 Homo sapiens	3.61 2.03
	414522	AW518944	Hs.76325	step II splicing factor SLU7	3.60 1.00
	440509	BE410132	Hs.134202	ESTs, Weakly similar to T17279 hypothet	3.58 1.04
	445182	AW189787		ESTs	3.57 2.70
20	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.56 1.48
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	3.28 3.25
	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	3.25 2.50
	430702	U56979	Hs.278568	H factor 1 (complement)	3.20 2.70
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.20 2.30
25	420729	AW964897	Hs.290825	ESTs	3.20 1.53
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.00 4.10
	420028	AE014680	Hs.3786	carbohydrate (N-acetylglucosamine-6-O) s	2.94 2.78
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfol	2.93 1.43
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	2.93 1.33
30	428030	AI915228	Hs.11493	Homo sapiens cDNA FLJ13536 fis, clone PL	2.92 2.47
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	2.89 3.33
	414407	AA147026	Hs.76704	ESTs	2.87 2.87
	450779	AW204145	Hs.156044	ESTs	2.78 1.86
	411243	AE039886	Hs.69319	CA11	2.73 1.00
35	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.68 2.32
	441619	NM_014056	Hs.7917	DKFZP564K247 protein	2.67 2.98
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.66 1.00
	440006	AK000517	Hs.5844	hypothetical protein FLJ20510	2.64 1.77
	426252	BE176980	Hs.28917	ESTs	2.63 7.30
40	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.60 2.53
	429429	AA829725	Hs.334437	hypothetical protein MGC4248	2.59 3.34
	427450	AE014526	Hs.178121	KIAA0626 gene product	2.57 2.28
	420180	AI004035	Hs.25191	ESTs	2.56 1.68
	434061	AW024973	Hs.283675	NPD009 protein	2.54 2.10
45	422070	AF149785	Hs.111126	pituitary tumor-transforming 1 interacti	2.54 3.25
	419355	AA428520	Hs.90061	progesterone binding protein	2.53 3.63
	446215	AW821329	Hs.14368	SH3 domain binding glutamic acid-rich pr	2.52 4.38
	432442	AI672516	Hs.178485	ESTs, Weakly similar to S65657 alpha-1C-	2.50 4.60
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	2.49 2.23
50	401155			Target Exon	2.48 2.30
	404530			Target Exon	2.48 1.00
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	2.48 2.35
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.47 2.88
	446535	AF257175	Hs.15250	peroxisomal D3,D2-enoyl-CoA isomerase	2.46 2.19
55	408636	BE294925	Hs.46680	CGI-12 protein	2.45 1.60
	420962	NM_005904	Hs.100602	MGI (mothers against decapentaplegic, Dr	2.44 3.75
	427008	Z45258	Hs.286013	short coiled-coil protein	2.42 3.40
	459711	BE386801	Hs.21858	trinucleotide repeat containing 3	2.40 2.78
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.40 1.00
60	410337	M83822	Hs.52354	cell division cycle 4-like	2.39 3.88
	435029	AF167706	Hs.19280	cysteine-rich motor neuron 1	2.39 3.23
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	2.39 1.00
	410968	AA199907	Hs.67397	homeo box A1	2.38 1.33
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.38 6.40
65	450775	AA902384	Hs.73853	bone morphogenetic protein 2	2.38 2.71
	442433	BE243044	Hs.8309	KIAA0747 protein	2.37 3.68
	454000	AA040620	Hs.5672	hypothetical protein AF140225	2.36 1.14
	447701	BE619526	Hs.255527	hypothetical protein MGC14128	2.36 2.02
	427985	AI770170	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	2.36 2.18
70	442257	AW503831	Hs.323370	Human EST clone 25257 mariner transposon	2.35 3.53
	454070	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	2.35 3.60
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	2.35 2.48
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	2.35 1.00
	407793	AW080879	Hs.236572	gb:xc38g04.x1 NCL_CGAP_Co20 Homo sapiens	2.35 1.21
75	442061	AA774284	Hs.285728	abl-interactor 12 (SH3-containing protei	2.34 3.03
	402845			ENSP0000246267:KIAA0444 PROTEIN (FRAGME	2.34 1.52
	411407	R00903	Hs.169793	ribosomal protein L32	2.34 0.77
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.34 0.72

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5	424637	NM_015057	Hs.151411	KIAA0916 protein	2.32	2.55
	413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	2.32	1.46
	411060	NM_006074	Hs.318501	Homo sapiens mRNA full length insert cDN	2.32	2.90
	430028	BE564110	Hs.227750	Target CAT	2.32	2.28
	417720	AA205625	Hs.208067	ESTs	2.32	2.09
10	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.31	1.13
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.30	4.38
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	2.30	1.86
	408179	AL042465	Hs.43445	poly(A)-specific ribonuclease (deadenyla	2.29	2.19
	442679	R53718	Hs.107882	hypothetical protein FLJ10659	2.29	2.79
15	458949	AW291777	Hs.346137	ESTs, Weakly similar to T08599 probable	2.28	1.85
	407191	AA608751		gb:ae56h07.s1 Stratagene lung carcinoma	2.27	2.42
	448367	AI955411	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	2.27	1.18
	405155			Target Exon	2.26	1.94
	445594	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	2.26	1.55
20	417458	NM_005655	Hs.82173	TGFB inducible early growth response	2.25	1.95
	430315	NM_004293	Hs.239147	guanine deaminase	2.24	1.84
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	2.24	2.73
	408937	AA210734	Hs.281386	ESTs	2.24	3.18
	431474	AL133990	Hs.180642	CEGP1 protein	2.23	1.00
25	434094	AA305599	Hs.238205	hypothetical protein PRO2013	2.22	4.08
	420997	AK001214	Hs.100914	hypothetical protein FLJ10352	2.22	2.15
	420164	AW339037	Hs.24908	ESTs	2.22	2.16
	414099	U11313	Hs.75760	sterol carrier protein 2	2.21	4.05
	424800	AL035588	Hs.153203	MyoD family inhibitor	2.21	3.53
30	459005	AA447679	Hs.144558	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.21	2.90
	416290	NM_000016	Hs.79158	acyl-Coenzyme A dehydrogenase, C-4 to C-	2.20	4.00
	439208	AK000299	Hs.180952	dynactin 4 (p62)	2.20	1.88
	401563			C15001262:gil7304961[ra]NP_038528.1[ca	2.20	1.77
	404687			C9000375*:gil11994617[dbj]BAB02754.1[A	2.19	2.60
35	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	2.19	2.08
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	2.19	2.21
	400835	AW853954		chromosome 2 open reading frame 2	2.18	3.00
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	2.18	2.45
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	2.17	1.83
40	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	2.17	2.87
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.17	1.71
	406038	Y14443		zinc finger protein 200	2.17	1.71
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.17	1.00
	441623	AA315805		desmoglein 2	2.17	1.81
45	459244	AW503990	Hs.142442	HP1-BP74	2.17	4.03
	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.17	2.93
	404204			ENSP00000252204*:Zinc finger protein 165	2.17	1.02
	453987	AA323750	Hs.235026	Homo sapiens, clone IMAGE:4247529, mRNA,	2.16	2.85
	411400	AA311919	Hs.69851	nucleolar protein family A, member 1 (H-	2.16	3.80
50	454949	AW947318	Hs.290131	KIAA1819 protein	2.16	1.96
	405223	AA312572	Hs.6241	phosphoinositide-3-kinase, regulatory su	2.16	1.48
	418030	BE207573	Hs.83321	neuromedin B	2.16	2.07
	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	2.16	2.32
	455511	AI142379		gb:qg64c01.r1 Soares_testis_NHT Homo sap	2.16	1.85
55	437559	AI678033	Hs.121476	ESTs	2.15	1.43
	418827	BE327311	Hs.47166	HT021	2.15	3.84
	417470	AF112219	Hs.82193	esterase D/formylglutathione hydrolase	2.15	1.74
	421012	X53281	Hs.101025	basic transcription factor 3	2.15	1.26
	448772	AW390822	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	2.15	4.05
60	439601	AB025032	Hs.6606	KIAA1109 protein	2.15	2.15
	434417	AL110157	Hs.3843	Homo sapiens mRNA; cDNA DKFZp586F2224 (f	2.15	1.45
	424865	AF011333	Hs.153563	lymphocyte antigen 75	2.15	2.63
	400752			NM_003105*:Homo sapiens sortilin-related	2.14	2.67
	438916	AW188464	Hs.101515	ESTs	2.14	2.38
65	430024	AI808780	Hs.227730	integrin, alpha 6	2.14	2.00
	409345	AI949109		hypothetical protein: FLJ20783	2.14	1.40
	421939	BE169531	Hs.109727	TAK1-binding protein 2; KIAA0733 protein	2.13	1.58
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.13	2.67
	419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	2.13	2.00
70	458025	AI275406	Hs.32450	gb:ql63c10.x1 Soares_NhHMPu_S1 Homo sapi	2.12	0.89
	428582	BE336659	Hs.185055	BENE protein	2.12	2.65
	422749	W01076	Hs.278573	CD59 antigen p18-20 (antigen identified	2.12	2.73
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.11	0.91
	456421	AL157485	Hs.91973	hypothetical protein	2.11	2.51
75	421508	NM_004833	Hs.105115	absent in melanoma 2	2.11	3.13
	402760			NM_021797*:Homo sapiens eosinophil chemo	2.09	1.79
	406274			Target Exon	2.09	1.60
	406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, pari	2.09	1.00
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	2.09	2.92
	445320	AA503887	Hs.167011	Homo sapiens cDNA: FLJ21362 fis, clone C	2.09	3.20
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	2.09	1.90

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	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.08	1.15
	405165			ENSP00000238974*:Homeobox protein NKX2-3	2.07	2.83
	418999	AW195747	Hs.21122	hypothetical protein FLJ11830 similar to	2.07	3.71
5	453865	AA307279	Hs.35947	methyl-CpG binding domain protein 4	2.07	1.71
	439924	AI985897	Hs.125293	ESTs	2.07	1.00
	439004	AW979062		gb:EST391172 MAGE resequences, MAGP Homo	2.07	2.13
	407955	BE536739	Hs.109909	ESTs	2.06	1.91
	412998	BE046254		gb:hn38g09.x2 NCI_CGAP_RDF2 Homo sapiens	2.06	2.58
10	414013	AA766605	Hs.47099	hypothetical protein FLJ21212	2.05	5.00
	415249	R40515	Hs.21248	ESTs	2.05	2.18
	427332	R09418	Hs.261101	ESTs, Weakly similar to I38022 hypotheti	2.05	3.35
	426521	AF161445	Hs.170219	hypothetical protein	2.05	1.00
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	2.05	6.03
	423851	R39505	Hs.133342	Homo sapiens clone 24566 mRNA sequence	2.05	1.88
15	410028	AW576454	Hs.346502	ESTs	2.04	1.95
	406575			Target Exon	2.04	1.56
	457148	AF091035	Hs.184627	KIAA0118 protein	2.04	3.11
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	2.04	2.42
20	429837	NM_003896	Hs.225939	sialyltransferase 9 (CMP-NeuAc)lactosylc	2.04	1.97
	440675	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	2.04	2.06
	411988	AA455459	Hs.164480	ESTs, Weakly similar to T50609 hypotheti	2.04	2.65
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	2.04	2.35
	446187	AK001241	Hs.14229	hypothetical protein FLJ10379	2.04	2.03
25	420838	AW118210	Hs.42321	ESTs	2.03	1.00
	445481	AW661846	Hs.346630	ESTs	2.03	2.49
	448175	BE296174	Hs.225160	hypothetical protein FLJ13102	2.03	2.25
	410600	AW575742		ESTs, Moderately similar to S65657 alpha	2.02	2.10
	401177			Target Exon	2.02	2.59
30	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	2.02	4.23
	434782	NM_005032	Hs.4114	plastin 3 (T isoform)	2.02	1.48
	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	2.02	2.93
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase kina	2.02	2.63
	424673	AA345051	Hs.294092	ESTs, Weakly similar to I38022 hypotheti	2.02	3.43
35	414721	X90392	Hs.77091	ribosomal protein L10	2.02	1.89
	429869	AI907018	Hs.15977	Target CAT	2.02	1.47
	439177	AW820275	Hs.76611	ESTs, Weakly similar to I38022 hypotheti	2.01	1.94
	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	2.01	1.64
	452046	AB018345	Hs.27657	KIAA0802 protein	2.01	4.31
40	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	2.01	6.75
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.00	2.75
	408232	AL137269	Hs.43899	Homo sapiens mRNA; cDNA DKFZp434C1714 (f	2.00	2.02
	408409	AW838181	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.00	1.95
	433256	AW604447	Hs.339408	ESTs, Weakly similar to S26689 hypotheti	2.00	0.91
45	429969	AI936504	Hs.2083	CDC-like kinase 1	2.00	3.60
	442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	2.00	1.95
	444916	AB028956	Hs.12144	KIAA1033 protein	2.00	1.23
	452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.00	5.30
	414906	AA157911	Hs.72200	ESTs	1.99	1.22
50	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	1.99	3.83
	414557	AA340111	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	1.99	2.31
	452946	AA082160	Hs.63368	ESTs, Weakly similar to TRHY_HUMAN TRICH	1.99	3.43
	408437	AW957744	Hs.278469	lactimal proline rich protein	1.98	2.15
	439205	AF087990	Hs.42758	Homo sapiens, clone IMAGE:3354845, mRNA,	1.98	2.28
	442506	BE566411		ESTs	1.98	3.95
55	447731	AA373527	Hs.19385	CGI-58 protein	1.98	2.57
	410579	AK001628	Hs.64691	KIAA0483 protein	1.97	2.43
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	1.97	2.50
	456141	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.97	3.03
60	419576	AK002060	Hs.91251	hypothetical protein FLJ11198	1.96	2.88
	407241	M34516		gb:Human omega light chain protein 14.1	1.96	1.09
	420684	AI681270	Hs.99824	BCE-1 protein	1.96	1.75
	448586	AF285120	Hs.283734	CGI-204 protein	1.96	3.28
	408089	H59799	Hs.42644	thioredoxin-like	1.95	4.00
65	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.95	2.12
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	1.95	3.45
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586C0724 (f	1.94	2.80
	434263	N34895	Hs.44648	ESTs	1.94	4.60
	409829	M33552	Hs.56729	lymphocyte-specific protein 1	1.94	1.79
70	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	1.94	2.30
	401835			Target Exon	1.94	2.27
	406557			C5000893:gl 6226859 sp P38525 EFG_THEMA	1.94	3.28
	440062	AI350518	Hs.129692	ESTs	1.94	3.18
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.94	2.70
75	457281	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.94	2.60
	420230	AL034344	Hs.284186	forkhead box C1	1.93	2.28
	452970	NM_012238	Hs.31176	sirtuin (silent mating type information	1.93	4.35
	403728			Target Exon	1.92	1.70

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5	415789	H01581	gb:33f08.r1 Soares placenta Nb2HP Homo	1.92	2.15
	406759	AA654582	Hs.77039 ATP synthase, H transporting, mitochondr	1.92	2.10
	442073	AW973443	Hs.8086 RNA (guanine-7-) methyltransferase	1.92	4.43
	438023	AF204883	Hs.6048 FEM-1 (C.elegans) homolog b	1.92	4.00
	445502	AW379160	Hs.12613 DKFZP434J214 protein	1.92	2.13
10	405474		NM_001093*:Homo sapiens acetyl-Coenzyme	1.92	2.58
	430007	NM_014892	Hs.227602 KIAA1116 protein	1.92	3.78
	439937	AF151906	Hs.6776 CGI-148 protein	1.91	2.32
	418068	AW971155	Hs.293902 ESTs, Weakly similar to ISHUS protein d	1.91	1.88
	444630	AI753230	Hs.323562 hypothetical protein DKFZp564K142	1.91	1.61
15	451184	T87943	Hs.173638 transcription factor 7-like 2 (T-cell sp	1.90	3.35
	414715	AA587891	Hs.904 amylo-1,6-glucosidase, 4-alpha-glucanotr	1.90	3.55
	445841	AL080115	Hs.13370 DKFZP564G0222 protein	1.90	1.46
	425284	AF155568	Hs.349043 NS1-associated protein 1	1.90	3.65
	437943	NM_016353	Hs.5943 rec	1.89	1.73
20	442426	AI373062	Hs.332938 hypothetical protein MGC5370	1.89	2.79
	400111		Eos Control	1.89	3.84
	437762	T78028	Hs.154679 synaptotagmin I	1.89	1.00
	404069		Target Exon	1.89	2.51
	434809	AW974687	gb:EST386776 MAGE resequences, MAGM Homo	1.88	2.35
25	414220	BE296094	Hs.323806 gb:601118231F1 NIH_MGC_17 Homo sapiens c	1.88	1.00
	422506	R20909	Hs.300741 sordin	1.87	2.99
	417439	AW602154	Hs.82143 E74-like factor 2 (els domain transcripti	1.87	1.13
	404391		Target Exon	1.87	3.00
	420187	AK001714	Hs.95744 hypothetical protein similar to ankyrin	1.86	2.93
30	446950	AA305800	Hs.5672 hypothetical protein AF140225	1.86	1.90
	400634		C10000818*:g[17651882]ref[NP_055697.1] K	1.86	2.80
	408455	C19034	Hs.288613 Homo sapiens cDNA FLJ14175 fis, clone NT	1.86	1.32
	422366	T83882	Hs.97927 ESTs	1.85	1.44
	452170	AF064801	Hs.28285 patched related protein translocated in	1.85	2.64
35	430604	AV650537	Hs.247309 succinate-CoA ligase, GDP-forming, beta	1.85	1.81
	426484	AA379658	Hs.272759 KIAA1457 protein	1.85	2.60
	411609	AW993680	gb:RC3-BN0034-290200-013-d08 BN0034 Homo	1.85	2.10
	431129	AL137751	Hs.263671 Homo sapiens mRNA; cDNA DKFZp434I0812 (f	1.84	3.70
	412843	AF007555	Hs.74624 protein tyrosine phosphatase, receptor t	1.84	2.58
40	401512		NM_014080:Homo sapiens dual oxidase-like	1.84	1.52
	415969	H11294	Hs.31047 ESTs	1.84	3.08
	444736	AA533491	Hs.23317 hypothetical protein FLJ14681	1.84	1.20
	426418	M90464	Hs.169825 collagen, type IV, alpha 5 (Alport syndr	1.84	2.35
	416968	AA412686	Hs.97955 ESTs	1.84	2.18
45	442961	BE614474	Hs.289074 F-box only protein 22	1.84	2.18
	418650	BE386750	Hs.86978 prollyl endopeptidase	1.84	1.98
	420923	AF097021	Hs.273321 differentially expressed in hematopoieti	1.84	1.00
	432834	F06459	Hs.289113 cytochrome b5 reductase 1 (B5R.1)	1.83	3.93
	442485	BE092285	Hs.29724 hypothetical protein FLJ13187	1.83	3.10
50	427699	AW965076	Hs.180378 hypothetical protein 669	1.83	3.03
	447387	AI268331	Hs.102237 lubby super-family protein	1.83	1.78
	418663	AK001100	Hs.41690 desmocollin 3	1.82	1.53
	419733	AW362955	Hs.224961 Homo sapiens cDNA FLJ14415 fis, clone HE	1.82	1.00
	409267	NM_012453	Hs.52515 transducin (beta)-like 2	1.81	1.57
55	413341	H78472	Hs.191325 ESTs, Weakly similar to T18967 hypotheti	1.81	2.05
	423810	AL132665	Hs.132955 BCL2/adenovirus E1B 19kD-interacting pro	1.81	1.98
	416274	AW160404	Hs.79126 guanine nucleotide binding protein 10	1.80	1.91
	400843		NM_003105*:Homo sapiens sortilin-related	1.80	4.88
	442187	N23532	Hs.288963 Homo sapiens cDNA: FLJ23034 fis, clone L	1.80	2.61
60	458285	AW296984	Hs.255595 ESTs, Weakly similar to A46302 PTB-assoc	1.80	2.33
	413753	U17760	Hs.75517 laminin, beta 3 (nicein (125kD), kalinin	1.80	3.17
	428004	AA445663	Hs.151393 glutamate-cysteine ligase, catalytic sub	1.80	1.00
	401613		Target Exon	1.79	2.66
	407173	T64349	gb:yc10d08.s1 Stratagene lung (937210) H	1.79	2.30
65	443145	AI049671	Hs.307763 EST, Weakly similar to I36022 hypothetic	1.79	2.00
	418596	AW976721	Hs.293327 ESTs	1.79	3.92
	437374	AL359571	Hs.44054 ninein (GSK3B interacting protein)	1.79	1.24
	439569	AW602166	Hs.222399 CEGP1 protein	1.79	2.39
	430677	Z26317	Hs.94560 desmoglein 2	1.78	2.02
70	436749	AA564890	Hs.5302 lectin, galactoside-binding, soluble, 4	1.78	0.96
	453016	AW295466	Hs.232051 ESTs, Weakly similar to dJ403A15.3 [H.sa	1.78	2.60
	426885	AA393130	Hs.193894 ESTs, Weakly similar to A47582 B-cell gr	1.78	2.47
	452848	AI417193	Hs.288912 hypothetical protein FLJ22604	1.78	2.17
	412560	R24601	CCR4-NOT transcription complex, subunit	1.78	3.13
75	411821	BE299339	Hs.72249 three-PDZ containing protein similar to	1.78	1.55
	428788	AF082283	Hs.193516 B-cell CLL/lymphoma 10	1.78	2.36
	443963	AA878183	Hs.17448 Homo sapiens cDNA FLJ13618 fis, clone PL	1.78	2.20
	435479	AF197137	Hs.259737 ATP synthase, H transporting, mitochondr	1.78	2.03
	413073	AL038165	Hs.75187 translocase of outer mitochondrial membr	1.77	2.29
	442473	W27992	gb:43d9 Human retina cDNA randomly prime	1.77	2.93
	418060	AA211589	Hs.208047 ESTs	1.77	4.19

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	400773		NM_003105*:Homo sapiens sortilin-related	1.77	1.76	
	400175		Eos Control	1.77	2.04	
	421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	1.77	2.32
5	451234	AI914901	Hs.24052	ESTs, Weakly similar to I38022 hypotheti	1.77	2.43
	423332	AI091466	Hs.127241	sorting nexin 7	1.76	1.82
	423960	AA164516	Hs.136309	SH3-containing protein SH3GLB1	1.76	2.00
	450489	AI697990	Hs.346002	ESTs	1.76	3.15
	457265	AB023212	Hs.225967	KIAA0995 protein	1.76	2.37
10	413076	U10564	Hs.75188	wee1 (S. pombe) homolog	1.75	2.18
	421948	L42583	Hs.334309	keratin 6A	1.75	1.00
	453578	R06875	Hs.81810	ESTs	1.75	3.10
	412430	AW675064	Hs.73875	fumarylacetoacetate hydrolase (fumarylac	1.75	2.14
	439396	BE562958	Hs.74346	hypothetical protein MGC14353	1.75	1.78
15	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	1.75	2.36
	449538	AI559444	Hs.104679	ESTs	1.75	3.07
	453146	AI338952	Hs.32194	ESTs	1.74	2.82
	426122	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5	1.74	2.88
	408989	AW361666	Hs.49500	KIAA0746 protein	1.74	2.07
20	441715	AI929453	Hs.342655	Homo sapiens cDNA FLJ13289 fis, clone OV	1.74	2.06
	412718	X79204	Hs.74520	spinocerebellar ataxia 1 (olivopontocere	1.74	2.46
	450798	AW167780	Hs.50438	ESTs	1.74	2.02
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.73	2.58
	400190			Eos Control	1.73	2.40
25	416309	R84694	Hs.79194	cAMP responsive element binding protein	1.73	1.48
	410219	T98226	Hs.171952	occludin	1.73	2.75
	419814	AW402478	Hs.93213	BCL2-antagonist/killer 1	1.73	2.70
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	1.73	2.07
	422387	AA309996	Hs.148656	ESTs, Weakly similar to T12453 hypotheti	1.73	2.02
30	417386	AL037228	Hs.82043	D123 gene product	1.73	2.44
	405812			Target Exon	1.72	2.94
	436270	C03769	Hs.339669	Homo sapiens, clone IMAGE:3947554, mRNA,	1.72	2.85
	409855	AW502461		gb:U1-HF-BR0p-ajv-b-08-0-U1.r1 NIH_MGC_5	1.72	2.63
	411442	N25956	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	1.72	1.88
35	400846			sortilin-related receptor, L(DLR class)	1.72	1.63
	401660			Target Exon	1.72	2.63
	402190			C19000835*.gij10946730[ref NP_067362.1]	1.72	3.33
	439191	AA281177	Hs.41182	Homo sapiens DC47 mRNA, complete cds	1.71	2.17
	410444	W73484	Hs.132554	gb:zd54e04.s1 Soares_fetal_heart_NbHH19W	1.71	2.70
40	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.71	1.33
	446066	AI343931	Hs.149383	ESTs	1.71	2.32
	411299	BE409857	Hs.69499	hypothetical protein	1.71	2.92
	408246	N55669	Hs.333823	mitochondrial ribosomal protein L13	1.71	2.00
	454054	AI336329	Hs.301519	Homo sapiens cDNA FLJ12536 fis, clone NT	1.71	1.93
45	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	1.70	3.70
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	1.70	1.60
	400750			Target Exon	1.70	2.82
	455842	BE145837		gb:MR0-HT0208-101299-202-c07 HT0208 Homo	1.70	2.17
50	429966	BE081342	Hs.283037	HS-PC039 protein	1.70	1.18
	418444	AI902899	Hs.85155	butyrate response factor 1 (EGF-response	1.70	2.47
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	1.70	3.03
	415738	BE539367	Hs.295953	ESTs, Weakly similar to AF220049 1 uncha	1.70	2.34
	405245			Target Exon	1.70	1.99
	408483	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypotheti	1.70	2.05
55	413611	BE153275		gb:PMO-HT0335-180400-008-e11 HT0335 Homo	1.70	2.05
	410190	AW072328	Hs.59728	Homo sapiens mRNA; cDNA DKFZp566C0546 (f	1.69	2.20
	434608	AA805443	Hs.179909	hypothetical protein FLJ22995	1.69	2.36
	432170	T56887	Hs.18282	KIAA1134 protein	1.69	1.83
	448182	AF244137	Hs.20597	host cell factor homolog	1.69	2.11
60	436293	AI601188	Hs.120910	ESTs	1.69	2.37
	448524	AB032948	Hs.21356	hypothetical protein DKFZp762K2015	1.68	2.48
	404231			Target Exon	1.68	2.50
	453906	AW444952	Hs.257054	ESTs	1.68	2.45
	437967	BE277414	Hs.5947	met transforming oncogene (derived from	1.68	1.00
65	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.68	3.51
	448813	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	1.68	1.69
	429162	AK001250	Hs.197642	hypothetical protein FLJ10388	1.68	3.13
	425555	H27225	Hs.9444	hypothetical protein FLJ13114	1.67	2.02
	405630			Target Exon	1.67	3.00
70	421405	AA251944	Hs.104058	CGI-29 protein	1.67	3.25
	422540	M37984	Hs.118845	tropoin C, slow	1.67	1.23
	450857	AA629075	Hs.190090	ESTs	1.67	2.48
	451668	Z43948	Hs.326444	cartilage acidic protein 1	1.66	2.55
	433821	AW182416		ESTs	1.66	2.65
75	405595			NM_000721*:Homo sapiens calcium channel,	1.66	2.23
	433892	AI929357	Hs.323966	Homo sapiens clone H63 unknown mRNA	1.66	1.97
	443558	AA376798	Hs.286122	MDS024 protein	1.66	2.00
	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	1.66	2.65

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	424685	W21223	Hs.151734	nuclear transport factor 2 (placental pr	1.66	2.88
	400845			NM_003105*:Homo sapiens sortilin-related	1.66	1.61
	447816	NM_007233	Hs.274329	TP53 target gene 1	1.66	2.63
5	404438			Target Exon	1.66	2.34
	451543	AA397651	Hs.301959	proline synthetase co-transcribed (bacte	1.65	2.08
	433233	AB040927	Hs.301804	KIAA1494 protein	1.65	3.13
	420938	AL049698	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	1.65	1.37
	435438	H84421	Hs.4890	ubiquitin-conjugating enzyme E2E 3 (homo	1.65	2.35
10	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.65	1.00
	433235	AB040929	Hs.35089	contactin 3 (plasmacytoma associated)	1.65	1.44
	439632	AW410714	Hs.334437	hypothetical protein MGC4248	1.65	2.35
	409324	W76202	Hs.343812	lipoic acid synthetase	1.65	2.00
	452207	NM_014517	Hs.28423	upstream binding protein 1 (LBP-1a)	1.65	2.33
15	423630	AB011132	Hs.129952	KIAA0560 gene product	1.65	2.13
	443358	H65417	Hs.17757	pleckstrin homology domain-containing, f	1.65	1.63
	427417	AA341061	Hs.177861	CGI-110 protein	1.64	1.28
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	1.64	1.60
	445677	H96577	Hs.6838	ras homolog gene family, member E	1.64	1.91
20	447503	AA115496	Hs.336898	Homo sapiens, Similar to RIKEN cDNA 1810	1.64	2.04
	431234	AL389585	Hs.301637	zinc finger protein 258	1.64	1.53
	418032	AW964695	Hs.9436	Homo sapiens, clone MGC:15763, mRNA, com	1.64	2.05
	407796	AA195509	Hs.39733	postsynaptic protein CRIFT	1.64	2.30
	446298	AF187813	Hs.14637	kidney- and liver-specific gene	1.64	2.05
25	439578	AW263124	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	1.64	2.26
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	1.64	2.10
	433646	AA603319	Hs.155195	ESTs	1.64	2.05
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	1.64	1.00
	419982	AA252544	Hs.55610	solute carrier family 30 (zinc transport	1.64	2.16
30	401603			NM_022041*:Homo sapiens giant axonal neu	1.64	2.73
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	1.64	2.75
	400788			C6000994*:gij10435784 dbj BAB14668.1 (A	1.63	2.04
	416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	1.63	2.64
	422491	AA338548	Hs.117546	neuronatin	1.63	0.96
35	424737	BE301883	Hs.152707	glioblastoma amplified sequence	1.63	3.45
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	1.63	1.39
	403988			C5001831:gil11056014 ref NP_067651.1 ac	1.62	2.11
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	1.62	2.63
	407874	AI766311	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE	1.62	2.19
40	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	1.62	3.03
	438184	AA779897	Hs.122125	ESTs	1.62	2.79
	405052			C7000609*:gil1062012 pir A53933 myosin I	1.62	2.55
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	1.62	2.48
	457961	AA772119	Hs.270721	ESTs, Weakly similar to I38022 hypotheti	1.62	2.30
45	436774	AW975810	Hs.159054	hypothetical protein FLJ13224	1.62	2.17
	414893	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	1.62	2.03
	458660	AI299739	Hs.99601	hypothetical protein FLJ12553	1.62	2.25
	405806			Target Exon	1.62	2.15
	421205	AL137540	Hs.102541	netrin 4	1.62	1.00
50	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	1.62	1.74
	427016	AA397525	Hs.191579	ESTs	1.61	2.16
	459182	AI147996	Hs.155833	ESTs, Weakly similar to spliceosomal pro	1.61	2.74
	455109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	1.61	2.59
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.61	1.78
55	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208655 1 BM-01	1.61	2.10
	447532	AK000614	Hs.18791	hypothetical protein FLJ20507	1.61	1.75
	439944	AA856767	Hs.124623	ESTs	1.61	2.41
	414692	H06831	Hs.154557	ESTs, Moderately similar to ALUC_HUMAN 1	1.60	3.05
	433187	R53995	Hs.293381	ESTs, Moderately similar to ALU7_HUMAN A	1.60	2.63
60	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	1.60	2.43
	441166	AA921738	Hs.132473	ESTs	1.60	2.69
	425571	AJ007292	Hs.158306	ephrin-A2	1.60	1.49
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	1.60	1.08
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	1.60	1.47
65	449268	AW369278	Hs.23412	hypothetical protein FLJ20160	1.60	2.89
	400772			NM_003105*:Homo sapiens sortilin-related	1.60	2.57
	445733	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	1.60	2.03
	428172	U09367	Hs.182828	zinc finger protein 136 (clone pHZ-20)	1.60	2.68
	421887	AW161450	Hs.109201	CGI-86 protein	1.59	1.39
70	418127	BE243982	Hs.83532	membrane cofactor protein (CD46, trophob	1.59	1.67
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	1.59	2.19
	434938	AW500718	Hs.8115	Homo sapiens, clone MGC:16169, mRNA, com	1.59	2.26
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	1.59	1.76
	418067	AI127958	Hs.83393	cystatin E/M	1.59	1.26
75	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	1.59	2.25
	451938	AI354355	Hs.16697	down-regulator of transcription 1, TBP-b	1.59	2.10
	407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	1.58	2.43
	410796	Z44547	Hs.3731	ESTs, Moderately similar to I38022 hypot	1.58	1.26

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	417343	AA197132	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	1.58	2.84
	416643	U62531	Hs.79410	solute carrier family 4, anion exchanger	1.58	1.26
	400847			NM_003105*Homo sapiens sortilin-related	1.58	1.48
5	436760	AW606927	Hs.5306	hypothetical protein DKFZp586F1122 simil	1.57	1.57
	433427	A1816449	Hs.171889	cholinephosphotransferase 1	1.57	1.64
	461986	BE246996	Hs.318401	hypothetical protein DKFZp584D1378	1.57	1.83
	428901	A1929568	Hs.146668	KIAA1263 protein	1.57	2.23
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	1.57	3.07
10	444604	AW327695	Hs.11441	chromosome 1 open reading frame 8	1.57	1.86
	439686	W40445	Hs.235857	ESTs, Weakly similar to I38022 hypotheti	1.57	3.07
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	1.57	2.01
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	1.57	2.83
	418942	A1566004	Hs.141269	Homo sapiens cDNA: FLJ21550 fis, clone C	1.57	1.21
15	418555	A1417215	Hs.87159	hypothetical protein FLJ12577	1.56	3.08
	402368			NM_021155*Homo sapiens CD209 antigen (C	1.55	2.05
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	1.56	2.08
	404977			Insulin-like growth factor 2 (somatomedi	1.56	5.50
	418772	BE567100	Hs.154938	hypothetical protein MDC5	1.56	2.30
20	415503	U36601	Hs.78473	N-deacetylase/N-sulfotransferase (hepara	1.56	2.56
	451743	AW074266	Hs.23071	ESTs	1.56	1.85
	423184	NM_004428	Hs.1624	ephrin-A1	1.56	1.41
	408041	AW138782	Hs.243607	ESTs	1.56	2.21
	416777	AF145760	Hs.79844	DKFZP564M1416 protein	1.56	2.00
25	428013	AF151020	Hs.181444	hypothetical protein	1.56	1.53
	410072	BE384447	Hs.16034	hypothetical protein MGC13186	1.55	1.52
	411495	AP000693	Hs.70369	KIAA0136 protein	1.55	2.88
	408162	AA993833	Hs.118527	ESTs	1.55	2.70
	413350	U02556	Hs.75307	t-complex-associated-testis-expressed 1-	1.55	1.99
30	422010	AA302049	Hs.31181	Homo sapiens cDNA: FLJ23230 fis, clone C	1.55	1.60
	426229	AU076961	Hs.155212	methylmalonyl Coenzyme A mutase	1.55	2.57
	425184	BE278288	Hs.155048	Lutheran blood group (Auerberg b antigen	1.55	1.45
	419011	H56244	Hs.39552	glutathione S-transferase A2	1.55	2.77
	417538	AW050865	Hs.275711	hypothetical protein MGC2452	1.55	2.76
35	409806	AW500960		gb:U1-HF-BP0p-aiy-b-01-0-U1.r1 NIH_MGC_5	1.55	2.45
	402737			Target Exon	1.54	2.58
	419825	A1754011	Hs.7326	ESTs	1.54	1.00
	410001	AB041036	Hs.57771	kallikrein 11	1.54	0.62
	407813	AL120247	Hs.40109	KIAA0872 protein	1.54	2.33
40	415906	A1751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.54	2.77
	427886	AA417083	Hs.104789	ESTs	1.54	2.60
	437018	AA889078	Hs.187033	ESTs	1.54	2.48
	415049	N67334	Hs.50158	ESTs	1.54	2.57
	422315	U16296	Hs.115176	T-cell lymphoma invasion and metastasis	1.54	2.57
45	413715	AW351121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	1.54	1.98
	447144	A1630759	Hs.17481	Homo sapiens clone 24606 mRNA sequence	1.54	2.48
	438924	BE535511		transmembrane trafficking protein	1.53	3.08
	445166	A1656116	Hs.147451	ESTs	1.53	2.08
	414073	AF068293	Hs.75737	pericentriolar material 1	1.53	1.70
50	402378			Target Exon	1.53	2.83
	452316	AA298484	Hs.51265	ESTs, Moderately similar to G786_HUMAN P	1.53	1.60
	450374	AA397540	Hs.50293	Homo sapiens clone 122482 unknown mRNA	1.53	3.59
	402617			C100355.1:gi 6678593 ref NP_033547.1 win	1.53	2.75
	406837	R70292	Hs.156110	immunoglobulin kappa constant	1.53	1.01
55	410573	AF151057	Hs.54595	aminoacidipate-semialdehyde dehydrogenase-	1.53	1.23
	426359	AA376409	Hs.10862	Homo sapiens cDNA: FLJ23313 fis, clone H	1.53	0.67
	434445	A1349306	Hs.11782	ESTs	1.53	2.80
	452717	AW160399	Hs.30376	hypothetical protein	1.53	2.01
	420465	AL080276	Hs.70488	similar to prokaryotic-type class 1 pept	1.53	2.25
60	437404	AA868974	Hs.180992	ESTs	1.53	2.00
	459192	AW176180		gb:RC2-BT0214-010999-001-E07 BT0214 Homo	1.52	3.20
	446457	A1300580	Hs.345281	ESTs, Moderately similar to ALU1_HUMAN A	1.52	2.35
	441466	AW573081	Hs.54828	ESTs	1.52	1.99
	421810	AK001718	Hs.108530	hypothetical protein FLJ10856	1.52	2.98
65	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	1.52	2.47
	414882	D79594	Hs.77546	Homo sapiens cDNA: FLJ21983 fis, clone H	1.52	2.55
	442169	W21813	Hs.8125	Homo sapiens mRNA: cDNA DKFZp586E1521 (f	1.52	1.31
	404349			Target Exon	1.52	2.74
	416278	AA366366	Hs.79137	protein-L-isoaspartate (D-aspartate) O-m	1.52	2.93
70	431846	BE019924	Hs.271580	uropod 1B	1.52	1.01
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.52	0.93
	442670	BE410050	Hs.11859	hypothetical protein FLJ13168	1.52	2.70
	441617	AA581863	Hs.178485	Homo sapiens cDNA FLJ13919 fis, clone Y7	1.52	1.65
	440079	A1557284	Hs.6900	ring finger protein 13	1.52	1.76
75	432831	A1821702	Hs.115959	ESTs, Weakly similar to I38022 hypotheti	1.52	2.13
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	1.52	2.13
	442149	AB014650	Hs.8118	KIAA0550 protein	1.52	1.00
	457747	AW975000		gb:EST387105 MAGE resequences, MAGN Homo	1.51	2.38

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5	419433	AA814807	Hs.7395	hypothetical protein FLJ23182	1.51	2.50
	431812	AA515902	Hs.130650	ESTs	1.51	1.64
	415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	1.51	2.62
	447590	A1953360	Hs.133487	ESTs	1.51	2.02
	416925	H03109	Hs.108920	HT018 protein	1.51	2.22
10	442755	W57656	Hs.109701	ubiquitin-like 5	1.51	1.34
	448594	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	1.51	2.24
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	1.51	1.49
	404397			ENSP00000251675: KIAA1550 protein (Fragm	1.51	2.18
	412927	AA284018	Hs.75063	human immunodeficiency virus type I enha	1.51	1.33
15	402371			Target Exon	1.51	3.22
	431730	AF208856	Hs.268122	hypothetical protein	1.51	1.57
	417715	AW69587	Hs.86366	ESTs	1.51	1.59
	451117	AA015752	Hs.205173	ESTs	1.50	2.70
	434727	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,	1.50	3.53
20	442297	NM_005202	Hs.89901	phosphodiesterase 4A, cAMP-specific (dun	1.50	2.24
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFp434K0322 (f	1.50	1.13
	452558	N88604	Hs.30212	thyroid receptor interacting protein 15	1.50	1.62
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	1.50	1.00
	438957	H30340	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H	1.50	1.05
25	419847	AW390601	Hs.184544	Homo sapiens, clone IMAGE:3355383, mRNA,	1.50	2.53
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (1.49	0.97
	433265	AB040971	Hs.35096	KIAA1538 protein	1.49	1.44
	408136	AL041135	Hs.42959	KIAA1012 protein	1.49	2.24
	455485	AA102287	Hs.25756	hypothetical protein FLJ20896	1.49	2.40
30	418863	AL135743	Hs.25566	ESTs, Weakly similar to 2004399A chromos	1.49	2.84
	405193			C7000789:gi1943947 gb AAC48716.1 (U901	1.48	2.20
	408948	AW296713	Hs.221441	ESTs	1.48	2.20
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	1.48	2.24
	405932			C15000305:gi13806122 gb AAC39198.1 (AF0	1.48	1.48
35	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.48	1.16
	422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	1.48	1.20
	428044	AA093322	Hs.301404	RNA binding motif protein 3	1.48	2.38
	416166	AW501907	Hs.261734	Homo sapiens cDNA: FLJ22807 fis, clone K	1.48	1.28
	430453	BE387060	Hs.3903	Cdc42 effector protein 4; binder of Rho	1.48	2.73
40	401600	BE247275		U5 snRNP-specific protein, 116 kD	1.48	2.53
	432638	AI017717		chromosome 21 open reading frame 15	1.48	2.03
	405194			C7000789:gi1943947 gb AAC48716.1 (U901	1.48	2.00
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.48	1.25
	450272	AI075170	Hs.20010	ESTs	1.48	2.35
45	413709	BE168687		gb:CM0-HT0395-280100-169-b09 HT0395 Homo	1.48	2.08
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	1.48	1.00
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.47	1.91
	436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	1.47	2.26
	404769			NM_007037*:Homo sapiens a disintegrin-li	1.47	1.24
50	420132	BE079847	Hs.301914	gb:RC6-BT0627-220300-012-D06 BT0627 Homo	1.47	2.00
	448356	AL120637	Hs.20993	high-glucose-regulated protein 8	1.47	2.90
	421628	AL121317	Hs.106210	hypothetical protein FLJ10813	1.47	4.08
	449059	AK000566	Hs.98135	hypothetical protein FLJ20559	1.47	3.13
	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.47	1.06
55	422119	AI277829	Hs.111862	KIAA0590 gene product	1.47	1.51
	438713	H16902		ESTs	1.47	2.39
	418248	NM_005000	Hs.83916	NM_005000*:Homo sapiens NADH dehydrogena	1.47	1.00
	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.46	2.20
	420548	AA278246	Hs.920	ESTs	1.46	2.13
60	424258	AA433848	Hs.107882	hypothetical protein FLJ10659	1.46	1.98
	414683	S78296	Hs.76888	hypothetical protein MGC12702	1.46	1.45
	427045	H86504	Hs.173328	protein phosphatase 2, regulatory subuni	1.46	2.31
	446646	BE552004	Hs.26192	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.46	1.30
	427257	AI026805	Hs.97726	ESTs	1.46	2.48
65	422971	AI879223	Hs.145409	RAB, member of RAS oncogene family-like	1.46	1.05
	451334	AI122691	Hs.13268	ESTs	1.46	2.12
	403326			C2000428*:gi17705383 ref NP_057536.1 GC	1.46	2.40
	453827	AF201948	Hs.35660	BUP protein	1.46	1.65
	423599	AI805664	Hs.31731	peroxiredoxin 5	1.46	1.56
70	410691	AW239226	Hs.65450	reticulon 4	1.46	1.49
	430688	AL022101	Hs.104991	hypothetical protein similar to preferen	1.46	2.45
	438083	AI949940	Hs.121924	ESTs	1.46	2.00
	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	1.45	1.60
	437325	AF142481	Hs.5548	f-box and leucine-rich repeat protein 5	1.45	1.26
75	403342			Target Exon	1.45	2.21
	438808	M73980	Hs.129053	Homo sapiens NOTCH 1 (N1) mRNA, complete	1.45	2.40
	446493	AK001389	Hs.15144	hypothetical protein DKFZp564O043	1.45	3.65
	414895	AW694856	Hs.116278	Homo sapiens cDNA FLJ13571 fis, clone PL	1.44	2.71
	442072	AI740832	Hs.12311	Homo sapiens clone 23570 mRNA sequence	1.44	1.08
	425723	NM_014420	Hs.159311	clckkopf (Xenopus laevis) homolog 4	1.44	2.24
	432901	AI554929	Hs.281866	ATPase, H transporting, lysosomal (vacuo	1.44	1.63

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5	412210	AW901492		gb:RC0-NN1012-270300-031-h10 NN1012 Homo	1.44	2.15
	421685	AF185723	Hs.105778	ATPase, Ca transporting, type 2C, member	1.44	1.83
	428115	AB023154	Hs.300355	KIAA0977 protein	1.44	1.31
	442358	BE567985	Hs.18585	ESTs, Moderately similar to ALU4_HUMAN A	1.44	2.47
	414665	L39874	Hs.76894	dCMP deaminase	1.44	1.25
10	413798	AA336708	Hs.75546	capping protein (actin filament) muscle	1.44	1.26
	410937	AA218564	Hs.67052	vacuolar protein sorting 26 (yeast homol	1.44	1.41
	400397	AJ270770		transcription factor 7-like 2 (T-cell sp	1.44	3.43
	405902			Target Exon	1.44	2.65
	433976	AA620987	Hs.190268	ESTs	1.44	2.46
15	405376			Target Exon	1.44	2.28
	436086	Z43133	Hs.9951	Homo sapiens cDNA: FLJ21954 fis, clone H	1.44	1.34
	418182	AW016405	Hs.16548	ESTs	1.44	2.35
	430307	BE513442	Hs.238944	hypothetical protein FLJ10631	1.43	1.55
	434924	AA443164	Hs.23259	hypothetical protein FLJ13433	1.43	2.05
20	417821	BE245149	Hs.82543	protein tyrosine kinase 9	1.43	2.15
	404744			Target Exon	1.43	1.99
	405418			Target Exon	1.43	2.83
	402869			Target Exon	1.43	2.40
	451608	AA384525	Hs.26745	hypothetical protein	1.43	1.22
25	424059	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1.43	2.45
	401041			C11000425:gij4507721[ref]NP_003310.1[i	1.43	2.90
	417839	A1815732	Hs.82712	fragile X mental retardation, autosomal	1.43	2.84
	405245	AA361037	Hs.288036	tRNA isopentenylpyrophosphate transferas	1.43	2.65
	447808	NM_007265	Hs.19673	suppressor of S. cerevisiae gcr2	1.43	2.00
30	456492	AA330047	Hs.191187	ESTs	1.43	2.73
	449244	AW859979	Hs.32204	ESTs	1.42	1.57
	413094	H24184	Hs.25413	TOLLIP protein	1.42	1.33
	452407	AA682909	Hs.29353	brain-specific protein p25 alpha	1.42	2.50
	407674	AW064061	Hs.279145	ESTs	1.42	2.35
35	441297	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	1.42	2.20
	421932	W51778	Hs.323949	kangei 1 (suppression of tumorigenicity	1.42	1.48
	426348	BE466586	Hs.17433	hypothetical protein FLJ20967	1.42	1.83
	432554	A1479813	Hs.278411	NCK-associated protein 1	1.42	2.46
	431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	1.42	1.30
40	425953	NM_004376	Hs.226581	COX15 (yeast) homolog, cytochrome c oxid	1.42	1.50
	444037	AV647686	Hs.42733	CHMP1.5 protein	1.42	1.38
	402144			Target Exon	1.42	2.38
	456758	AA325170	Hs.224627	ESTs, Weakly similar to FAHUA alpha-acl	1.42	2.23
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	1.42	2.18
45	426663	AL137657	Hs.172803	hypothetical protein MGC10327	1.41	1.38
	410684	AA088500	Hs.170298	ESTs	1.41	1.28
	401784			NM_002280*:Homo sapiens keratin, hair, a	1.41	1.37
	427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	1.41	1.32
	449269	A1564682	Hs.175870	ESTs	1.41	1.37
50	406467			Target Exon	1.41	1.80
	444339	T96555	Hs.31562	ESTs	1.41	2.94
	431663	A1027643	Hs.120912	ESTs	1.41	1.41
	413343	BE392026	Hs.334346	hypothetical protein MGC13045	1.41	1.21
	447537	AW295072	Hs.346408	ESTs, Weakly similar to AF193556 1 sacsi	1.41	2.07
55	428211	AA424211	Hs.183176	ESTs	1.41	1.25
	406248			Target Exon	1.41	2.40
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.41	1.39
	414653	M24486	Hs.76768	procollagen-proline, 2-oxoglutarate 4-di	1.41	1.33
	403885			Target Exon	1.41	2.58
60	439459	AF086279	Hs.58013	ESTs	1.41	2.08
	419075	T84266	Hs.123927	ESTs	1.41	2.84
	405022			Target Exon	1.40	2.55
	401346	BE041451		hypothetical protein	1.40	2.38
	415660	A1909007	Hs.78563	ubiquitin-conjugating enzyme E2G 1 (homo	1.40	2.38
65	448023	A1693299	Hs.170388	ESTs	1.40	2.38
	435962	AA702820	Hs.291294	ESTs	1.40	2.10
	432480	AA205475	Hs.275865	ribosomal protein S18	1.40	1.37
	414309	AK000639	Hs.75884	DKFZF586A011 protein	1.40	1.18
	440256	U25641	Hs.18851	hypothetical protein FLJ10875	1.40	1.91
70	413809	L25851	Hs.851	integrin, alpha E (antigen CD103, human	1.40	2.80
	408176	AK001553	Hs.43436	adenylate kinase 3 alpha like	1.40	2.73
	433960	AW629188	Hs.188929	ESTs	1.40	1.99
	404178			C5001430*:gij4503521[ref]NP_001559.1[mu	1.40	2.83
	402449			Target Exon	1.40	1.51
75	455604	BE011183		gb:PM3-BN0218-100500-003-d09 BN0218 Homo	1.40	2.30
	429221	A1821060	Hs.198271	Target CAT	1.40	1.22
	422122	AA383642	Hs.111894	lysosomal-associated protein transmembra	1.40	1.42
	406231			Target Exon	1.40	2.60
	405879			Target Exon	1.40	2.73
	450936	A1033745		gb:ow23a10.x1 Soares_parathyroid_tumor_N	1.40	1.13
	403381			ENSPC0000231844*:Ecotropic virus Integra	1.39	6.03

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5	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	1.39	3.20
	448261	BE244072	Hs.20815	macrophage erythroblast attach	1.39	1.33
	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	1.39	2.30
	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.39	1.53
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.39	1.34
10	430138	AA936296	Hs.234265	DKFZP586G011 protein	1.39	2.38
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	1.39	2.88
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	1.39	1.34
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.39	1.61
	450092	AW139606	Hs.221057	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.39	2.78
15	400275			NM_008513*:Homo sapiens seryl-tRNA synth	1.39	2.03
	403725			Target Exon	1.39	2.03
	443211	AI128388	Hs.143655	ESTs	1.39	1.83
	421510	AK000919	Hs.105191	hypothetical protein: FLJ10057	1.39	2.83
	430071	AA355986	Hs.232068	transcription factor 8 (represses interl	1.38	3.54
20	451545	AI802128	Hs.208647	ESTs	1.38	2.21
	439897	NM_015310	Hs.6763	KIAA0942 protein	1.38	3.65
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	1.38	1.00
	410344	AW978436	Hs.62515	KIAA0494 gene product	1.38	2.25
	404439			ENSP00000067222*:Mitochondrial 28S ribos	1.38	2.25
25	448581	NM_002709	Hs.21537	protein phosphatase 1, catalytic subunit	1.38	1.47
	408569	BE086047	Hs.86412	chromosome 9 open reading frame 5	1.38	1.27
	447643	H10767	Hs.238465	nGAP-like protein	1.38	1.22
	401593			Target Exon	1.38	2.58
	405807			NM_031889:Homo sapiens enamelin (ENAM),	1.38	2.38
30	406356	N47812		CGI-35 protein	1.38	2.25
	401886			NM_021783:Homo sapiens XEDAR (XEDAR), mR	1.38	2.00
	421110	AJ250717	Hs.1355	cathepsin E	1.38	8.93
	427449	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAIL	1.38	1.44
	427451	AI690916	Hs.178137	transducer of ERBB2, 1	1.38	2.81
35	440681	AW449656	Hs.166547	ESTs	1.38	2.95
	419590	AF005043	Hs.91390	poly (ADP-ribose) glycohydrolase	1.38	2.10
	446044	H67567	Hs.13572	calcium modulating ligand	1.37	2.62
	400967			Target Exon	1.37	3.12
	414506	AF075337	Hs.76293	thymosin, beta 10	1.37	1.18
40	402599			NM_021186*:Homo sapiens zona pellucida g	1.37	2.68
	422932	AI191813	Hs.308220	ESTs	1.37	2.38
	433889	AK002082	Hs.3623	hypothetical protein FLJ11220	1.37	2.23
	429802	H09548	Hs.5367	ESTs, Weakly similar to I38022 hypotheti	1.37	2.25
	443856	AK000574	Hs.9908	nitrogen fixation cluster-like	1.37	1.28
45	453489	AA300067	Hs.33032	hypothetical protein DKFZp434N185	1.37	2.15
	424670	W61215	Hs.116651	epithelial V-like antigen 1	1.37	1.66
	428995	AW004975	Hs.194716	MAD (mothers against decapentaplegic, Dr	1.37	1.33
	441551	AA318224	Hs.296141	ESTs	1.37	2.95
	450528	NM_014072	Hs.25063	PRO0461 protein	1.37	1.19
50	427605	NM_000997	Hs.337445	ribosomal protein L37	1.37	1.31
	459237	AA031675	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	1.37	2.50
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	1.37	1.31
	404906			NM_025213:Homo sapiens spectrin, beta, n	1.36	3.08
	436246	AW450963	Hs.119991	ESTs	1.36	1.00
55	441478	AA360018	Hs.301342	hypothetical protein MGC4342	1.36	1.43
	419715	AF070523	Hs.92384	vitamin A responsive; cytoskeleton relat	1.36	1.28
	426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	1.36	2.16
	400129			Eos Control	1.36	2.03
	450447	AF212223	Hs.25010	hypothetical protein P15-2	1.36	2.13
60	434697	AL133033	Hs.4084	KIAA1025 protein	1.36	2.01
	430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	1.36	2.03
	434767	AF153201		C2H2 (Kruppel-type) zinc finger protein	1.36	2.87
	459729	AL037285	Hs.289848	EST, Weakly similar to ALU4_HUMAN ALU SU	1.36	1.27
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.35	2.20
65	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	1.35	2.68
	409844	AW502336		gb:U1-HF-BR0p-aka-b-05-0-U1.r1 NIH_MGC_5	1.35	2.29
	402517			Target Exon	1.35	2.10
	447042	AB035863	Hs.182217	succinate-CoA ligase, ADP-forming, beta	1.35	1.25
	405000			Target Exon	1.35	2.32
70	452065	AK000360	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	1.35	2.36
	404866			C9000748:gi 8324209 gb AAE34384.2 (S775	1.35	2.55
	451081	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	1.35	1.70
	427979	BE379776	Hs.181309	proteasome (prosome, macropain) subunit,	1.35	2.23
	435825	R16702	Hs.91147	ESTs	1.35	2.39
75	426469	BE297886	Hs.293970	methylmalonate-semialdehyde dehydrogenas	1.35	1.40
	447002	BE242866	Hs.16933	HepA-related protein	1.34	2.88
	410946	AW811502		gb:QV2-ST0145-061299-015-b04 ST0145 Homo	1.34	2.02
	454383	AW500332	Hs.11114	hypothetical protein dJ1181N3.1	1.34	2.13
	440512	AA887845	Hs.19573	suppressor of S. cerevisiae gcr2	1.34	2.05
	409865	AW502208		gb:U1-HF-BR0p-aju-e-09-0-U1.r1 NIH_MGC_5	1.34	2.63
	447390	X95384	Hs.18426	translational inhibitor protein p14.5	1.34	1.00

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	450293	N36754	Hs.171118	hypothetical protein FLJ00025	1.34	2.45
	445831	NM_006055	Hs.13351	LanC (bacterial lantibiotic synthetase c	1.34	1.60
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	1.34	1.39
5	441946	AW298716	Hs.120775	ESTs	1.34	2.30
	446192	H49944	Hs.14231	selenoprotein W, 1	1.34	1.17
	415285	BE537973	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	1.34	2.22
	425590	AI954686	Hs.158321	beaded filament structural protein 2, ph	1.34	2.50
	407498	U28131		gb:Human HMGI-C chimeric transcript mRNA	1.34	2.13
10	441331	AI216764	Hs.149971	ESTs, Moderately similar to ALUB_HUMAN I	1.34	2.05
	411789	AF245505	Hs.72157	Adlican	1.34	1.27
	420542	NM_000505	Hs.1321	coagulation factor XII (Hageman factor)	1.33	1.25
	413892	AI878921	Hs.75607	myristoylated alanine-rich protein kinas	1.33	1.41
	439750	AL359053	Hs.57654	Homo sapiens mRNA full length insert cDN	1.33	1.99
15	414861	AL119396	Hs.77508	glutamate dehydrogenase 1	1.33	1.66
	421687	AL035306	Hs.106823	hypothetical protein MGC14797	1.33	2.18
	410846	AW807057		gb:MR4-ST0062-031199-018-b03 ST0062 Homo	1.33	2.07
	443937	R86571	Hs.24601	ESTs	1.33	2.02
	432360	BE045243	Hs.274416	Target CAT	1.33	1.12
20	443119	AA312264	Hs.7980	hypothetical protein MGC12966	1.33	2.68
	438464	AA689735	Hs.324743	protein phosphatase 4 regulatory subunit	1.33	1.99
	401371			ENSP00000198192:BA436F9.1 (novel protei	1.33	1.10
	405443			Target Exon	1.33	2.11
	453764	BE008180	Hs.282846	Homo sapiens cDNA FLJ14353 fis, clone Y7	1.33	2.88
25	424924	AL039103	Hs.153834	pumilio (Drosophila) homolog 1	1.33	1.24
	453555	N23574	Hs.123649	ESTs, Moderately similar to ALU7_HUMAN A	1.33	2.23
	404343			C7002191:g 5053028 gb AAD38811.1 AF155	1.33	1.04
	412383	AW947577		gb:RC0-MT0004-140300-031-b09 MT0004 Homo	1.33	2.06
	404250			Target Exon	1.33	2.53
30	413899	AF083892	Hs.75608	tight junction protein 2 (zona occludens	1.33	2.81
	422716	AI702835	Hs.124475	ESTs, Weakly similar to YEF4_YEAST HYPOT	1.33	2.30
	448862	AI351979	Hs.152717	hypothetical protein FLJ13725	1.33	1.08
	409540	AW409569		gb:fn01e09.x1 NIH_MGC_17 Homo sapiens cD	1.33	2.18
	431186	NM_012249	Hs.250697	ras-like protein	1.32	1.39
35	402754			NM_022469*:Homo sapiens hypothetical pro	1.32	1.16
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	1.32	2.02
	459710	AI701596	Hs.121592	ESTs	1.32	2.70
	435192	AK000739	Hs.4835	eukaryotic translation initiation factor	1.32	2.22
	401383			Target Exon	1.32	2.18
40	453394	AW960474	Hs.40289	ESTs	1.32	2.20
	421820	AW662990	Hs.294133	heme-binding protein	1.32	1.24
	444047	AI097452	Hs.135095	ESTs	1.32	2.95
	440860	R10482	Hs.132876	ESTs	1.32	2.83
	425808	AA364109	Hs.177990	ESTs	1.32	2.11
45	456558	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	1.32	2.05
	447015	AB033029	Hs.16953	KIAA1203 protein	1.32	1.30
	414015	AA340987	Hs.75693	prolylcarboxypeptidase (angiotensinase C	1.32	1.39
	414843	BE385038	Hs.77492	heterogeneous nuclear ribonucleoprotein	1.32	1.26
	424058	AL121516	Hs.138617	thyroid hormone receptor interactor 12	1.32	2.01
50	401196			Target Exon	1.32	2.13
	450147	AW373713	Hs.146324	CGI-145 protein	1.32	1.32
	422599	BE410590	Hs.119257	ems1 sequence (mammary tumor and squamou	1.32	1.33
	405172			Target Exon	1.32	2.11
	434087	AF116875	Hs.334476	hypothetical protein PRO1942	1.32	2.30
55	416720	H05435	Hs.11110	hypothetical protein MGC2508	1.32	2.18
	426621	NM_001329	Hs.171391	C-terminal binding protein 2	1.32	1.53
	442685	AB033017	Hs.8594	KIAA1191 protein	1.32	1.43
	443879	Z28462	Hs.9927	Homo sapiens mRNA; cDNA DKFZp564D156 (fr	1.31	2.24
	405180	NM_002649		phosphoinositide-3-kinase, catalytic, ga	1.31	1.36
60	417365	D50683	Hs.82028	transforming growth factor, beta recepto	1.31	0.98
	402087			Target Exon	1.31	1.31
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	1.31	2.05
	409935	AW511413	Hs.278025	ESTs	1.31	1.20
	430235	BE268048	Hs.236494	RAB10, member RAS oncogene family	1.31	1.31
65	400172			Eos Control	1.31	1.05
	421742	AW970004	Hs.107528	androgen induced protein	1.31	1.79
	404273			Target Exon	1.31	2.35
	416204	AW972270	Hs.144054	ESTs	1.31	2.15
	435076	AW298113	Hs.92909	SON DNA binding protein	1.31	2.05
70	452497	AA732153	Hs.27865	Homo sapiens cDNA: FLJ21333 fis, clone C	1.30	1.57
	404596			Target Exon	1.30	2.23
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	1.30	1.15
	427195	W27230	Hs.173912	eukaryotic translation initiation factor	1.30	1.34
	438129	AA778547		gb:af87d03.s1 Soares_testis_NHT Homo sap	1.30	2.55
75	402138			Target Exon	1.30	2.09
	404029			NM_018936*:Homo sapiens protocadherin be	1.30	2.83
	402731	AL042818		E3 ubiquitin ligase SMURF1	1.30	3.32
	458766	AW183618	Hs.55610	solute carrier family 30 (zinc transport	1.30	1.56

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5	434585	AW451715	Hs.184075	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.30	2.73
	417219	AW973473	Hs.220936	ESTs	1.30	2.45
	423125	AA393071	Hs.182579	leucine aminopeptidase	1.30	2.00
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.30	1.00
	444681	AJ243837	Hs.288316	chromosome 6 open reading frame 9	1.30	0.94
10	408621	X57809	Hs.181125	immunoglobulin lambda locus	1.29	1.02
	436663	AW410458	Hs.5258	chromosome 11 open reading frame 2	1.29	1.20
	417250	N58241	Hs.332115	ESTs	1.29	3.43
	434978	AA321238	Hs.4310	eukaryotic translation initiation factor	1.29	1.91
	448079	R76981		thyroid hormone receptor-associated prot	1.29	2.01
15	450626	AW190989	Hs.1508	insulin-degrading enzyme	1.29	2.09
	456059	BE543127	Hs.336948	Homo sapiens, clone IMAGE:3530891, mRNA,	1.29	2.23
	417809	H75797	Hs.233550	zinc finger protein 208	1.29	2.20
	454771	AW819939	Hs.273629	ESTs	1.29	2.10
	413895	BE178160		gb:RC3-HT0600-060400-022-h10 HT0600 Homo	1.29	2.08
20	404649			Target Exon	1.29	1.32
	440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like doma	1.29	2.08
	405891			Target Exon	1.29	2.00
	418965	A1002238	Hs.11482	splicing factor, arginine/serine-rich 11	1.29	2.41
	412824	AW558075	Hs.11261	small proline-rich protein 2A	1.29	1.27
25	420037	BE299598	Hs.135569	hypothetical protein FLJ14708	1.29	1.23
	459221	BE246522	Hs.306121	leukocyte receptor cluster (LRC) encoded	1.28	2.48
	458651	AW612481	Hs.104105	ESTs	1.28	2.35
	422984	W28614		chorionic somatomammotropin hormone 1 (p	1.28	1.37
	459365	BE067754		gb:MR4-BT0358-140400-006-g10 BT0358 Homo	1.28	1.06
30	418254	AA732511	Hs.86650	ESTs	1.28	2.38
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.28	1.99
	448456	A1521830	Hs.171050	ESTs	1.28	2.18
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.28	1.68
	405053			Target Exon	1.28	3.23
35	423915	A1041278	Hs.87908	Snf2-related CBP activator protein	1.28	4.25
	443721	AW450451	Hs.266355	ESTs	1.28	1.15
	452047	N35953	Hs.43510	ESTs, Weakly similar to BOX B BINDING FA	1.28	2.30
	440213	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	1.28	1.19
	452900	AAG26794		prothymosin, alpha (gene sequence 28)	1.28	1.27
40	418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalyti	1.28	2.76
	458911	AA373131	Hs.24322	ATPase, H transporting, lysosomal (vacuo	1.28	1.21
	444250	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	1.28	2.43
	431631	AA548906	Hs.122244	ESTs	1.27	1.51
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	1.27	3.08
45	430316	NM_000875	Hs.239176	insulin-like growth factor 1 receptor	1.27	1.37
	416272	AA178882		gb:zp38b09.r1 Stratagene muscle 937209 H	1.27	2.00
	437456	AL047045	Hs.60293	Homo sapiens clone 122482 unknown mRNA	1.27	3.18
	456327	H58741	Hs.38774	ESTs	1.27	2.35
	403349	NM_001406		ephrin-B3	1.27	2.28
50	428821	H91282	Hs.286232	Homo sapiens cDNA: FLJ23190 fis, clone L	1.27	2.13
	454555	AW807095		gb:MR4-ST0062-040100-024-e02 ST0062 Homo	1.27	2.05
	406372	A1760903		gb:w09h08.x1 NCL_CGAP_CLL1 Homo sapiens	1.27	1.44
	4001720			NM_014587:Homo sapiens SRY (sex determi	1.27	2.07
	400082			Eos Control	1.27	1.26
55	420183	W92885	Hs.143408	ESTs	1.27	2.24
	411579	AC005258	Hs.70830	U5 snRNA-associated Sm-like protein LSM7	1.27	1.17
	402191			NM_021733:Homo sapiens testis-specific	1.27	2.44
	457118	A1245525	Hs.182469	Homo sapiens mRNA; cDNA DKFZp564K1972 (f	1.27	2.17
	408576	NM_003542	Hs.46423	H4 histone family, member G	1.27	2.78
60	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	1.27	3.15
	414909	R80316	Hs.132569	PP2135 protein	1.27	1.37
	416114	A1695549	Hs.183868	glucuronidase, beta	1.26	2.48
	455476	AW948172		gb:RCO-MT0013-280300-021-b06 MT0013 Homo	1.26	2.18
	445926	AF054284	Hs.334826	splicing factor 3b, subunit 1, 155kD	1.26	1.35
65	432647	A1807481	Hs.278581	fibroblast growth factor receptor 2 (bac	1.26	1.16
	405436			Target Exon	1.26	2.38
	406140			Target Exon	1.26	3.20
	426201	AW182614	Hs.128499	ESTs	1.26	1.17
	433334	A1927208	Hs.231958	matrix metalloproteinase 28	1.26	2.30
70	423262	NM_005479	Hs.126057	frequently rearranged in advanced T-cell	1.26	2.61
	422929	AA356694	Hs.94011	ESTs, Weakly similar to MGB4_HUMAN MELAN	1.26	2.11
	445605	A1906088	Hs.87159	hypothetical protein FLJ12577	1.26	3.11
	425050	BE391854	Hs.7970	gb:601285394F1 NIH_MGC_44 Homo sapiens c	1.25	2.18
	420539	AA282735	Hs.44004	AD031 protein	1.25	2.03
75	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	1.25	1.19
	456535	AA305079	Hs.1342	cytochrome c oxidase subunit Vb	1.25	1.18
	434202	BE382411	Hs.3764	guanylate kinase 1	1.25	1.14
	439528	BE613180	Hs.288368	Homo sapiens cDNA: FLJ21314 fis, clone C	1.25	2.12
	400178			Eos Control	1.25	2.15
	430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	1.25	1.20
	412841	A1751157	Hs.101395	hypothetical protein MGC11352	1.25	1.39

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5	425655	BE614551	Hs.738	ribosomal protein L14	1.25	1.22
	449536	AI656808	Hs.281328	ESTs, Weakly similar to T00378 KIAA0641	1.25	3.00
	418406	X73501	Hs.84905	cyokeratin 20	1.24	2.11
	414570	Y00285	Hs.75473	insulin-like growth factor 2 receptor	1.24	1.14
	436967	AA761729	Hs.135705	ESTs	1.24	2.53
10	457216	AA452554	Hs.283697	ESTs, Weakly similar to A41796 neural re	1.24	2.18
	418414	J04977	Hs.84981	X-ray repair complementing defective rep	1.24	1.35
	423217	NM_000094	Hs.1540	collagen, type VII, alpha 1 (epidermolys	1.24	0.92
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	1.24	2.71
	402329			NM_006505*:Homo sapiens poliovirus recep	1.24	1.13
15	447525	AF151031	Hs.300631	hypothetical protein	1.24	1.07
	445939	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	1.24	2.23
	421936	AB040884	Hs.109694	KIAA1451 protein	1.24	2.15
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.24	2.15
	426717	N90977	Hs.49690	Homo sapiens mRNA; cDNA DKFZp434D2328 (f	1.24	2.14
20	404751	T70445		ribosomal protein L9	1.24	1.30
	411456	AW847588		gb L3-CT0213-161299-038-G09 CT0213 Homo	1.24	2.35
	425417	AF058948	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	1.24	2.88
	434508	AI648601	Hs.118012	ESTs	1.24	2.03
	428284	AA635762	Hs.183435	NM_004545:Homo sapiens NADH dehydrogenas	1.24	1.59
25	418597	AK001678	Hs.86337	similar to DNA-directed RNA polymerase I	1.24	2.27
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	1.24	1.53
	449210	AI635363	Hs.345517	ESTs	1.24	2.18
	439551	W72062	Hs.11112	ESTs	1.24	2.13
	426244	AI064808	Hs.168289	succinate dehydrogenase complex, subunit	1.23	1.06
30	453635	BE148082	Hs.24724	MFH-amplified sequences with leucine-ric	1.23	1.34
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	1.23	2.27
	434943	AI929819	Hs.92909	chromosome Z1 open reading frame 50	1.23	2.10
	417010	NM_006225	Hs.80776	phospholipase C, delta 1	1.23	1.21
	426508	W23184	Hs.170171	glutamate-ammonia ligase (glutamine synt	1.23	1.37
35	434055	AF168712	Hs.3726	x 003 protein	1.23	1.58
	438363	AI886351	Hs.22353	hypothetical protein FLJ21952	1.23	2.44
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	1.23	2.28
	407018	U45869		NM_018955:Homo sapiens ubiquitin B (UBB)	1.23	1.44
	444981	AW856398	Hs.12210	hypothetical protein FLJ13732 similar to	1.23	1.19
40	440112	AA099014	Hs.231029	Homo sapiens, clone MGC:15961, mRNA, com	1.22	2.07
	426672	AW270555	Hs.171774	hypothetical protein	1.22	1.16
	404956			C1003210*:gi 6912582 ref NP_036524.1 pe	1.22	2.18
	435088	NM_000481	Hs.102	aminomethyltransferase (glycine cleavage	1.22	1.08
	438588	AW274454	Hs.6318	peroxisomal short-chain alcohol dehydrog	1.22	1.02
45	434454	AF217793	Hs.3850	LIS1-interacting protein NUDEL; endoolig	1.22	1.27
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	1.22	2.52
	428755	D87454	Hs.192966	KIAA0265 protein	1.22	1.16
	420685	AA279362		gb zs84d04.r1 NCI_CGAP_GCB1 Homo sapiens	1.22	2.75
	458991	AI743502		gb w63h12.x2 Soares_NFL_T_GBC_S1 Homo s	1.22	2.39
50	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	1.22	1.00
	434023	AI277863	Hs.146141	ESTs	1.22	2.12
	430801	AI580935	Hs.105698	ESTs	1.22	2.53
	414880	AW247305	Hs.119140	eukaryotic translation initiation factor	1.21	1.16
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	1.21	1.04
55	404790			C12001707*:gi 7305215 ref NP_038599.1 k	1.21	2.05
	403943			C5000355:gi 4503225 ref NP_000765.1 cyt	1.21	2.05
	400201			NM_006156*:Homo sapiens neural precursor	1.21	1.35
	421005	AW293089	Hs.33263	ESTs	1.21	2.02
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.21	1.11
60	400789			C11001367*:gi 1076205 pir J50754 hypoth	1.21	1.06
	412853	M34175	Hs.74626	adaptor-related protein complex 2, beta	1.21	1.24
	449709	BE410592	Hs.23918	hypothetical protein PP5395	1.20	1.27
	413726	AJ278465	Hs.75510	annexin A11	1.20	1.14
	428485	NM_002950	Hs.2280	ribophorin I	1.20	1.24
65	405163			C5000561*:gi 7513700 pir T14151 Inv pro	1.20	1.11
	415887	NM_003375	Hs.78902	voltage-dependent anion channel 2	1.20	1.16
	434468	N29309	Hs.39288	ESTs	1.20	3.20
	446843	AW135925	Hs.98798	hypothetical protein MGC11332	1.20	2.25
	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1.20	2.18
70	448242	R60646	Hs.20768	HSPC189 protein	1.20	1.22
	415753	U52819	Hs.78781	vascular endothelial growth factor B	1.20	1.05
	442156	AI690566	Hs.29403	hypothetical protein FLJ22060	1.20	1.18
	408824	L80005	Hs.48375	small nuclear ribonucleoprotein polypept	1.20	1.45
	430012	NM_015373	Hs.227637	chromosome 22 open reading frame 2	1.20	1.03
75	413392	AW021404	Hs.13021	ESTs	1.20	2.07
	401286			Target Exon	1.20	2.08
	415665	AI097276	Hs.274430	surfeit 6	1.20	2.53
	456562	AA306049	Hs.102669	DKFZP434O125 protein	1.20	2.40
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	1.20	3.45
	427818	AW511222	Hs.193765	ESTs	1.19	2.99
	406404			NM_002162*:Homo sapiens intercellular ad	1.19	1.17

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	400124		Eos Control	1.19	2.12
	416023	AA173029	gb:zp05e01.r1 Stralagene ovarian cancer	1.19	2.45
	427751	AF000152	conserved gene amplified in osteosarcoma	1.19	1.07
5	401204		ENSP00000252232*:Sterol regulatory elem	1.19	2.40
	446771	AA128965	TATA box binding protein (TBP)-associate	1.19	2.03
	429673	AA884407	protein tyrosine phosphatase, non-recept	1.18	2.36
	400130		Eos Control	1.18	2.58
	405365		CX001212*:gi7861932[gb]AAF70445.1 (AF2	1.18	2.38
10	406181		Target Exon	1.18	2.18
	422559	AW247696	hypothetical protein MGC12934	1.18	2.13
	409524	AW402151	tumor necrosis factor (ligand) superfam	1.18	1.07
	438446	AW137476	Homo sapiens cDNA FLJ13884 fis, clone TH	1.18	2.11
	447980	AI703397	ESTs	1.18	2.02
15	425503	W92517	actin binding LIM protein 1	1.18	1.29
	411469	T09997	cysteine-rich protein 2	1.18	0.99
	409162	H25530	solute carrier family 22 (organic cation	1.17	1.04
	429986	AF092047	sine oculis homeobox (Drosophila) homolo	1.17	1.00
	420869	X58964	regulatory factor X, 1 (influences HLA c	1.17	2.58
20	425943	H46986	ESTs	1.17	2.25
	415376	R35960	Homo sapiens, Similar to hypothetical pr	1.17	2.13
	420588	AF000982	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.17	2.38
	457205	AI905780	Target CAT	1.17	1.11
	407970	AW403814	BCL2-associated athanogene	1.16	3.60
25	440214	AA247118	hypothetical protein FLJ11305	1.16	2.15
	405646		C12000200:gi4557225[ref]NP_000005.1 al	1.16	1.11
	438438	AA257992	Janus kinase 1 (a protein tyrosine kinas	1.16	1.08
	431427	AK000401	Homo sapiens cDNA FLJ20394 fis, clone KA	1.16	2.08
	419885	AA251561	ESTs	1.16	2.07
30	427679	AA973904	ESTs, Moderately similar to MYPH_HUMAN M	1.16	2.15
	443885	AW296385	hypothetical protein FLJ12610	1.15	2.05
	415511	AI732617	ESTs	1.15	3.44
	417988	AA210878	ESTs, Moderately similar to ALU1_HUMAN A	1.15	2.09
	405058		Target Exon	1.15	1.16
35	446623	AF279865	kinesin family member 13B	1.15	1.21
	419754	H52299	Homo sapiens mRNA; cDNA DKFZp586i0523 (f	1.15	1.15
	420003	AA256906	ESTs, Weakly similar to ubiquitous TPR m	1.15	2.06
	422988	AW673847	ESTs	1.15	1.00
	426371	M63967	aldehyde dehydrogenase 1 family, member	1.15	2.31
40	422895	NM_015958	CGI-30 protein	1.15	2.08
	426295	AW367283	zinc finger protein 6 (CMPX1)	1.15	2.13
	448323	AI492298	ESTs	1.14	2.54
	414244	AA287801	ESTs, Moderately similar to Z195_HUMAN Z	1.14	2.23
	442872	AI471987	ESTs	1.14	2.09
45	425318	AU076845	BCL2/adenovirus E1B 19kD-interacting pro	1.14	2.33
	415667	F11582	developmentally regulated GTP-binding pr	1.14	1.10
	401058		Target Exon	1.14	2.20
	409838	AW502928	gb:U1-HF-3P0p-aiw-e-10-0-UI.r1 NIH_MGC_5	1.14	2.15
	438493	AI130740	phosphoinositide-3-kinase, regulatory su	1.14	1.00
50	404392		C7001460:gi12667420[gb]AAK01436.1 AF332	1.14	2.82
	433220	AI076192	ESTs	1.14	2.78
	405166		Target Exon	1.14	2.23
	401038		C11000425:gi14507721[ref]NP_003310.1 ti	1.14	2.71
	414052	AW578849	ESTs, Weakly similar to unnamed protein	1.14	2.08
55	442043	BE567620	ESTs	1.13	2.17
	419727	AW160796	DKFZP564O243 protein	1.13	1.14
	425206	NM_002153	hydroxysteroid (17-beta) dehydrogenase 2	1.13	2.07
	414682	AL021154	inhibitor of DNA binding 3, dominant neg	1.13	1.47
	402712		C1003562*:gi10047177[dbj]BAB13382.1 (A	1.13	1.18
60	452289	BE568205	mitogen-activated protein kinase kinase	1.12	2.16
	401496		Target Exon	1.12	1.10
	459249	AI970399	ESTs	1.12	2.67
	447495	AW401864	programmed cell death 8 (apoptosis-induc	1.12	2.03
	428422	AI557280	capping protein (actin filament) muscle	1.11	2.60
65	421762	AA297546	gb:EST113074 Fetal brain III Homo sapien	1.11	2.15
	405855		Target Exon	1.11	1.98
	428972	AK001470	cysteine desulfurase	1.11	2.19
	406761	AI241715	ATP synthase, H transporting, mitochondr	1.10	3.33
	432425	AF070619	Homo sapiens clone 24481 mRNA sequence	1.10	2.30
70	446241	AI004677	chromosome 14 open reading frame 4	1.10	2.28
	424454	AB011139	optic atrophy 1 (autosomal dominant)	1.10	2.18
	418242	AW976183	BTB and CNC homology 1, basic leucine zi	1.10	2.07
	437407	AI479332	ESTs	1.10	2.09
	447459	AI380255	ESTs	1.10	2.22
75	426682	AV660038	UDP glycosyltransferase 1 family, polype	1.09	2.33
	403655		NM_003071:Homo sapiens SWI/SNF related,	1.09	2.25
	433156	R59206	Homo sapiens cDNA: FLJ22539 fis, clone H	1.09	2.70
	403826		Target Exon	1.09	1.10

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	433333	AI016521	Hs.71816	v-akt murine thymoma viral oncogene homo	1.09	1.06
	451382	H86180	Hs.221513	ESTs	1.08	2.75
	454717	AW815123		gb:QV4-ST0212-261199-045-b01 ST0212 Homo	1.08	1.98
5	422743	BE304678	Hs.119598	ribosomal protein L3	1.08	1.00
	411672	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.08	1.00
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	1.08	2.45
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.08	2.15
	447703	AI420277		gb:tf06c12.x1 NCI_OGAP_Pr28 Homo sapiens	1.08	2.05
10	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	1.07	2.03
	455234	R41084		gb:Hk763-f Adult heart, Clontech Homo sa	1.07	2.08
	413945	NM_000591	Hs.75627	CD14 antigen	1.07	0.91
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	1.07	1.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.07	1.11
15	455630	AV655701	Hs.75183	cytochrome P450, subfamily 11E (ethanol-	1.06	2.14
	455424	AW937733		gb:QV3-DT0045-210100-063-d06 DT0045 Homo	1.05	2.03
	438324	AI792660	Hs.6162	KIAA0771 protein	1.05	2.27
	421604	AW293880	Hs.248367	MEGF11 protein	1.05	2.00
	422614	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	1.04	2.33
20	404058			Target Exon	1.04	2.10
	453085	AW954243		KIAA0251 protein	1.04	2.18
	417500	H59970		gb:yr16f04.r1 Soares fetal liver spleen	1.04	2.40
	408653	AW410189	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	1.04	2.73
	440439	N92818	Hs.64754	ESTs, Weakly similar to potential CDS [H	1.04	2.05
25	409209	AA460160	Hs.73217	ESTs	1.04	2.73
	456107	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosyl	1.03	2.18
	415403	F07923	Hs.26744	ESTs	1.02	2.43
	455591	BE008018		gb:QV0-BN0147-290400-214-c01 BN0147 Homo	1.02	2.08
30	428491	AF091035	Hs.184627	KIAA0118 protein	1.02	2.81
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	1.02	2.11
	434540	NM_016045	Hs.3945	CGI-107 protein	1.02	2.78
	442174	AI690080	Hs.128907	ESTs, Weakly similar to ARIX homeodomain	1.02	2.05
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	1.02	1.00
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	1.02	2.25
35	454412	AW582568		gb:RC1-ST0278-080100-011-h04 ST0278 Homo	1.00	2.20
	428955	AA393669	Hs.238094	ESTs	1.00	2.18
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	1.00	2.10
	405710			CX000682:gi12741327[ref][XP_008833.2] zi	1.00	2.00
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1.00	1.00
40	402001			Target Exon	1.00	1.00
	402812			NM_004930*:Homo sapiens capping protein	1.00	1.00
	402892			Target Exon	1.00	1.00
	403329			Target Exon	1.00	1.00
	407202	N58172	Hs.109370	ESTs	1.00	1.00
45	408684	R61377	Hs.12727	hypothetical protein FLJ21610	1.00	1.00
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	1.00	1.00
	413573	AI733659	Hs.149089	ESTs	1.00	1.00
	414343	AL036166	Hs.323378	coated vesicle membrane protein	1.00	1.00
	414422	AA147224	Hs.249195	Homeo box A13	1.00	1.00
50	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	1.00	1.00
	421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	1.00	1.00
	423349	AF010258	Hs.127428	homeo box A9	1.00	1.00
	424273	W40460	Hs.144442	phospholipase A2, group X	1.00	1.00
	424649	BE242035	Hs.151461	embryonic ectoderm development	1.00	1.00
55	426827	AW067805	Hs.172665	methylene tetrahydrofolate dehydrogenase	1.00	1.00
	427308	D26067	Hs.174905	KIAA0033 protein	1.00	1.00
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	1.00	1.00
	430261	AA305127	Hs.237225	hypothetical protein HT023	1.00	1.00
	431078	U82827	Hs.249195	homeo box A13	1.00	1.00
60	433222	AW514472	Hs.238415	clckkopf (Xenopus laevis) homolog 4	1.00	1.00
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	1.00
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	1.00
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	1.00	1.00
	443564	AI921685	Hs.199713	ESTs	1.00	1.00
65	444542	AI161293	Hs.280380	aminopeptidase	1.00	1.00
	445413	AA151342	Hs.12677	CGI-147 protein	1.00	1.00
	446706	AW291095	Hs.21814	interleukin 20 receptor, alpha	1.00	1.00
	448807	AI571940	Hs.7549	ESTs	1.00	1.00
	449448	D60730	Hs.57471	ESTs	1.00	1.00
70	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	1.00	1.00
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	1.00
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	1.00	1.00
	452039	AI922988	Hs.172510	ESTs	1.00	1.00
	452795	AW392555	Hs.18978	hypothetical protein FLJ21620	1.00	1.00
75	453096	AW294631	Hs.11325	ESTs	1.00	1.00
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1.00	1.00
	453966	BE146734	Hs.63325	transmembrane protease, serine 4	1.00	1.00
	405580			Target Exon	1.00	1.00

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5	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	1.00	1.00
	450377	AB033091	Hs.74313	KIAA1265 protein	1.00	1.00
	433226	AW503733	Hs.9414	KIAA1486 protein	1.00	1.00
	412719	AW018610	Hs.816	ESTs	1.00	1.00
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	1.00	1.00
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.00	1.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	1.00	1.00
	439817	AI023799	Hs.163242	ESTs	1.00	1.00
10	455474	AW948094		gb:RC0-MT0012-290300-031-c10 MT0012 Homo	0.99	2.00
	420148	U34227	Hs.95361	myosin VIIA (Usher syndrome 1B (autosoma	0.99	2.33
	428466	AF151063	Hs.184456	hypothetical protein	0.98	2.20
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12976 fis, clone NT	0.98	3.09
	444654	AV650572	Hs.23440	KIAA1105 protein	0.98	2.00
15	409759	N40285	Hs.81182	histamine N-methyltransferase	0.97	2.20
	401936			Target Exon	0.97	2.39
	403463			Target Exon	0.96	2.58
	434421	AI915927	Hs.34771	ESTs	0.96	2.15
	412636	NM_004415		desmoplakin (DPI, DPII)	0.95	2.01
20	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	0.93	2.55
	421938	AA405951		gb:zu66c01.r1 Soares_testis_NHT Homo sap	0.93	3.10
	447470	BE618324	Hs.263561	ESTs, Weakly similar to A53531 oncofetal	0.92	2.08
	448369	AW268962	Hs.111335	ESTs	0.91	2.35
	421710	AE007930	Hs.107089	KIAA0461 protein	0.91	2.63
25	406605	AI686003	Hs.296031	ESTs	0.91	2.21
	447475	AI380797	Hs.158992	ESTs	0.90	3.25
	426892	U82828	Hs.194382	ataxia telangiectasia mutated (includes	0.90	2.02
	450222	U75308	Hs.24644	TATA box binding protein (TBP)-associate	0.89	2.73
	401572			C15001384*:g 12737057 ref XP_012129.1	0.88	2.00
30	429226	AA913330	Hs.53542	choreoacanthocytosis gene; KIAA0986 prot	0.88	2.37
	421979	AW062518	Hs.233150	hypothetical protein MGC5560	0.87	3.70
	407614	NM_001932	Hs.37144	membrane protein, palmitoylated 3 (MAGUK	0.86	2.02
	417912	R25269	Hs.50547	ESTs	0.86	2.00
	401654			NM_007242:Homo sapiens DEAD/H (Asp-Glu-A	0.86	2.11
35	403149			NM_001450:Homo sapiens four and a half L	0.86	2.19
	413000	BE046280		gb:hn43c09.x2 NCL_CGAP_RDF2 Homo sapiens	0.85	2.40
	425166	AK001456	Hs.154919	KIAA0625 protein	0.85	2.18
	447371	AA334274	Hs.18368	DKFZP564B0769 protein	0.84	2.13
	452601	AI935587	Hs.34447	ESTs	0.84	2.55
40	400957			Target Exon	0.83	2.15
	426420	BE383808	Hs.322430	NDRG family, member 4	0.83	2.14
	429354	AA451666	Hs.269363	ESTs	0.80	2.25
	417831	H16423	Hs.82685	CD47 antigen (Rb-related antigen, integr	0.78	2.43
	443368	BE568891	Hs.199210	ESTs, Moderately similar to bK116F5.2 [H	0.78	2.00
45	441901	AI914445	Hs.126103	ESTs	0.76	2.06
	429462	AI890356	Hs.127804	Homo sapiens, clone IMAGE:3536432, mRNA,	0.76	2.03
	403010			C21000152:g 6226483 sp Q52118 YMO3_ERWS	0.75	2.43
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	0.75	2.42
	448332	AW293110	Hs.171068	ESTs	0.74	2.00
50	421674	T10707	Hs.296355	hypothetical protein FLJ23138	0.71	2.18
	450645	AL117441	Hs.301997	hypothetical protein FLJ13033	0.67	2.06
	448514	AE020526	Hs.301866	KIAA0819 protein	0.67	2.03
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.60	2.54
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmbl	0.60	2.00
55	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	0.57	2.15
	408077	AL133574	Hs.42458	Homo sapiens mRNA; cDNA DKFZp586C1817 (f	0.53	2.29

TABLE 9B

60 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

65	Pkey	CAT Number	Accession
	409345	112147_1	AI949109 AW118631 AI833146 AW117691 R45932 R80970 AA733110 AW269428 T27024 R97693 AI149202 AI475492 H98845 AA609655 AI125598 AW663742 AI140029 AW103164 AA126682 N66829 W65398 H94509 W65300 R07712 R36955 AA812477 AA609576 AI754304 Z41075 AA970004 AW274661 AA923584 AI673108 AA070706 AA541812 T09038
	409540	1138613_1	AW409569 BE297044 BE295828
70	409806	1155259_1	AW500960 AW501280 AW500814
	409838	1155987_1	AW502928 AW505608 AW501576 AW501577
	409844	1156139_1	AW502336 AW502339 AW501736 AW501839
	409855	1156256_1	AW502461 AW503000 AW502207 AW501862
	409865	1156518_1	AW502208 AW502366 AW502148
75	410600	121108_1	AW575742 BE549623 AI335824 BE463447 AA729043 AW408712 AW499616 AA086179 AW499617 AA191322
	410846	1223902_1	AW807057 AW807054 AW807189 AW807193 AW807369 AW807429 AW807364 AW807365 AW807078 AW807256 AW807160 AW807331
	410946	1227589_1	AW811502 AW811521 AW811548 AW811471 AW811511 AW811508
	411456	1246706_1	AW647588 AW847716 AW847664 AW847592

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5	411609	1251530_1	AW993680 AW853769
	412210	1283615_1	AW901492 AW947725 AW901448
	412383	1292509_1	AW847577 AW947574 AW947576 AW947734 AW947733 AW947732
	412560	130601_1	R24601 R23657 AA194467 AI948584 AI678666 AA194383 AI765219 AA702993 AA813511 AA620965 AI990303 AI624882 AI003925
			AI338870 AI004669 AI004690 AI127228 Z25302 F29302 BE044308 F32992 AA112966 T30825 F24958 F18071 C00537 T30841 R24502
10			AI934786 AI770075 AI144132 AA812597 AW203978 H82735 AI813349 AI142908 C04694 AI208243 AI203044 N89963 AI767866 AI290470
			AI665963 H63611 BE463806 AI082639 AA507760
	412636	13165_1	NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789
			AW361413 AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561
			BE143155 AW890965 BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211
15			BE082576 BE082584 BE004047 AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933
			AI905935 AW747877 AW748114 BE148516 AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175
			AW365157 AW365154 AW068840 BE005272 AW365145 BE001925 BE182166 BE144243 BE001923 AI951786 AI434518 BE184920
			BE184933 AI284090 BE184941 AW804674 BE184924 C04715 W39488 AW995615 BE184948 BE159646 AW606653 AA099891 AA131128
			AA337270 AA340777 AW384371 AA852212 R58704 AW366566 AW364859 AA025851 AA025852 AA455100 AA719958 AW352220
20			AW998245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090
			AA056401 H91011 AW368529 AW390272 C18467 AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654
			AW177786 BE092134 BE092137 BE092136 AW177784 AI022852 BE061653 AW376811 AW848592 AA040018 BE185331 BE182164
			AA368584 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767
			H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470 AI392926 AF139065 AW370813 AW370827 AW798417 AW798780
25			AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866 AW370829 AA247685 BE002273 AI760816 AI439101 AW879451
			AI700963 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975 AI470146 AA946936 BE067737 BE067786 W19267
			AA644381 AA702424 AI417612 AI306554 AI686869 AI568892 AW190555 AI571075 AI220673 AA056527 AI471874 AI304772 AW517828
			AI915596 AI627383 AI270345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070 AI494069 AI911702 AA149191 AA026854
			AI830049 AI867258 AW780435 AI910434 AI819584 AI658282 AI078449 AI025932 AI860584 AI635878 AA026047 AA703232 D12082
30			AW192085 AA658154 AW514597 AW591892 T87181 AA782066 AW243815 AW150038 AW268383 AW004633 AI927207 AA782109
			AW473233 AI804485 AW169216 AI572669 AA602182 AW015480 AW771865 AI270027 AA961816 AA283207 AI076962 AI498487 AI348053
			AI783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 AI905927 AA022701 W38382 R20795 T77861 AW860878
	412998	1343218_1	BE046254 BE046673 BE046253
	413000	1343239_1	BE046280 BE046763 BE046676
35	413611	1380017_1	BE153275 BE153189 BE153329 BE153022 BE153030 BE152974
	413709	1384144_1	BE158667 BE158668
	413804	1390710_1	T64662 BE168190 BE168256
	413895	1397743_1	BE178160 BE177986 BE178330 BE178480
	415789	1555357_1	H01581 H12950 R65905 H13053
40	416023	156696_1	AA173029 BE467711 AA176710
	416272	158407_1	AA178882 AA179898 AA178897
	417500	168443_1	H59970 AA203382 R08822
	419555	185884_1	AA244416 AA244401
	420685	195591_1	AA279362 AA454496 AA584871
45	421762	206590_1	AA297546 AA297410 AA297401 AA297465 AA297268 AW966174
	421938	209376_1	AA405951 AA300675 AA412243 AA412383
	422895	22276_1	NM_015958 AF132964 AA088658 N28882 AI197842 AA338679 AA405666 W16871 AA385447 AI928315 AI928318 AW846613 AW960005
			AI860687 AI205534 AI961336 T64873 AI735559 H58826 AA657710 AW337576 BE242131 AA339340 AA371380 AA334618 AA316398
			R96579 AW771996 AA366110 W07461 H77948
50	422984	223466_3	W28614 W27435 AI983043 AA364395 AW572472 AW190386 AI129278 AI913081 AW473549 AA830713 AI982871 AI638647 AI826466
			AW572486 N52583 N89687 AW075557 AI571047 AI887479 AI559469 AI685802 AA805256 AI458777 AA974369 AI868929 AI886032
			AI823925 AI823556 AW198135 AI287510 AI565910 AA765775 AI866019 AI263697 AI355625 R42668 AA894603 AW105585 AI824555
			AW339175 D20479
			AI017717 AA349996 AA350286 BE501310 R48207 AI372769 AJ003450 AA915976 AI261513 AI033019 AI222825 AW150983 AA420700
55	432638	35173_4	AA420670 AW884784 Z40157
			AW182416 AA918195 AA778707 AA927922 AA868718 AA853991 AA609856 AA634398
	433821	374566_1	AF153201 AW888811 AW888810 AW842970 AA383181 F35832 F26805 X78930 AF026094 N83362 AA206766 AW874294 AA284205
	434767	39297_1	AI091885 AA206800 AW370684 AA904608 AA806352 AA894757 AW068376 AA807284 AA311341 AW958314
			AW974687 AA649656 AA652145
60	434809	393566_1	AA778647 AW070999 R42302
	438129	450500_1	H16902 AA814856 T65225 AI523569 F09869 F04737 AI538427 AI051714 AW172603 F02602 F01437 AI684417 AI801950 F02970 Z39367
	438713	463722_1	F02882 T16704 H14597 AW952332 R52080 H10427 T06175 T31057 AI381431 R60918 R41255 R43059 R39905 H19330 R36968
			BE535511 M62098 AA306787 AW691766 AA348998 AA338869 AA344013 AW955561 AW389343 AW403607 L40391 AW408435 AA121738
	438924	4669_1	AI568978 H13317 R20373 AW948724 AW948744 AA335023 AA436722 AA448690 C21404 AW884390 AA345454 AA303292 AA174174
65			BE092290 T90614 AA035104 R76028 AA126924 AA741086 AW022056 AW118940 AA121666 AI832409 AA683475 AI140901 AI623576
			AW519084 AW474125 AI953923 AI735349 AW150109 AI436154 AW118130 AW270782 AI804073 N27434 AA876543 AA937815 AI051166
			AA505378 AI041975 AI335355 AI089540 AA662243 AI127912 AI925604 AI250880 AI366874 AI564386 AI815196 AI683526 AI435885
			AI160934 H79030 AI801493 AA448691 AI673767 AI076042 AI804327 AA813438 AA680002 AI274492 T16177 AI287337 AI935050 AA907805
			AA911493 AI589411 AI371358 AW576236 AI078866 AW516168 AA346372 AI560185 AA471009 R75857 AA296025 AA523155 AA853168
70			AI686593 AI658482 AI566601 AW072797 AA128047 AAC35502 AW243274 AA992517 R43760
	439004	467743_1	AW979062 AA848000 AA847958 AA829138
	441623	52182_1	AA315805 AA376906 BE539395 AW579186 H44349 BE328145 BE041644 AW579187 AW366504 H26241 H25318 W37573 AW600919
			AA528775 R75904 AW780125 AA149420 AI672414 AI122760 AA345675 AW172758 AI37912 AI961291 AW090300 AI090244 BE219837
			AI623661 BE501576 AI742232 AW887496 BE501734 AI023964 AI288904 AA975373 AA860325 AI458424 AI984583 N32562 AI358102
75			AW241694 AI038448 AA576391 AI018389 AI672071 AA977874 W37448 AW189392 AA612894 AI373653 H89551 H89365 AI699774
			AI277548
	442473	543413_1	W27992 AF056988
	442506	54405_1	BE566411 AL121194 AW976385 AW366882 AI767324
	445182	632151_1	AW189787 AI216430 AW268499 AW205930 AI392907 BE093017 BE093019 BE093010
	447703	733191_1	AI420277 AW747989 W26555

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5	448079	74834_1	R76981 AA101801 AA101722 AA122297 AA098802 BE006483 AA343200 AW963375 BE090425 AA213871 BE621402 AA309094 AW960171 AI275045 Z44230 AW243724 AI051487 AI376624 R68631 AW978550 C00116 AI984051 AA122265 AI379941 AW205843 AW205839 AW190219 AW129532 AI954133 AI658869 AI383948 AI537386 AA213788 AI088416 AI360826 AA101802 AI619505 AA101795 AA101723 AW614392 R64287 AA927599 AI251904 AI803003 AI675123 AW023079 AW134959 AI926156 AA831069 AI638324 F29901 R46085 F03383 C17731 R20584 T90131
10	450936	85190_2	AI033745 AI034133 AA844424 AW166024 AI831699 AI971097 AA011685 H70852 H70851
15	451844	888230_1	T61430 AI820546 AI821336
20	452900	93691_1	AA626794 AA626779 AA071274 AA928041 AI954235 N71035 N70230 AW674412 AI871136 AI563955 AI954237 AA649543 AI340231 AI368586 AI868721 W44486 T63736 AA126250 AI343619 H94297 T47633 AI672897 AA496355 R23240 AI814680 AA902119 AA644262 N67040 AW074273 AI357512 AA865354 AI027942 R33837 H95828 N63928 AI418701 AI186469 AA693672 AA778429 AA128352 AW954072 C00015 AA861853 AW022016 AI955645 AI753118 AI755095 AA029523 T70086 AA029458 AW675640 N79606 AI659597 AI417119 AI804089 AI383091 AA128493 T83907 T47632 AA094118 AA496405 H94191 AW887759 N98454 AA512988 AI623761 AW028373 AW249740 AI187029 AA991733 AI683085 AI336036 D60550 D60466 D60009 D60248 AW262673 AI524080 AA205643 AI969141 AW674989 AA093704 R81248 R73069 W01019 R23316 C14688 W44485 AA093663 T70157 H57883 R94790 D81287 D81788 AA364340 AA383533 N41706 BE295144 D60973 D81466 D60551 R33836 D60249 AA354560 W01933 T71478 AA515461 F27984 BE064745 W19084 R81247 AI080252 AI382863 AA205642
25	454412	1174764_1	AW954243 AA829930 AA412478 AA828434 AA814538 AI927418 AI192435 W52697 AA443666 AA031913 AI683306 AA918481 AI183314 D83907 AI206832 AA876122 D83836 D83838 D82533 AI761290 AI191125 AI143749 AW771909 AI241436 AI767267 W56507 AA847787 AA568692 T10502 AI247870 AA715017 AA643304 AA890233 AA811387 AA897470 AA907729 AI708679 AI078010 AA452830 AW419160 AI783713 N80205 W56778 AA676899 AI888718 N69930 AI338935 AI217580 AA639508 AA575836 BE046852 AI312651 AI038406 AA4628649 AA643838 AI493761 AA032024 W38849 AA340178 AA447052 AA452969 W19369 AA296364 H44229 W58767 C05751 C05835 AI741989 N98532 AW102617 AA412583 AI922246 W38495 AA355375 AA928571 C06275 AA352500 N93132
30	454555	1223870_1	AW562568 AW618656 AW818647 AW818655 AW818637 AW818234
35	454717	1230516_1	AW807095 AW807022 AW845880 AW807096 AW807461 AW846116 AW807070
40	455234	1265385_1	AW815123 AW815138 AW815259
45	455424	1289247_1	R41084 AW875856
50	455474	1292960_1	AW937733 AW937727 AW937883
55	455591	1335166_1	AW948094 AW948118 AW948070 AW948093 AW948084 AW948088 AW948074 AW948079 AW948117 AW948085 AW948081 AW948096 AW948102 AW948087 AW948080 AW948061 AW948091 AW948098 AW948089 AW948104 AW948119 AW948065 AW948100 AW948112 AW948121 AW948068 AW948109 AW948105 AW948097 AW948120 AW948108 AW948111 AW948114 AW948115 AW948072 AW948083 AW948095 AW948116 AW948078 AW948077 AW948071 AW948067 AW948107 AW948122 AW948065 AW948064 AW948113 AW948063 AW948062
60	455804	1337197_1	AW948172 AW948178 AW948169 AW948176 AW948191 AW948192 AW948186 AW948184 AW948187 AW948188 AW948189 AW948181
65	455842	1374629_1	AW948177 AW948171 AW948183 AW948173
70	457747	397222_1	BE008018 BE008025 BE008026 BE007959 BE007994 BE008016 BE008019 BE008024 BE008022 BE008027 BE008029 BE008020
75	458891	850804_1	BE008015 BE008021 BE008028 BE008023 BE008030 BE008014
	459192	923891_1	BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169
			BE145837 BE145894
			AW975000 AA656945 AA661558
			AI743502 AI807438
			AW176180 AW176212 AI909464 AW176218 AW176171 AW176203 AW176181 AW176213

TABLE 9C

45	Pkey:	Unique number corresponding to an Eos probe set		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
50	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
55	400634	8567750	Minus	101102-101223,101886-102018
	400750	8119067	Plus	198991-199168,199316-199548
	400752	7331445	Minus	36215-36461
	400772	8131629	Minus	34896-35021,41078-41197
	400773	8131629	Minus	44116-44238,48208-48321
	400788	7342055	Plus	184369-184715
60	400789	8307741	Plus	82281-83893
	400835	8954121	Plus	89366-89622
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
	400844	9188605	Plus	24746-24872,25035-25204
	400845	9188605	Plus	34428-34612
65	400846	9188605	Plus	39310-39474
	400847	9188605	Plus	44643-44835
	400957	7705148	Minus	66959-67241
	400967	7770682	Minus	32697-32999
70	401038	7232177	Minus	4277-4469
	401041	7232177	Plus	44750-45076
	401058	8117654	Minus	45226-45414
	401155	9438289	Plus	31381-31526
	401177	9438503	Minus	62773-63330
	401196	9719673	Plus	33138-33834
75	401204	9743388	Minus	33694-33872
	401286	9801342	Minus	147036-147318
	401346	9925605	Minus	12031-13032
	401371	9650602	Plus	80901-81283

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	401383	6721135	Minus	155543-157381
	401496	7381769	Minus	82790-83002
	401512	7622346	Plus	136399-136557
5	401563	8247910	Plus	91395-91763
	401572	8570271	Minus	78651-78889
	401593	7230957	Plus	10368-10572,11293-12356
	401600	4388746	Minus	27363-27518,28727-28891,29526-29731
	401603	7689963	Minus	116659-116780
10	401613	4878062	Plus	22461-22831
	401654	9097132	Minus	64695-64797
	401660	9100664	Minus	173662-174024
	401720	6468551	Plus	7783-8468
	401784	7249190	Plus	148362-148606,149453-149535,149731-149962
15	401835	7139700	Plus	142257-142742
	401886	7229913	Minus	79215-79393
	401936	3806091	Plus	46817-46943
	402001	9501818	Plus	68062-68223
	402087	8117546	Plus	137069-137213,138678-138828,138969-139050
20	402138	7704985	Plus	14173-15108
	402144	7242326	Plus	115425-115977
	402190	8576067	Minus	76488-76959
	402191	8576073	Minus	69410-69583
	402329	7798735	Plus	15833-16180,18419-18715,22507-22624
25	402368	9558577	Minus	47218-47330,48052-48203
	402371	9558584	Plus	68736-68956
	402378	9625333	Minus	41312-41468,48313-48720
	402449	9796674	Plus	59667-60039,62588-62828,63465-63623,64923-65108
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
30	402517	9798106	Plus	17569-17721
	402599	7239666	Plus	5835-5987
	402617	9930797	Minus	69466-69945
	402712	8969253	Minus	10941-11138
	402731	9211639	Minus	117913-118004,121110-121211,121327-121457,125478-125623,126540-126663
35	402737	9212184	Minus	13358-13552
	402754	9213730	Plus	15345-15852
	402760	9213869	Plus	136829-136952,137336-137521
	402812	6010110	Plus	25026-25091,25844-25920
	402845	9369286	Plus	160451-160617,160788-161009
40	402869	6434643	Minus	138639-139335
	402892	8086844	Minus	194384-194645
	403010	3132346	Plus	78385-79052
	403149	9799833	Plus	25034-25185
	403326	8440025	Minus	110959-111122
45	403329	8516120	Plus	96450-96598
	403342	7233487	Minus	42312-43750
	403349	8569773	Minus	167815-168374
	403381	9438267	Minus	26009-26178
	403463	9929538	Plus	102596-102879
50	403655	8736093	Plus	65668-65859
	403725	7534031	Plus	86737-86943
	403728	7534291	Minus	34481-34671
	403807	8439933	Minus	162963-165773
	403826	9838209	Plus	121197-121358
55	403885	7710403	Minus	53259-53524
	403943	7711864	Plus	100742-100904,101322-101503
	403988	8576087	Plus	16251-16462
	404029	7871252	Plus	108716-111112
	404068	3548785	Plus	99397-101808
60	404069	3168619	Plus	47310-47450
	404178	7630978	Minus	178075-178383
	404204	3169112	Minus	79868-80321
	404231	8218035	Minus	61077-61322
	404250	9187145	Minus	36099-36212,37928-38075
65	404273	9885189	Plus	97789-98285,99601-99855
	404343	9838093	Plus	122664-122931
	404349	7630858	Minus	61006-61187
	404391	3135305	Minus	26030-26173,27852-27997
	404392	3135305	Minus	29738-29857
70	404397	9558608	Minus	104042-104232
	404438	6984205	Plus	63413-63553
	404439	7139680	Plus	55316-55585
	404530	6479107	Plus	3157-3304
	404596	9958262	Minus	104807-105043
75	404649	9796926	Minus	100027-100399
	404666	7272179	Minus	18677-18993
	404687	9797554	Minus	128456-128565
	404744	9187237	Plus	71776-71852,72885-73019,73700-73822,74692-74850

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	404751	7630939	Plus	113799-114252,114393-114715
	404769	8099713	Minus	175801-176823
	404790	7230958	Plus	38611-38761
5	404906	7331453	Minus	100985-101126
	404966	7387343	Plus	55883-56203
	404977	3738341	Minus	43081-43229
	405000	8957544	Minus	88854-89993
	405022	7330304	Plus	217163-217439
10	405053	7651944	Minus	157134-157430
	405068	7655685	Plus	150740-151556
	405155	9966228	Plus	130469-130723
	405163	9966267	Minus	161171-161299
	405165	9966302	Plus	6461-6845
15	405166	9966302	Plus	40526-40891
	405172	9966752	Plus	153027-153262
	405180	7139743	Plus	65438-65740
	405193	7230072	Plus	128187-128383
	405194	7230072	Plus	190465-190645,193346-193610
20	405245	7249293	Minus	57560-58312
	405365	2275192	Minus	119867-120372,120481-120824,121029-121357
	405376	1552533	Plus	28875-29099
	405418	6997292	Plus	51839-51953
	405436	7408068	Minus	55716-55979
25	405443	7408143	Plus	90716-90887,101420-101577
	405474	8439781	Plus	172005-172175
	405502	9211311	Minus	50360-50584
	405580	4512267	Plus	169232-169647
	405595	7159256	Plus	47585-47688
30	405630	4508116	Minus	103218-103291,105858-105993,110051-110126
	405646	4914350	Plus	741-969
	405710	5531256	Minus	66203-66832
	405806	7274891	Minus	224961-226780
	405812	4775630	Minus	29424-29764
35	405855	7652031	Minus	60377-60795
	405879	6758747	Minus	54789-55457
	405891	6758795	Plus	41062-41861
	405902	6758795	Minus	82322-83110
	405932	7767812	Minus	123525-123713
40	406038	8389537	Plus	37764-37877
	406140	9168231	Minus	49887-50219
	406181	5923650	Plus	16586-16855
	406231	7417725	Plus	17206-17641,17772-17968
	406248	7417725	Plus	49711-50227
45	406274	7543787	Plus	932-1123
	406356	7107907	Plus	18761-18973
	406404	9256305	Minus	152569-152874
	406467	9795551	Plus	182212-182958
	406557	7711569	Minus	5446-5574,6170-6352
50	406575	7711679	Plus	142034-142473

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TABLE 10A: Genes preferentially expressed in non-invasive bladder tumors

5	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1	80th percentile of T4 tumor Als divided by the 80th percentile of T2-T4 tumor Als		
10	Pkey	ExAccn	UnigeneID	Unigene Title
	421110	AJ250717	Hs.1355	cathepsin E
	428651	AF196478	Hs.188401	annexin A10
	451668	Z43948	Hs.326444	cartilage acidic protein 1
	415511	AI732617	Hs.182362	ESTs
15	428336	AA503115	Hs.183752	microseminoprotein, beta-
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte
	400752			NM_003105*:Homo sapiens sortilin-related
	430315	NM_004293	Hs.239147	guanine deaminase
	403010			C21000152:gi 6226483 sp Q52118 YMO3_ERWS
20	404977			Insulin-like growth factor 2 (somatomedi
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport
	400409	AF153341		Homo sapiens winged helixforkhead trans
	400844			NM_003105*:Homo sapiens sortilin-related
	406081			Target Exon
25	417275	X63578	Hs.295449	parvalbumin
	402230			Target Exon
	454219	X75042	Hs.44313	v-rel avian reticulocendrotheliosis viral
	403381			ENSP00000231844*:Ecolotropic virus integra
	426088	AF038007	Hs.166196	ATPase, Class I, type 6B, member 1
30	452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC
	434051	AW024973	Hs.283675	NPD009 protein
	418406	X73501	Hs.84905	cytokeratin 20
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT
35	403383			Target Exon
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu
	424800	AL035588	Hs.153203	MyoD family inhibitor
	404606			Target Exon
	418205	L21715	Hs.83760	troponin I, skeletal, fast
40	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abi subst
	413786	AW613780	Hs.13500	ESTs
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C
	416540	BE262478	Hs.79404	neuron-specific protein
	420729	AW964897	Hs.290825	ESTs
45	402844			C1000118*:gi 9951913 ref NP_062632.1 pr
	401093			C12000586*:gi 6330167 dbj BAA86477.1 (A
	417720	AA205625	Hs.208067	ESTs
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278
	403818			Target Exon
50	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L
	418060	AA211589	Hs.208047	ESTs
	400843			NM_003105*:Homo sapiens sortilin-related
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5
	401512			NM_014080:Homo sapiens dual oxidase-like
55	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H
	417094	NM_006895	Hs.81182	histamine N-methyltransferase
	436293	AI601168	Hs.120910	ESTs
	436246	AW450963	Hs.119991	ESTs
	447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314 CDC28/cdc
60	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein
	415025	AW207091	Hs.72307	ESTs
65	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA
	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin
	411880	AW872477		gb:hm30f03.x1 NCL_CGAP_Thy4 Homo sapiens
70	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P
	413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib
	405364			ENSP00000239138*:Guanine nucleotide-bind
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)
75	401929			C1700169C:gi 6005701 ref NP_009099.1 AT
				1.00

TABLE 10B

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Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

5

Pkey	CAT Number	Accession
411880	1263110_1	AW872477 BE088101 T05990
413804	1390710_1	T64682 BE168190 BE168256

10

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

15

20

Pkey	Ref	Strand	Nt_position
400752	7331445	Minus	36215-36461
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
401093	8516137	Minus	22335-23168
401512	7622346	Plus	136399-136557
401929	3810670	Minus	3167-3286,4216-4310
402230	9966312	Minus	29782-29932
402844	9369286	Plus	54958-55313
403010	3132346	Plus	78385-79052
403381	9438267	Minus	26009-26178
403383	9438267	Minus	119837-121197
403818	8962065	Minus	138360-138512,144656-144796
404606	9212936	Minus	22310-23269
404977	3738341	Minus	43081-43229
405364	2281075	Minus	48325-48491,49136-49252
406081	9123861	Minus	38115-38691

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TABLE 11A: Genes preferentially expressed in muscle-invasive bladder tumors

	Pkey:	Unique Eos probeset Identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
5	UnigenelD:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1	80th percentile of T2-T4 tumor AIs divided by the 80th percentile of T1 tumor AIs			
10	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	423961	D13666	Hs.136348	periostin (OSF-2os)	11.22
	421948	L42583	Hs.334309	keratin 6A	10.87
	401780			NM_005557*:Homo sapiens keratin 16 (foca	9.16
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	8.40
15	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	7.88
	439926	AW014875	Hs.137007	ESTs	7.73
	408243	Y00787	Hs.624	Interleukin 8	7.54
	414183	AW957446	Hs.301711	ESTs	7.00
	411573	AB029000	Hs.70823	KIAA1077 protein	6.52
20	414522	AW518944	Hs.76325	step II splicing factor SLU7	6.42
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.14
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	6.04
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	5.66
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	5.62
25	422168	AA566894	Hs.112408	S100 calcium-binding protein A7 (psorias	5.51
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	5.48
	401781			Target Exon	5.46
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	5.41
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	5.41
30	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	5.32
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	5.32
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	5.27
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	5.22
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.17
35	406663	U24683	Hs.293441	immunoglobulin heavy constant mu	5.08
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	4.93
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.89
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.74
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	4.64
40	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	4.39
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.30
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	4.29
	433470	AW960564		transmembrane 4 superfamily member 1	4.23
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	4.22
45	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	4.22
	413324	V00571	Hs.75294	corticotropin releasing hormone	4.20
	436729	BE621807		transmembrane 4 superfamily member 1	4.18
	450455	AL117424	Hs.25035	chloride intracellular channel 4	4.15
	413731	BE243845	Hs.75511	connective tissue growth factor	4.09
50	412429	AV650262	Hs.75765	GRO2 oncogene	4.00
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	4.00
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.00
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	3.97
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	3.95
55	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	3.94
	413441	AI929374	Hs.75367	Src-like-adaptor	3.91
	404854			Target Exon	3.81
	431319	AA873350	Hs.302232	ESTs	3.77
	452432	AW206008	Hs.283378	Homo sapiens cDNA; FLJ21778 lis, clone H	3.76
60	429679	NM_006290	Hs.211600	tumor necrosis factor, alpha-induced pro	3.72
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.58
	408380	AF123050	Hs.44532	diubiquitin	3.58
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.57
	422545	X02761	Hs.287820	fibronectin 1	3.52
65	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.49
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	3.48
	406687	M31126		matrix metalloproteinase 11 (stromelysin	3.41
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.36
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	3.32
70	417497	AW402482	Hs.82212	CD53 antigen	3.30
	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	3.25
	445033	AV652402	Hs.72901	mucin 13, epithelial transmembrane	3.23
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	3.23
	427527	AI809057	Hs.293441	immunoglobulin heavy constant mu	3.22
75	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.18
	453331	AI240665		ESTs	3.15
	428036	AW068302		Homo sapiens mRNA for caldesmon, 3' UTR	3.10
	417366	BE185289	Hs.1076	small proline-rich protein 1B (corniflin)	3.09

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5	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	3.07
	416478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.02
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	2.77
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibitor	2.75
	406755	N80129	Hs.94360	metallothionein 1L	2.75
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	2.67
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	2.65
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.64
10	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	2.51
	410204	AJ243425	Hs.326035	early growth response 1	2.46
	438973	AW959503	Hs.60440	ESTs, Weakly similar to serin protease w	2.46
	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	2.44
	422626	AA344932	Hs.118786	metallothionein 2A	2.44
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.43
15	413902	AU076743	Hs.75613	CD36 antigen (collagen type I receptor,	2.42
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	2.42
	407207	T03651	Hs.336780	tubulin, beta polypeptide	2.30
	438855	AW946276	Hs.5441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	2.29
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.20
20	424909	S78187	Hs.153752	cell division cycle 25B	2.18
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	2.17
	416819	U77735	Hs.80205	pim-2 oncogene	2.11
	422562	AI962060	Hs.119397	AE-binding protein 1	2.07
	414081	AW969976	Hs.279009	matrix Glia protein	2.07
25	426406	AI742501	Hs.169756	complement component 1, s subcomponent	2.03
	443950	NM_001425	Hs.9999	epithelial membrane protein 3	2.01
	418323	NM_002116	Hs.1162	major histocompatibility complex, class	1.94
	414420	AA043424	Hs.76095	immediate early response 3	1.90
30	415149	X12451	Hs.78056	cathepsin L	1.72
	415213	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea	1.70
	421848	X15880	Hs.108885	collagen, type VI, alpha 1	1.69
	452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.64
	427676	AA394062	Hs.300772	tropomyosin 2 (beta)	1.64
	415198	AW009480	Hs.943	natural killer cell transcript 4	1.60
35	424390	AW815557	Hs.182241	interferon induced transmembrane protein	1.59
	426825	AL133415	Hs.297753	vimentin	1.51
	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	1.46
	407694	U77594	Hs.37682	retinoic acid receptor responder (tazaro	1.44

TABLE 11B

Pkey: Unique Eos probe set identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
428036	28620_1	<p>AW068302 AI754558 AI750727 AI752631 AA302174 AA327522 M64110 AW859944 AW859989 AI751995 AA769620 AI858829 AI924875 AI888836 AA864291 AI685060 AW086029 AI624908 AW466326 AI093800 AA991651 AI254501 BE004703 AA334442 AW938852 AA194330 AL046953 AA852866 AW391995 W30846 AW562926 W25261 AA042863 R99045 H97060 W03910 H94687 T88984 AL048165 T29632 N31556 N36484 AI798679 AA989355 W23832 AA873789 AI743646 AA363587 AI814748 AW338990 N73740 N83666 AL047316 R24137 R63433 AA524984 AA234043 AA195131 N99903 AA453669 AI240302 AA370271 AI950026 AW771049 AA121476 AA569557 AI752632 AI355594 AI471993 AI159941 N94555 AI753138 N21537 H97881 N25769 AW068044 AA608425 R63380 AA384736 AA384738 AA852352 AI073645 AA527960 AA525036 AA044414 AI752460 AA703064 R01216 AA897183 AI751996 T81078 H95047 AA573642 D58348 N20953 AA437143 N95439 AA579540 AW867056 AA770090 AI085180 AI806799 AA426421 AI572513 R24081 AA853189 AA295620 AA234044 AA371020 AW994984 H20896 AW964436 AA318516 AA318499 AA318727 AA318211 AA318478 AA318444 AA318307 AA318497 AA318448 AA318309 AA318496 AA318213 AA318435 AA318424 AA318217 AA318523 AA318438 AA318487 AA318724 AA593185 AW994985 T69842 AI251813 AA478174 AA447737 T68350 F07712 AA121145 H08973 AA345212 BE000667 AW068210 W45394 AW795667 R73973 N42354 H85516 BE147991 T28113 R32662 AA384678 AW239275 H82382 AW840700 D58229 C04082 W45394 AW795667 R73973 BE002409 AA042828 AA363555 AJ223612 AA344709 BE149590 BE149590 AW579469 AW365135 AW365134 AW994353 AW972886 AW069166 AA062957 D79947 W46960 AW959278 AA295997 AA026215 AW579469 AW365135 AW365134 AW994353 AW972886 AW069166 AA343690 AW888731 AI751527 AA937490 AA937506 AI826715 BE465604 AI925532 AI858109 AW339097 AI858524 AI720571 BE046506 AW364981 AA043906 AA375983 AA525181 AW068366 AW070577 AW891837 N83985 AW182753 AI422979 AI679733 BE006555 AL048166 AI081401 AI888821 AI626043 N37087 AI624140 AI801298 AA600048 AI753947 H89615 N66424 AW069756 AI814880 AI982806 AI754287 AI971816 AW069022 AW069069 AW069454 AA342989 AI077712 AI311467 AI087361 AI801015 W46993 AI281324 AW191963 AI421675 AI300881 AI356570 AA873156 AI004219 AI189685 AA478018 AA076063 AI445222 AI753124 AI521569 AI625026 AI022366 AI475993 H20846 AI223234 AI635123 AA579170 N30442 AW117889 AA807935 AA556975 AI306636 AA888963 AI952591 AI935835 AI445293 H16713 AW139633 AA621222 AA572051 AI280828 H09543 AI453725 AW069613 AI865615 AI753921 AI368782 AI633206 AI446651 W46961 N22201 H82276 C16555 AA291477 AW440535 AW517755 AA669921 AI926777 AW662118 AA553369 N57873 AW023948 C15861 C16601 AI251465 AW079167 BE045090 AI273006 C16390 C16503 AI620823 F13661 N66664 Z21311 C16108 C16089 C16400 AA758273 AI287781 AA854676 AW680874 AW385583 AI589944 AA665817 AW192979 AW469065 AA564048 H84715 C16417 AA731072 AA661674 C16487 N29477 AW189997 AI370492 C16471 AA652809 AA936687 AA506512 C16306 AW028413 AI537935 AA528347 C16255 AW029046 C16202 AI868152 AI524662 T94414 AI567041 AI619654 AW008486 AI075624 AA577434 AA345104 T30105 AA932002 C16585 AI750390 AW294265 AI619552 AA669781 AA026678 AW132002 AW263919 C16562 AA759137 AA593351 Z40779 C16577 AA885045 AW073763 R45484 AI520895 U54708 T49285 AI568126 AW008569 AI093317 AL119781 T61046 AI053563 H51958 AF114144 AA305739 AW950394 AW793928 AW793910 AL047737 AV659047 AV659632 AI750389 AA092053 AA092798 H65367 T61587 R23745 Z20418 T76485 AI751528 AW068121 AA853188 AI752459 AA853711 AW950663 R76964 R36359 R21626 R21522</p>

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433470 3672_1 AW960564 AA092457 T55890 D56120 T92525 A1815987 BE182608 BE182595 AW080238 M90657 AA347236 AW961686 AW178446
AA304671 AW583735 T61714 AA316968 A1446815 AA343532 AA083489 AA488005 W52095 W39480 N57402 D82638 W25540 W52647
D62729 D58990 BE319182 AA315188 AA308636 AA112474 W76162 AA088544 H52265 AA301631 H80982 AA113786 BE620997 AW651691
AA343799 BE613669 BE547180 BE546656 F11933 AA376800 AW239185 AA376086 BE544387 BE619041 AA452515 AAD01806 AA190873
AA180483 AA159546 F00242 A1940609 A1940602 A1189753 T97663 T66110 AW062896 AW062510 AW062902 A1051622 A1828930
AA102452 A1685095 A1819390 AA557597 AA383220 A1804422 A1633575 AW338147 AW603423 AW606800 AW750567 AW510672 A1250777
AA083510 AW629109 AW513200 AA921353 A1677934 A1148698 A1955858 AA173825 AA453027 A1027865 AW375542 AA454099 AA733014
A1591384 R79300 R60023 AA843106 AA625058 AA844898 AW375550 AA869018 A1474275 AW205937 A1052270 AW388117 AW388111
AA699452 A1242230 N47475 H38178 AA365621 AA113196 AA130023 H39740 T61629 A1885973 AW083671 AA179730 AA305757 A1285455
N83956 AA216013 AA336155 AW999959 T97525 AA345349 T91762 AA771981 A1265092 A1591386 BE392486 BE385852 AA682601
A1682884 AA345840 T85477 AA292949 AA932079 AA088791 D82607 T48574 AW752038 C06300
436729 42585_1 BE621807 A1445481 A1346835 A1453743 A1564644 A1928364 AW984527 BE156214 A1694111 A1591358 C17504 C17476 C17963 C18304
AW071625 A1678712 C17732 D57559 H61762 A1720939 A1262930 H27252 AA479712 A1927769 AA291465 AA155661 A1963432 A1567995
AA421676 A1925607 AA292956 AA192448 AW192553 A1865838 A1696905 A1871950 A1911921 BE619741 BE439796 A1161312 A1597801
A1424384 A1093510 A1240988 AW820230 A1492554 BE044033 AW262737 AW008570 AA043216 AW629505 AA136645 AA037722 AA706057
AA088439 AW606193 AW806183 AA479834 BE501957 AA129574 R36114 AA649494 AA524526 BE327120 AW572531 BE219764 BE349186
AW015724 AA043217 AW772000 A1799814 A1671727 AW779725 AA502632 A1470033 AA129575 W38161 A1972739 AA04570 AA627686
AA723200 AA147228 AA903050 A1990245 A1075878 T32487 C06123 AA157944 A1800106 W60075 A1659160 AA478326 AW673152
AA182640 A1990827 AW275048 AW103470 A1298935 AW471421 R79190 AW085158 W45410 A1333170 AW300456 AA682517 T55840
A1623466 A1692846 AA962397 AW191997 AA136658 A1251817 BE044134 AW339104 AW517762 AA724739 R79933 AA411100 AA191349
AA037696 AA190966 AA757735 AW772283 AA010631 H80983 A1769516 H64985 A1061065 A1950693 AA065492 A1245632 H26594
AW088968 BE156360 A1349390 A1621320 A1736844 AW194272 AA148284 AA953883 C06365 AA487693 A1927217 A1918523 A1453453
A1798502 A1189366 A1261359 A1032559 AW338678 A1972899 A1500576 A1872628 A1693030 Z28771 A1985583 A1363829 AW339301
AA581093 A1650338 W60032 AA603566 A1686240 AW242958 AA719173 A1745717 AW675302 A1582462 A1244845 A1565439 F09579
A1918453 AA035576 A1472527 AW351556 AA191414 AW674145 D57558 A1446740 D57845 A1589264 C05782 AA722206 A1432033 R21752
BE157510 A1829640 A1468237 AW384233 AA989662 A1865912 AW197954 A1344941 X75684 A1344943 AW583310 AA988297 A1334860
A1346677 A1798415 D11921 A1377596 A1983655 A1744233 C06111 A1248307 AA948565 A1224807
453331 96214_1 A1240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73959 A1095755 T49904 H03868 AA411580 R33395 AA410586 T48869
D63292 R31981 H12498 H02668 AA035018 R75957 A1803329 R27528 R36203 A1809932 A1808765 R78948 AA411449 AA976929 A1378760
A1378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 A1360919 H03502 BE208298 R68598
A1350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933

TABLE 11C

Pkey:	Unique number corresponding to an Eos probeset		
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
Strand:	Indicates DNA strand from which exons were predicted.		
Nt_position:	Indicates nucleotide positions of predicted exons.		
Pkey	Ref	Strand	Nt_position
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
404854	7143420	Plus	14260-14537

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TABLE 12A: Genes preferentially expressed in muscle-invasive bladder tumors

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	Seq ID No.:	Sequence Identification Number linking information in Table 12A to sequences in Table 13			
10	Pkey	ExAccn	UnigeneID	Unigene Title	Seq ID No.
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID No. 1 & 2
15	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	Seq ID No. 3 & 4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. 5 & 6
20	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID No. 7 & 8
	406964	M21305		FGENES predicted novel secreted protein	Seq ID No. 9 & 10
25	429276	AF056085	Hs.198612	G protein-coupled receptor 51	Seq ID No. 11 & 12
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	Seq ID No. 13 & 14
30	410102	AW246508	Hs.279727	ESTs; homologue of PEM-3 [Clona savignyi	Seq ID No. 15 & 16
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. 17 & 18
35	424735	U31875	Hs.272459	short-chain alcohol dehydrogenase family	Seq ID No. 19 & 20
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	Seq ID No. 21 & 22
40	415511	AI732617	Hs.182362	ESTs	Seq ID No. 23 - 25
	452461	N78223	Hs.108106	transcription factor	Seq ID No. 26 & 27
45	413324	V00571	Hs.75294	corticotropin releasing hormone	Seq ID No. 28 & 29
	443211	AI128388	Hs.143655	ESTs	Seq ID No. 30
50	439926	AW014875	Hs.137007	ESTs	Seq ID No. 31 & 32
	432222	AI204995		gb:an03c03.x1 Stralagene schizo brain S1	Seq ID No. 33
55	408908	BE296227	Hs.250822	serine/threonine kinase 15	Seq ID No. 34 & 35
	443171	BE281128	Hs.9030	TONDU	Seq ID No. 36 & 37
60	432829	W60377	Hs.57772	ESTs	Seq ID No. 38 & 39
	410553	AW016824	Hs.272068	hypothetical protein MGC14128	Seq ID No. 40 & 41
65	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	Seq ID No. 42 & 43
	425721	AC002115	Hs.155309	uroplakin 1A	Seq ID No. 44 & 45
70	420370	Y13645	Hs.97234	uroplakin 2	Seq ID No. 46 & 47
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dj365012.1 [H.sa	Seq ID No. 48 & 49
75	428664	AK001666	Hs.168095	similar to SALL1 (sal [Drosophila]-like	Seq ID No. 50 & 51
	456034	AW450979		gb:U1-H-B13-ala-a-12-O-U1.s1 NCL_CGAP_Su	Seq ID No. 52
80	421110	AJ250717	Hs.1355	cathepsin E	Seq ID No. 53 & 54
	451668	Z43948	Hs.326444	cartilage acidic protein 1	Seq ID No. 55 - 60
85	408243	Y00787	Hs.624	interleukin 8	Seq ID No. 61 & 62
	440304	BE159984	Hs.125395	ESTs	Seq ID No. 63 & 64
90	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	Seq ID No. 65 & 66
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	Seq ID No. 67 & 68
95	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	Seq ID No. 69 & 70
	405033			C1002652*:gij544327[sp]Q047399FMO5_RABIT	Seq ID No. 71 & 72
100	422282	AF019225	Hs.114309	apolipoprotein L	Seq ID No. 73 & 74
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	Seq ID No. 75 & 76
105	400844			NM_003105*:Homo sapiens sortilin-related	Seq ID No. 77 & 78
	404875			NM_022619*:Homo sapiens phospholipase A2	Seq ID No. 79 & 80
110	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	Seq ID No. 81 & 82
	431347	AI133461	Hs.251664	Insulin-like growth factor 2 (somatomedi	Seq ID No. 83 & 84
115	413804	T64682		gb:yc48b02.r1 Stralagene liver (937224)	Seq ID No. 85 & 86
	444163	AI126098		FGENESH predicted RNaseH domain-containi	Seq ID No. 87 - 89
120	444444	AI149332	Hs.14855	ESTs	Seq ID No. 90 & 91
	427747	AW411425	Hs.180655	serine/threonine kinase 12	Seq ID No. 92 & 93
125	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. 94 & 95
	420281	AI623693	Hs.323494	Predicted cation efflux pump	Seq ID No. 96 & 97
130	402305			C19000735*:gij4508027[ref]NP_003414.1 z	Seq ID No. 98 - 100
	436608	AA628980		down syndrome critical region protein DS	Seq ID No. 101 & 102
135	427239	BE270447		ubiquitin carrier protein	Seq ID No. 103 & 104
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	Seq ID No. 105 & 106
140	424008	R02740	Hs.137555	putative chemokine receptor, GTP-binding	Seq ID No. 107 & 108
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	Seq ID No. 109 & 110
145	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No. 111 & 112
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	Seq ID No. 113 & 114
150	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	Seq ID No. 115 & 116
	401093			C12000586*:gij6330167[dtbj]BAA86477.1 {A	Seq ID No. 117 - 119
155	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	Seq ID No. 120 & 121
	449722	BE280074	Hs.23960	cyclin B1	Seq ID No. 122 & 123
160	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. 124 & 125
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	Seq ID No. 126 - 133
165	439606	W79123	Hs.58561	G protein-coupled receptor 67	Seq ID No. 134 & 135
	418543	NM_005329	Hs.85862	hyaluronan synthase 3	Seq ID No. 136 & 137
170	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	Seq ID No. 139 - 141
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	Seq ID No. 142 & 143
175	427335	AA448542	Hs.251677	G antigen 7B	Seq ID No. 144 & 145
	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini	Seq ID No. 146 & 147

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404440			NM_021048:Homo sapiens melanoma antigen,	Seq ID No. 148 & 149
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	Seq ID No. 150 & 151
408380	AF123050	Hs.44532	diubiquitin	Seq ID No. 152 & 153
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	Seq ID No. 154 & 155
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	Seq ID No. 156 & 157
438817	AI023799		ESTs	Seq ID No. 158
421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	Seq ID No. 159 & 160
431515	NM_012152	Hs.258583	EDG-7 (endothelial differentiation, lys	Seq ID No. 161 & 162
433159	AB036898	Hs.150587	kinesin-like protein 2	Seq ID No. 163 & 164
432441	AW292425	Hs.163484	ESTs	Seq ID No. 165
425726	AF085808	Hs.159330	uropod 3	Seq ID No. 166 & 167
448045	AJ297436	Hs.20166	prostate stem cell antigen	Seq ID No. 168 & 169
431846	BE019924	Hs.271580	uropod 1B	Seq ID No. 170 & 171
437044	AL035864	Hs.69617	differentially expressed in Fanconi's an	Seq ID No. 172 & 173
444381	BE387335	Hs.263713	ESTs, Weakly similar to S64054 hypotheti	Seq ID No. 174 & 175
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	Seq ID No. 176 & 177
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	Seq ID No. 178 & 179
400297	AI127076	Hs.306201	hypothetical protein DKFZp564C1278	Seq ID No. 180 & 181
428484	AF104032	Hs.164601	solute carrier family 7 (cationic amino	Seq ID No. 182 & 183
429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. 184 & 185
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	Seq ID No. 186 & 187
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	Seq ID No. 188 & 189
423961	D13666	Hs.136348	perostin (OSF-2os)	Seq ID No. 190 & 191
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	Seq ID No. 192 & 193
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein homolog	Seq ID No. 194 & 195
430486	BE062109	Hs.241551	chloride channel, calcium activated, family member 2	Seq ID No. 196 & 197
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	Seq ID No. 198 & 199
409103	AF251237	Hs.112208	XAGE-1 protein	Seq ID No. 200 & 201
129404	AI267700		ESTs	Seq ID No. 202
403047			NM_005555*:Homo sapiens transmembrane protease	Seq ID No. 203 & 204
439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig), transmem	Seq ID No. 205 & 206

TABLE 12B

35 Pkey: Unique Eos probe identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

40	Pkey	CAT Number	Accession
	413804	1390710_1	T64682 BE168190 BE168256
	427239	27647_1	BE270447 AW409921 BE207288 BE207170 D56355 BE263223 BE408171 BE262243 BE392439 BE292738 BE261776 BE314300 BE267719
45			BE288715 BE513876 BE295291 BE297066 AA210923 BE407519 H51344 BE322905 AW248281 AW250313 T19021 AA355115 AA316879
			BE289633 BE621936 AA290724 AA380031 AA593616 BE301331 W79220 H73020 AW797850 BE274611 BE314315 BE542407 BE562063
			BE312868 BE278817 BE252503 AA426470 M91670 NM_014501 BE264533 AI884863 AI884942 AI678077 AA829937 AI869333 AW273060
			AA906924 AI571293 AW172642 AA582906 AW674596 AW300936 AW615753 AW615587 AW665495 AI859296 AA594105 AA928110
			AI038859 AI589898 AA828316 AA938955 AA283711 AW170665 BE047759 AW732128 AI015067 AW070748 AW248955 AA975490
50			AA211097 AI826097 AA826730 AA994072 AI367867 W74508 AI086474 AA827720 AI922589 AW000868 W58033 AA991461 BE048131
			M91218 AA676186 AA661759 AI123679 AI089508 AW272915 AI566244 AW245061 AA686299 AW250988 AI953468 AI891144 AW089131
			AI471577 AA293354 AA464019 BE044549 T29587 AW956171 BE537716 BE269400 AA918328 AI538087 AA969243 AW075033 BE139361
			AI340599 AI250128 AI247038 BE138953 AW075177 AI307208 BE049086 AW302327 AI054335 AI345565 AI334881 AI252075 AI254494
55			AW075006 AW302733 AW302738 AI054057 AI054217 AI054172 AI054302 AI053722 AI054060 AI054079 AW075181 AI307473 AI312145
			AI340734 AI334909 AW071374 BE138502 AW074809 AW301901 AI251662 AI307559 BE139228 AI254764 AW073049 AI251264 AI802837
			AW271867 AI307442 AW075100 AW073456 AW072496 AI270787 AW271039 AW071307 AI610913 AW071289 AI251232 AI251262
			AW073656 AW072901 AI307493 AI255068 AI251269 AI271496 AI252160 AI271496 AI252427 AW073469 AW071420 AI270156 AI252926 AI252639
			AI252858 AW072520 AW073433 AI340643 AI802854 AI334733 AI563896 AW071311 AI802853 AI289711 AI345036 AW072513 AI348921
			AI307478 AI305762 BE139315 AW271034 AI334886 AI340619 AW470478 BE139260 BE138965 AW302085 BE041872 AW268964
60	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
	436608	42361_3	AA628980 AI126603 BE504035
	438817	465592_1	AI023799 AA826307 AI683094 AI307373 AI870547 AW979007
	444163	593658_1	AI126098 AI184746 AI148521
	456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE166945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 12C

70 Pkey: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

75	Pkey	Ref	Strand	Nt_position
	400844	9188605	Plus	24746-24872,25035-25204
	401093	8516137	Minus	22335-23166

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402305	7328724	Plus	40832-41362
404440	7528051	Plus	80430-81581
404875	9801324	Plus	96588-96732,97722-97831
405033	7107731	Minus	142358-142546

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Table 13
Seq ID NO: 1 DNA sequence:
Nucleic Acid Accession #: NM_002205
Coding sequence: 24..3173

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1	11	21	31	41	51	
CAGGACAGGG	AAGAGCGGG	GCTATGGGA	GCCGGACGCC	AGAGTCCCT	CTCCACGCCG	60
TGCAGCTGCG	CTGGGGCCCC	CGGCGCCGAC	CCCCGCTCGT	GCCGCTGCTG	TTGCTGCTCG	120
TGCCGCGGCC	ACCCAGGGTC	GGGGGCTTCA	ACTTAGACGC	GGAGGCCCA	GCAGTACTCT	180
CGGGGCCCCC	GGGCTCCTTC	TTGCGATTCT	CAGTGGAGTT	TTACCGCGCG	GGAACAGACG	240
GGGTCACTGT	GCTGGTGGGA	GCACCCAAGG	CTAATACCAG	CCAGCCAGGA	GTGCTGCAGG	300
GTGGTGTCTG	CTACCTCTGT	CCTTGGGGTG	CCAGCCCCAC	ACAGTGCACC	CCCATTGAAT	360
TTGACAGCAA	AGGCTCTCGG	CTCCTGGAGT	CCTCACTGTC	CAGCTCAGAG	GGAGAGGAGC	420
CTGTGGAGTA	CAAGTCTCTT	CAGTGGTTTG	GGGCAACAGT	TCCAGCCCTG	GGCTCCTCCA	480
TCTTGGCATG	CGCTCCACTG	TACAGCTGGC	GCACAGAGAA	GGAGCCACTG	AGCGACCCCG	540
TGGGCACCTG	CTACCTCTCC	ACAGATAACT	TCACCCGAAT	TCTGGAGTAT	GCACCTTGCC	600
GCTCAGATTT	CAGCTGGGCA	GCAGGACAGG	GTTACTGCCA	AGGAGGCTTC	AGTGCAGAGT	660
TCACCAAGAC	TGGCCCTGTG	GTTTATAGTG	GACCAGGAAG	CTATTTCTGG	CAAGGCCAGT	720
TCCTGTCTGC	CAGTCAGGAG	CAGATTGCAG	AATCTTATTA	CCCCGAGTAC	CTGATCAACC	780
TGTTTCAGGG	GCAGCTGCAG	ACTCGCCAGG	CCAGTTCCAT	CTATGATGAC	AGCTACCTAG	840
GATACCTCTG	GGCTGTGGT	GAATTCAGTG	GTGATGACAC	AGAAGACTTT	GTGCTGGTGT	900
TGCCCAAGGG	GAACCTCACT	TACGGCTATG	TCACCATCCT	TAATGGCTCA	GACATTCGAT	960
CCCTCTACAA	CTTCTCAGGG	GAACAGATGG	CCTCCTACTT	TGGCTATGCA	GTGGCCGCCA	1020
CAGAAGTCAA	TGGGACGGGG	CTGGATGACT	TGCTGGTGGG	GGCACCCCTG	CTCATGGATC	1080
GGACCCCTGA	CGGCGGGCCT	CAGGAGGTGG	GCAGGGTCTA	CGTCTACCTG	CAGCACCCAG	1140
CCGGCATAGA	GCCACGCCCC	ACCCCTTACC	TCAGTGGCCA	TGATGAGTTT	GGCCGATTGT	1200
CGAGCTCCTT	GACCCCTCTG	GGGACCTGG	ACCAGGATGG	CTACAATGAT	GTGGCCATCG	1260
GGGCTCCTTT	TGGTGGGGAG	ACCCAGCAGG	GAGTAGTGTT	TGTATTTCTT	GGGGGCCCGC	1320
GAGGGCTGGG	CTCTAAGCCT	TCCAGGTTT	TGCAGCCCTT	GTGGGCAGCC	AGCCACACCC	1380
CAGACTTCTT	TGGCTCTGCC	CTTCGAGGAG	GCCGAGACCT	GGATGGCAAT	GGATATCCTG	1440
ATCTGATTTT	GGGCTCCTTT	GGTGTGGACA	AGGCTGTGGT	ATACAGGGGC	CGCCCATCG	1500
TGTCCGCTAG	TGCCCTCCCT	ACCATCTTCC	CCGCGATGTT	CAACCCAGAG	GAGCGGAGCT	1560
GCAGCTTAGA	GGGGAACCTT	GTGGCTGCA	TCAACCTTAG	CTTCTGCCTC	AATGCTTCTG	1620
GAACACAGT	TGCTCACTCC	ATTGGTTTCA	CAGTGGAACT	TCACTGGAC	TGGCAGAAGC	1680
AGAAAGGAGG	GGTACGGCGG	GCAGTGTTC	TGCCCTCCAG	GCAGCAACC	CTGACCCAGA	1740
CCCTGTCTAT	CCAGAATGGG	GCTCGAGAGG	ATTGCAGAGA	GATGAAGATC	TACCTCAGGA	1800
ACGAGTCAGA	TTTCGAGAC	AACTCTCGC	CGATTCAAT	CGCTCTCAAC	TTCTCTTGG	1860
ACCCCAAGC	CCAGTGGAC	AGCCACGGCC	TCAGGCCAGC	CCTACATTAT	CAGAGCAAGA	1920
GCGCGATAGA	GGACAAGGCT	CAGATCTTGC	TGGACTGTGG	AGAAGACAAC	ATCTGTGTGC	1980
CTGACCTGCA	GCTGGAAGTG	TTTGGGGAGC	AGAAACCATG	GTACCTGGGT	GACAAGAATG	2040
CCCTGAACCT	CACCTTCCAT	GCCCAAGATG	TGGGTGAGGG	TGGCGCCTAT	GAGGCTGAGC	2100
TTCTGGGTAC	GGCCCTTCCA	GAGGCTGAGT	ACTCAGGACT	CGTCAGACAC	CCAGGGAATC	2160
TCTCCAGCCT	GAGCTGTGAC	TACTTTGCCG	TGAACCAAG	CCGCTGCTGT	GTGTGTGACC	2220
TGGGCAACCC	CATGAAGGCA	GGAGCCAGTC	TGTGGGTGG	CCTTCGTTT	ACAGTCCCTC	2280
ATCTCCGGGA	CACCTAAGAA	ACCATCCAGT	TTGACTTCCA	GATCCTCAGC	AAGAATCTCA	2340
ACAACTCGCA	AAGCGAGCTG	GTTTCCCTTC	GGCTCTCCGT	GGAGGCTCAG	GCCCAAGTCA	2400
CCCTGAACGG	TGCTCCAAG	CCTGAGGCAG	TGCTATTCCC	AGTAAGCGAC	TGGCATCCCC	2460
GAGACCAAGC	CCAGAGCTCC	ATTAGCCAGG	GTGTGTGGA	ACTCAGCTGT	CCCCAGGCTC	2520
TCAACCAAGG	CCAGAGCTCC	TATGTGACCA	GAGTTACGGG	ACTCAACTGC	ACCAACCAATC	2580
TGAAAGGTCA	GCAGCTCCTA	CTGAGGTTGG	ATCCCGAGGG	TTCCCTGCAC	CACCAGCAAA	2640
ACCCCATTA	CCCAAGGGC	AGCTCTGCTT	CCTCGGGACC	TCAGATCCTG	AAATGCCCGG	2700
AACGGGAAGC	TCCAAGCCGC	CGCTGTGAGC	TCCGGCCCCC	GCACCAACAA	GAGAGCCMAA	2760
AGGCTGAGTG	TTTCAGGCTG	CGCTGGGCCA	AGACTTTCTT	GCAGCGGGAG	CACCAGCCAT	2820
GTCTGAGATT	GCATTTCCGA	GTGTACAAAG	CCCTGAAGAT	GCCCTACCGA	ATCCTGCCTC	2880
TTAGCTGCA	GTGTGAGGCT	CGTCAGGTGG	CCACAGCTGT	GCAATGGACC	AAGGCGAAG	2940
GGCAGCTGCC	CCAAAAGAG	TGGATCATCA	TCTAGCCAT	CCTGTTTGGC	CTCCTGCTCC	3000
GCAGCTATGG	CGTCCCACTG	CTCTACAAGC	TTGGATTCTT	CAAAOGCTCC	CTCCCATATG	3060
TAGGTCTACT	CATCTACATC	CTCCAGCCAC	CTCTGATGCC	TGAGTCTCTC		3120
GCACCGCCAT	GGAAAAGCT	TGAAGAACCA	GTCCCCCAC	CCTCATTTCTA	CTGAAAAGGA	3180
CAATTTGAGA	CTCCCATCTC	AGGTGCTGAC	GGCCAGGGAG	AAGCTCTCT	CCCCAGCCCA	3240
GGGGTCTGGG	TACTTCTTGA	GAGCCAGGGG	GGTGAGGAGC	TGGGGATCCC	TCCCCCCCAT	3300
GAGACATACT	TGAAGGGCCA	GAGCCAGGGG	GGTGAGGAGC	TGGGGATCCC	TCCCCCCCAT	3360
GCAGTGTGAA	GGACCTCTGT	TTACACATAC	CCTCTTCATG	GATGGGGGAA	CTCAGATCCA	3420
GGGACAGAGG	CCAGCCTCC	CTGAAGCCTT	TGCATTTTGG	AGAGTTTCTT	GAAACAACTG	3480
GAAAGATAAC	TAGGAAATCC	ATTACAGATT	CTTTGGGCCA	GACATGCCAC	AAGGACTTCC	3540
TGTCCAGCTC	CAACCTGCAA	AGATCTGTCC	TCAGCCTTGC	CAGAGATCCA	AAAGAAGCCC	3600
CCAGTAAGAA	CCTGGAACCT	GGGAGTTTAA	GACCTGGCAG	CTCTGGACAG	CCCCACCTTG	3660
GTGGGCCAAC	AAAGAACACT	AACTATGCAT	GGTGCCCCAG	GACCACTCTA	GGACAGATGC	3720
CACAAGGATA	GATGCTGGCC	CAGGGCCAGA	GCCCACTCTC	AAGGGGAATC	AGAACTCAAA	3780
TGGGGCCAGA	TCCAGCCTGG	GGTCTGGAGT	TGATCTGGAA	CCGAGACTCA	GACATTGGCA	3840
CCAAATCCAGG	CAGATCCAGG	ACTATATTGG	GGCCTGTCTC	AGACCTGATC	CTGAGGCCCC	3900
AGTTACACCT	GATTTAGGAG	AAGCCAGGAA	TTTCCCAGGA	CCTGAAGGGG	CCATGATGGC	3960
AACAGATCTG	GAACCTGAGC	CTGGCCAGAC	ACAGGCCCTC	CCTGTTCCCC	AGAGAAAGGG	4020
GAGCCCACTG	TCCTGGGCCCT	GCAGAAATTT	GGTTCTGCCT	GCCAGCTGCA	CTGATGCTGC	4080
CCCTCATCTC	TCTGCCCAAC	CCTTCCCTCA	CCTTGGCACC	AGACACCCAG	GACTTATTTA	4140
AACCTCTGTT	CAAGTGCAAT	AAATCTGACC	CAGTGCCCCC	ACTGACCAGA	ACTAGAAAAA	4200

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AAAA

Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_002196.1

1 11 21 31 41 51
MGSRTFESPL HAVQLRWGPR RRPPLVPLLL LHVPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
10 GFSVEFYRPG TDGVSVLVGA PKANTISQPGV LQGGAVLYCP WGASPTQCTP IEFDSKGSRL 120
LESSLSSESSE EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCTYLS 180
DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFKTGTGRVV LGGPGSYFWQ GQILSATQEQ 240
IABSYYPEYL INLVQQLQT RQASSIYDDS YLGYSVAVGE FSGDDTDEFV AGVPKGNLTY 300
15 GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ 360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDEFB RFGSSSLTPLG DLDQDGYNDV AICAPFGGET 420
QQGVVYVYFPG GPGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRDLDDNG YPDLVGSFSG 480
VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLBGNPV ACINLSFCLN ASGKHVADSI 540
20 GFTVELQLDW QKQKGVVRRR LFLASQATL TQTLIIQNGA REDCREMKIY LRNESEFRDK 600
LSPIHIALNF SLDPQAPVDS HGLRPAHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660
GEQNHVYLG D KNALNLTFHA QNVGEGGAYE AELRVTAPE AEYSGLVHRP GNFFSLSCDY 720
FAVNQSRLLV CDLGNPMKAG ASLWGLRFT VPHLRDTKKT IQPDFQILSK NLNNSQSDVV 780
SFRLSVEBAQ QVTINGVSKP EAVLFPVSDW HPRDQPKKE DLGPAVHHVY ELINQGPSSI 840
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPESGLHH QQKREAPSR 900
25 SASSGPQILK CPBABCFLIR CELGPLHQOE SQSLQLHFRV WAKTFLOREH QPFSLQCEAV 960
YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020
YKLGFFKRSL PYGTAMEKAQ LKPPATSDA

Seq ID NO: 3 DNA sequence:
Nucleic Acid Accession #: NM_002425
Coding sequence: 23..1453

1 11 21 31 41 51
35 AAAGAAGGTA AGGCGAGTGA GAATGATGCA TCTTGCAITC CTTGTGCTGT TGTGTCTGCC 60
AGTCTGCTCT GCCTATCCTC TGAGTCGGCC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
TGCCACAGCAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTT TTAATAAAAT CCAAGGAATG CAGAAGTTCC TTGGGTGTTGA 240
40 GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCTTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT 420
TGAGAAAGCT CTGAAAGTCT GGAAGAGAGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTTCCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
45 TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCTCT 660
CGTGTGCTGT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACACCTGAAGC 720
TTTGTGTATC CCACTCTACA ACTCATTAC AGAGCTCGCC CAGTTCCGCC TTTCCGAAGA 780
TGAITGTAAT GGCATTCACT CTCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT 840
50 GGTGCCACCA AAATCTGTTT CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
GTCTCTCGAT GCCATCAGCA CTCTGAGGG AGAATATCTG TTCTTTAAAG ACAGATATT 960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTTCA TTGATTTCTG CATTTTGGCC 1020
CTCTCTTCCA TCATATTTTG ATGCTGCATA TGAAGTTAAC AGCAGGGACA CCGTTTTTAT 1080
TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAATGAG GTACAAGCAG GTTATCCAAG 1140
55 AGGCATCCAT ACCCTGGGTT TTCCTCCAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200
CAAGGAAAAAG AAGAAAACAT ACTTCTTTGC AGCGGACAAA TACTGGAGAT TTGATGAAA 1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTT CAGGAGTTGA 1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC 1380
ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GTGCACAC ATATTAAAGA GTAACAGCTG 1440
60 GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
ATTATTATC TAAATGTATTA TGAGCCAAAA TGGTTAATTT TTCCTGCATG TTCTGTGACT 1560
GAGAAGATG AGCCTTGCA ATATCTGCAT GTGTCTGAA GAATGTTTCT GGAATTCTTC 1620
ACTTGCTTTT GAATTGCAT TAACAGAAAT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCTGTTC 1740
CTT

Seq ID NO: 4 Protein sequence:
Protein Accession #: NP_002416

1 11 21 31 41 51
70 MMHLAFLVLL CLPVCASAYPL SGAKEEDSN KDLAQQYLEK YYNLEKDVVK FRRKDSNLIV 60
KKIQGMQKFL GLEVTGKLDL DTLEVMRKPR CGVPDVGHFS SPPGMPKWRK THLTYRIVNY 120
TPDLPRDAVD SAIEKALKVW EEVTPLTFSR LYEGEADIMI SFAVKEHGF YSFDGPGHSL 180
75 AHAYPPGPGY YGDIHFDDDE KWTEDASGTN LFLVAHELGL HSLGLFHSAN TEALMYPLYN 240
SFTELAQFRL SQDDVNGIQS LYGPPPPASTE EPLVETKSV SGSEMPAKCD PALSFDAIST 300
LRGEYLFEDK RYFWRSHWN PEPEFHLSA FWPSLPSYLD AAYEVNSRDT VFIFKGNFV 360
AIRGNEVQAG YPRGIHTLGF PPTIRKIDAA VSDKEKKKTY FFAADKYWRF DENSQSMEQG 420

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FPRLIADDFP GVEPKVDAVL QAFGFFYFFS GSSQFEFDPN ARMVTHILKS NSWLHC

Seq ID NO: 5 DNA sequence:
Nucleic Acid Accession #: NM_002421
Coding sequence: 72..1481

5

	1	11	21	31	41	51	
10	GGGATATTGG	AGTAGCAAGA	GGCTGGGAAG	CCATCACTTA	CCTTGCACTG	AGAAAGAAGA	60
	CAAPGGCCAG	TATGCACAGC	TTTCCTCCAC	TGCTGCTGCT	GCTGTTCTGG	GCTGTGGTGT	120
	CTCACAGCTT	CCCAGCGACT	CTAGAAACAC	AAGAGCAAGA	TGTGGACTTA	GTCCAGAAAT	180
	ACCTGGAAAA	ATACTACAAC	CTGAAGAATG	ATGGGAGGCA	AGTTGAAAAG	CGGAGAAATA	240
	GTGCCCCAGT	GGTIGAAAAA	TTGAAGCAAA	TGCAGGAATT	CTTTGGGCTG	AAAGTGACTG	300
15	GGAAACCAGA	TGCTGAAACC	CTGAAGGTGA	TGAAGCAGCC	CAGATGTGGA	GTGCCCTGATG	360
	TGGCTCAGTT	TGCTCTCACT	GAGGGGAACC	CTCGCTGGGA	GCAACACATC	CTGACCTACA	420
	GGATTGAAAA	TTACACGCCA	GATTTGCCAA	GAGCAGATGT	GGACCATGCC	ATTGAGAAAG	480
	CCITCCAAC	CTGGAGTAAT	GTCACACCTC	TGACATTAC	CAAGGTCTCT	GAGGGTCAAG	540
	CAGACATCAT	GATATCTTTT	GTCAGGGGAG	ATCATCGGGA	CAACTCTCCT	TTTGATGGAC	600
20	CTGGAGGAAA	TCTTGCTCAT	GCTTTTCAAC	CAGGCCCAGG	TATTGGAGGG	GATGCTCATT	660
	TTGATGAAGA	TGAAGGTGG	ACCAACAATT	TCAGAGAGTA	CAACTTACAT	CGTGTGCGG	720
	CTCATGAAC	CGGCCATTCT	CTTGGACTCT	CCCATTCTAC	TGATATCGGG	GCTTTGATGT	780
	ACCCTAGCTA	CACCTTCACT	TGCGATGTTT	AGCTAGCTCA	GGATGACATT	GATGGCATCC	840
	AAGCCATATA	TGGACCTTCC	CAAAATCCTG	TCCAGCCCAT	CGGCCACAA	ACCCCAAAAG	900
25	CGTGTGACAG	TAAGCTAAC	TTTGATGCTA	TAACCTACGT	TGGGGAGGAA	GTGATGTTCT	960
	TTAAAGACAG	ATTCTACATG	CGCACAAATC	CCTTCTACCC	GGAGGTTGAG	CTCAATTTCA	1020
	TTTCTGTTTT	CTGCCACAA	CTGCCAAATG	GGCTTGAAGC	TGCTTACGAA	TTTGCCGACA	1080
	GAGATGAAGT	CCGTTTTTTC	AAAGGGAATA	AGTACTGGGC	TGTTTCAAGG	CAGAATGTGC	1140
	TACACGAGTA	CCCCAAGGAC	ATCTACAGCT	CCTTTGGCTT	CCCTAGAACT	GTGAAGCATA	1200
30	TGCGATGCTG	TCITTTCTGAG	GAAACACCTG	GAAAAACCTA	CTTCTTTGTT	GCTAACAAAT	1260
	ACTGGAGGTA	TGATGAATAT	AAACGATCTA	TGGATCCAGG	TTATCCCAAA	ATGATAGCAC	1320
	ATGACTTTCC	TGGAATTGGC	CACAAAGTTG	ATGCAGTTTT	CATGAAGAGT	GGATTTTTCT	1380
	ATTTCTTTCA	TGGAACAAGA	CAATACAAAT	TTGATCTCTA	AACGAAGAGA	ATTTTGACTC	1440
	TCCAGAAAGC	TAATAGCTGG	TCAACTGCA	GGAAAAATTG	AACATTACTA	ATTTGAATGG	1500
35	AAAACACATG	GTGTGAGTCC	AAAGAAGGTG	TTTTCTGAA	GAACGTGCTA	TTTTCTCAGT	1560
	CATTTTTAAC	CTCTAGAGTC	ACTGATACAC	AGAATATAAT	CTTATTTATA	CCTCAGTTTG	1620
	CATATTTTTT	TACTATTTAG	AATGTAGCCC	TTTTTGTACT	GATATAATTT	AGTTCACAA	1680
	ATGCTGGGTA	CAAAAAGTCA	AGTTTGTGGC	TTATGGATTC	ATATAGGCCA	GAGTTGCAAA	1740
40	GATCTTTTCC	AGAGTATGCA	ACTCTGACGT	TGATCCCAGA	GAGCAGCTTC	AGTGACAAAC	1800
	ATATCCTTTC	AAGACAGAAA	GACACAGGAG	ACATGAGTCT	TTGCCGGAGG	AAAAGCAGCT	1860
	CAAGAACACA	TGTGCAGTCA	CTGGTGTGAC	CCTGGATAGG	CAAGGGATAA	CTCTTCTAAC	1920
	ACAAAATAAG	TGTTTTATGT	TTGGAATAAA	GTCAACTTGG	TTTCTACTGT	TTT	

45

Seq ID NO: 6 Protein sequence:
Protein Accession #: NP_002412

	1	11	21	31	41	51	
50	MHSFPPLLLL	LFMGVVSHSF	PATLETQEQD	VDLVQKYLEK	YYNLKNDGRQ	VEKRRNSGPV	60
	VHKLKMQEAF	FGLKVTGKPD	AETLKVMKQP	RCGVDPVAQF	VLTEGNRNE	QTHLTYRIEN	120
	YTPDLPRADV	DHAIEKAFQL	WSNVTPLTFT	KVSEGGADIM	ISFVRGDHRD	NSPFDGPGGN	180
	LAHAFQPPGP	IGDHAHFDED	ERWTNNFREY	NLHRVAABEL	GHLGLSHST	DIGALMYPSY	240
55	TFSGDVQLAQ	DDIDGIQAIY	GRSQNPVQPI	GPQTPKACDS	KLTFDAITTI	RGEVMFFKDR	300
	FVMRTNPFYP	EVELNFIISV	WPQLPNGLFA	AYEFADRDEV	RFFKGNKYWA	VQQQNVLHGY	360
	PKDIYSSPFG	PRTVKHIDAA	LSEENTGKTY	FFVANKYWRY	DEYKRSMDFG	YPKMIAHDFP	420
	GIGHKVDAVF	MKDGFFYFFH	GTRQYKFDPK	TKRILTLQKA	NSWFNCRKN		

60

Seq ID NO: 7 DNA sequence:
Nucleic Acid Accession #: NM_014331
Coding sequence: 1..1506

	1	11	21	31	41	51	
65	ATGTCAGAA	AGCCTGTTGT	GTCCACCATC	TCCAAAGGAG	GTTACCTGCA	GGGAAATGTT	60
	AACGGGAGGC	TGCCTTCCCT	GGGCAACAAG	GAGCCACCTG	GGCAGGAGAA	AGTGACGCTG	120
	AAGAGGAAAG	TCACTTTACT	GAGGGGAGTC	TCCATTATCA	TGGCACCATT	CATTGGAGCA	180
70	GGAATCTTGA	TCTCTCTTAA	GGGCGTGCTC	CAGAACACGG	GCAGCGTGGG	CATGTCTCTG	240
	ACCATCTGGA	CGGTGTGTGG	GCTCCTGTCA	CTATTGGAG	CTTTGTCTTA	TGCTGAATTG	300
	GGAACAACCTA	TAAAGAAATC	TGGAGGTCAT	TACACATATA	TTTTGGAAGT	CTTTGGTCCA	360
	TTACCACTCT	TTGTACGAGT	CTGGGTGGAA	CTCCTCATAA	TACGCCCTGC	AGCTACTGCT	420
	GTGATATCCC	TGGCATTGGG	ACGCTACATT	CTGGAACCAT	TTTTTATTCA	ATGTGAAATC	480
75	CCTGAACCTG	CGATCAAGCT	CATTACAGCT	GTGGGCATAA	CTGTAGTGAT	GGTCTCTAAT	540
	AGCATGAGTG	TCAGCTGGAG	CGCCCGGATC	CAGATTTTCT	TAACCTTTTG	CAAGCTCACA	600
	GCAATTCTGA	TAATTATAGT	CCCTGGAGTT	ATGCAGCTAA	TTAAAGGTCA	AACGCAGAAC	660
	TTTAAAGACG	CGTTTTTCAG	AAGAGATTCA	AGTATTACGC	GTTTGCCACT	GGCTTTTTTAT	720

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TATGGAATGT ATGCATATGC TGGCTGGTTT TACCTCAACT TTGTTACTGA AGAAGTAGAA 780
AACCCCTGAAA AAACCATTCCT CCTTGCAATA TGTATATCCA TGCCCAATTGT CACCATTGGC 840
TATGTGCTGA CAAATGTGGC CTACTTTACG ACCATTAATG CTGAGGAGCT GCTGCTTTCA 900
AATGCAGTGG CAGTGACCTT TTCTGAGCGG CTACTGGGAA ATTTCTCATT AGCAGTTCCG 960
ATCTTTGTTG CCCTCTCCTG CTTTGGCTCC ATGAACGGTG GTGTGTTTGC TGTCTCCAGG 1020
TTATTCTATG TTGCGTCTCG AGAGGGTCAC CTTCCAGAAA TCCTCTCCAT GATTCATGTC 1080
CGCAAGCACA CTCTCTACCC AGCTGTTATT GTTTTGCAACC CTTTGACAAT GATAATGCTC 1140
TTCTCTGGAG ACCTCGACAG TCCTTTGAAT TTCCTCAGTT TTGCCAGGTG GCTTTTTTAT 1200
GGGCTGGCAG TTGCTGGGCT GATTTATCTT CGATACAAAT GCCCAGATAT GCATCGTCTC 1260
TTCAAGGTGC CACTGTTCAAT CCCAGCTTTG TTTTCCTTCA CATGCCCTCT CATGGTTGCC 1320
CTTTCCCTCT ATTCGGACCC ATTTAGTIACA GGGATTGGCT TCGTCATCAC TCTGACTGSA 1380
GTCCCTGCGT ATTATCTCTT TATTATATGG GACAAGAAAC CCAGGTGGTT TAGAATAATG 1440
TCAGAGAAAA TAACCAGAAC ATTACAAATA ATACTGGAAG TTGTACCAGA AGAAGATAAG 1500
TTATGAACTA ATGCACTTGA GATCTTGCCA ATCTGCCCAA GGGGAGACAC AAAATAGGGA 1560
TTTTTACTTC ATTTTCTGAA AGTCTAGAGA ATTACAACCT TGGTGATAAA CAAAAGGAGT 1620
CAGTTATTTT TATTTCATATA TTTTAGCATA TTCGAACTAA TTTCTAAGAA ATTTAGTTAT 1680
AACTCTATGT AGTTATAGAA AGTGAATATG CAGTTATTCT ATGAGTCGCA CAATTCTTGA 1740
GTCTCTGATA CCTACCTAAT GGGGTTAGGA GAAAGACTA GACAATTACT ATGTGGTCAT 1800
TCTCTACAA ATATGTTAGC ACGGCAAGA ACCTTCAAA TGAAGACTGA GATTTTCTG 1860
TATATATGGG TTTTGTAAG ATGGTTTAC ACACTACAGA TGCTATACT GTGAAAAGT 1920
TTTTCAATTC TGAAGAAAAG CATACATCAT GATTATGGCA AAGAGGAGAG AAAGAAATTT 1980
ATTTTACATT GACATTGCAT TGCTTCCCT TAGATACCAA TTTAGATAAC AAACACTCAT 2040
GCTTTAATGG ATTATACCA GAGCACTTTG AACAAAGTC AGTGGGAGT GTTGAATACA 2100
TTAAAGAAGA GTTCTAGGG GCTACTGTTT ATGAGACACA TCCAGGAGT ATGTTTAAGT 2160
AAAAATCCTT GAGAATTAT TATGTCAGAT GTTTTTTCT TCAATTACAG GAAGTTTATG 2220
TTATCTGTCA TTTTCTTTT TCACATCAGT TTGATCAGGA AAGTGTATAA CACATCTTAG 2280
AGCAAGAGTT AGTTTGTAT TAAATCCTCA TTAGAACAA CACCTGTTTC ACTAATAACT 2340
TACCCTGAT GAGTCTATCT AAACATATGC ATTTTAAGCC TTCAAATTAC ATTATCAACA 2400
TGAGAGAAAT AACCAACAAA GAAGATGTTT AAAATAATAG TCCCATATCT GTAATCATAT 2460
CTACATGCAA TGTTAGTAAT TCTGAAAGTT TTAAATTTA TGGCTATTTT TACACGATGA 2520
TGAATTITGA CAGTTTGTGC ATTTTCTTTA TACATTTTAT ATTCTTCGT TAAAATATCT 2580
CTTCAGATGA AACTGTCCAG ATTAATTAGG AAAAGGCATA TATTAACATA AAAATTGCAA 2640
AAGAAATGTC GCTGTAAATA AGATTACAA CTGATGTTTC TAGAAAATTT CCACTTCTAT 2700
ATCTAGGCTT TGTGAGTAAT TTCCACACCT TAATTATCAT TCAACTTGCA AAAGAGACAA 2760
CTGATAAGAA GAAATTTGAA ATGAGAACTCT GTGGATAAGT GTTTGTGTTT AGAAGATGTT 2820
GTTTGGCCAG TATTAGAAAA TACTGTGAGC CGGGCATGGT GGCTTACATC TGTAAATCCCA 2880
GCACCTTGGG AGGCTGAGGG GGTGGATCAC CTGAGGTCGG GAGTTCTAGA CCAGCCTGAC 2940
CAACATGGAG AAACCCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGCCAT 3000
GCTGGTAATC TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTGAAC CCGGAGGCG 3060
GAGGTTGACG TGAGCCAAGA TTGCACCACT GTACTCCAGC CTGGGTGACA AAGTCAGACT 3120
CCATCTCCAA AAAAAAAAAA AAAA

45 Seq ID NO: 8 Protein sequence:
Protein Accession #: NP_055146

50
55
60

1 11 21 31 41 51
MVRKPVVSTI SKGGYLGQNV NGRLP SLGNK EPPGQEKVQL KRKVTLRGV SIIIGTIIGA 60
GIFISPKGV L QNTGSVGM SL TIWTVCGVLS LFGALS YAE L GTTIKKS GGH YTYILEVFGP 120
LPAFVRVWVE LLII RPAATA VISLAFGRYI LEPFFIQCEI PELA IKLITA VGITVVMVLN 180
SMSVSW SARI QIFLT FCKLT AILII IVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY 240
YGM YAYAGWF YLNFVITEVE NPEKTIPLAI CISM AIVTIG VVLIN VAYFT TINAE LLLS 300
NAVAVTF SER LLGN FSLAVP IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHP 360
RKHTPLPAVI VLHPLTMI ML FSGDLDSL LN FLSFARWLFI GLAVAGLIYL RYKCPDMHRP 420
FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLTC VPAYYLFIIW DKKPRWFRIM 480
SEKITRTLQI ILEVVPEDK L

60 Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: FGENESH
Coding sequence: 1..546

65
70
75

1 11 21 31 41 51
ATGGCCTTGG GCAGCTCCGC CCTGTGGCT TTGCAGGSTA ATGCCCACTT CCTGCTGCT 60
TTCATGGCTG GCATTAAAGT TCTGTGGCTT TTCCAGGTAG TCCCCCTGGG GCTCCCCGAG 120
TTGGTGCAAA GCCTCCTGGG TGGAGCTCGA ACTGAAACTC GCTTTGTGCC CGCAGCCCTG 180
CAGCTCGCGG GTGCCCCGCA CCTGCCCGCT GGGTCTGTG CTTTGAAGA GAGCACTTGC 240
GGCTTTGACT CCGTGTGGC CTCTCTGCCG TGGATTTTAA ATGAGGAAGG CCAGCAACCT 300
TTCTGTCCTT CAGGAGACAT GTCTGACTGG GACTACTGGG TTGGCTGGCG GAAGTTAATT 360
CATTTCTCTT TGAGCACTCC AGGGTGGAGC AGGCAGGTTA GGCTCCAGTT GTTCCAGCTT 420
CAGTTTGTC AAGGCCAGAA CTTGGACGTA ACAGTGTACT GCAGGCTCCA GGCAGTGAG 480
AAACCCCTTG AAATCGGTT CATGGTTCCA TTCACCTTCA TGTACTGGAT CCACCATGGA 540
AAGTAG

Seq ID NO: 10 Protein Sequence
Protein Accession #: FGENESH

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1 11 21 31 41 51
5 MALGSSAPVA LQGNAPFAA FMAGIKLWL FQVPLGLPE LVQRLLGGAR TETRFVPAAL 60
QLAGALDLPA GSCAFESTC GFDSVLASLP WILNEBQQP FWSSGDMSDW DYWWGWRKLI 120
HSPLSTPGWS RQVRLQLFQL QFVKQQLDV TVYCRLQGSSE KPFETGSMVP FTFMYWIHHG 180
K

10 Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 461-3286

1 11 21 31 41 51
15 GCCGCCCCCTG AGCAGCCTCG CCTTCGCCTC CCGCGTTTCC TGCCGTCCTCG CCTCCCCCGG 60
CCGAGCTCCA GGGGCTGCCG CCTAGCAGCT CCCGGCGGGA GAGCGGTTC A GAGCGCGCAC 120
GGGGCGGGC GAGGCGGCGC CGGTGCGGGG CGGCGCGCTT GGAGAGAGGC GCGCGCGGAG 180
AGCGCGGGCC CCTCTCCCGC GTTGTCTCGC TTGCTCCCGC CCTCCCGCAC TCCGCTCGCT 240
20 CCCACCCCTT CCGCGGTGA TTGATCCGTC ACGGCGCGCG CCGCTGCCGC CGCGCGCGCC 300
GCGGCGGTTC TGAGCCGAGC CGGAACCTTA GCCCGAGAGC GAGCGCGGGC CCGGCGCGGC 360
GCCATTGCGC GGGCGCGCGG GGAAGACCTT GCGCGCGGGC GCGCGCGCGC GCCAGGCCAT 420
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CGGCGAGCCC GGGCGCGCGC CTCTGCGGCC CGGGCGCTGG GGCTGGGCGC GGGGCGCCCC 540
25 GCTGTGCGCC CTGCTGCTGC CTCTGCGGCC CGGGCGCTGG GGCTGGGCGC GGGGCGCCCC 600
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30 CTTGATGGTG TTTGGAGGCG TCTGTCCATC COTCACATCC ATCAATGCAG AGTCCCTCCA 900
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35 AGACACCGAG AGCTTCTCCA ACGATCCCTG TACCAAGTGC AAAAAGCTGA AGGGAATGA 1200
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CTTCAACTAC ACGGACCACA CGCTGGGCGG GATCATCTCT AATGCCATGA ACGAGACCAA 1680
CTTCTTGGGG GTACGCGGCT AAGTTGTATT CCGGAATGGG GAGAGAATGG GGACCATTA 1740
45 ATTTACTCAA TTTCAAGACA GCAGGGAGGT GAAGGTGGGA GAGTACAACG CTGTGGCCGA 1800
CACACTGGAG ATCATCAATG ACACCATCAG GTTCCAAGGA TCCGAACCA CAAAGACAA 1860
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Protein Accession #: EOS sequence

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Seq ID NO: 13 DNA sequence
Nucleic Acid Accession #: NM_001565.1
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5 Seq ID NO: 14 Protein sequence:
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GTAGCACCAT GGCAGGACTG GGGGAACCTG AGTGTCTTGT CTGTATCCCT GTTGTGAGGT 1860
TCCTTCCAGG GGCTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCCT CAGCCCTGGC 1920
TGAGCAACTG GGTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCCTGC 1980
ATCTGTCTGC TTCTGGCTG ACAATCCTGG AATCTGTTT TCCGAATCC AGGCCAAAAA 2040
GTTCAAGTGC AATGGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGAGGGCTG 2100
CAACATACCT CAATCTGTTC CCAGGCCGGA TCCTCCTGAA GCCCTTTTCG CAGCACTGCT 2160
ATCTCCAAA GGCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCCTTTTTT 2220
TTTTTAACT GAGGATTGTC ATTAAACACA GTTGTTTTCT
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Seq ID NO: 18 Protein sequence:
Protein Accession #: NP_005931.1

25
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35

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1 11 21 31 41 51
| | | | |
MAPAAWLRS AARALLPPL LLLQLPPL ARALPPDVH LHAERRGPQ WHAALPSSPA 60
PAPATQEAER PASSLRPPRC GVPDPDSGLS ARNRQKRFVL SGRWRKEDL TYRILRFPWQ 120
LVQEQVRQTM AEALKVWSDV TFLTFTVEHE GRADIMIDFA RYVHGDDLFF DPGGILAHA 180
FFPKTHREGD VHPDYDETWT IGDDQGTDL LQVAAHEFGHV LGLQHTTAAK ALMSAFYTFR 240
YPLSLSPDDC RGVOHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDPAD PDACEASFDA 300
VSTIRGELFF KAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAFEDA QGHIWFFQGA 360
QYWWYDGEKP VLGPAPLTBL GLVRFPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVDS 420
PVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFDP VKVKALEGFP RLVGPDFFGC 480
AEPANTFL
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Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: NM_005794.1
Coding sequence: 434-1276

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45
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55
60
65

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1 11 21 31 41 51
| | | | |
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CTCACTCGTT GGGTCCGTGC CACCTTTAAG AGCTGTAAAC CTCACCGCGA AGGTCTGCAA 120
CTTCACTCCT GGGGCCAGCA AGACCACGAA TGCAACGAGA GGAATGAACA ACTCTGGACA 180
CACCATCTTT AAGAACCGTA ATACTCACCG CAAGGGCTCT CAACTTCATT CTTGAAGTCA 240
GTGAGGCCAA GAACCCATCA ATTCCGTACA CATTTTGGTG ACTTTGAAGA GACTGTCAAC 300
TATCACCAAG TGGTGAGACT ATTGCCAAGC AGTGAGACTA TTGCCAAGTG GTGAGACCAT 360
CACCAGCGG TGAGACTATC AOCATATGCC AAGTGGCCTG ATTGAGCAGG AAGCATCTCA 420
GACACCAACC ACTATGCTGT CAGCAGTTGC CCGGGGCTAC CAGGGCTGGT TTCATCCCTG 480
TGCTAGGCTT TCTGTAGGCA TGAGCAGCAC CGGGATAGAC AGGAAGGGCG TCCTGGCTAA 540
CCGGGTAGCC GTGGTCAAGG GGTCCACCA CCGGATCGGC TTTGCCATCG CCCGACGTCT 600
GGCCCGGGAC GGGGCCACG TGGTCATCAG CAGCCGGAAG CAGCAGAAGC TGGACCGGGC 660
CATGGCCAAG CTGCAGGGGG AGGGGCTGAG TGTGGCGGGC ATTGTGTGCC ACGTGGGGAA 720
GGCTGAGGAC CGGAGCAGC TGGTGGCCAA GGCCCTGGAG CACTGTGGGG GCCTCGACTT 780
CCTGGTGTGC AGCGCAGGGG TCAACCTCTT GGTAGGAGC ACTCTGGGGA CCAGTGAGCA 840
GATCTGGGAC AAGATCCTAA GTGTGAACGT GAAGTCCCCA GCCCTGTCTG TCAGCCAGTT 900
GCTGCCCTAC ATGAGAAACA GGAGGGGTGC TGTATCCTG GTCTCTTCCA TTGCAGCTTA 960
TAATCCAGTA GTGGCGCTGG GTGTCTACAA TGTGAGCAAG ACAGCGCTGC TGGGTCTCAC 1020
TAGAACACTG GCATTGGAGC TGGCCCCCAA GGACATCCG GTAAACTGCG TGGTTCAGG 1080
AATTATAAAA ACTGACTTCA GCAAGGTGTT TCATGGGAAT GAGTCTCTCT GGAAGAAGTT 1140
CAAGGAACAT CATCAGCTGC AGAGGATTGG GGAGTCAGAG GACTGTGAGG GAATCGTGTC 1200
CTTCTGTGTC TCTCCAGATG CCAGCTACGT CAACGGGGAG AACATTGCGG TGGCAGGCTA 1260
CTCCACTCGG CTCTGAGAGC AGTGGGGGCG GCTGCGTAGC TGTGTCCTCA GCCCAGGAGC 1320
CTGAGGGGGT GTCTAGGTGA TCATTGGGAT CTGGAGCAGA GTCTGCCATT CTGCCAGACT 1380
AGCAATTTGG GGGCTTACTC ATGCTAGGCT TGAGGAAGAA GAAAAACGCT TCGCATTTCT 1440
CC
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Seq ID NO: 20 Protein sequence:
Protein Accession #: NP_005785.1

70
75

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1 11 21 31 41 51
| | | | |
MLSAVARGYQ GWFHPCARLS VRMSSTGIDR KGVLANRVAV VTGSTSGIGF AIARRLRDGC 60
AHVVISRRKQ QNVDRAMAKL QGEGLSVAGI VCHVGKAEDR EQLVAKALEH CGGVDFLVCS 120
AGVNPVVGST LGTSEQIWDK ILSVNVKSPA LLLSQLLPYM ENRRGAVILV SSIAAYNPVV 180
ALGVYVNSKT ALLQLTRTLA LELAPKDIRV NCVVPGIIKT DFSKVFGHNE SLWKNFKEHH 240
QLQRIGESGD CAGIVSFLCS PDASYVNGEN IAVAGYSTRL
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WO 03/003906

PCT/US02/21338

Seq ID NO: 21 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 77-904

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      GCGCGGTTTT GCGTCCGCGAG CAGCTCTGGG CTCTTCTCAG CTGCGCGGAGC AGCTGCTCCA 60
      ATGCCCCCGGA GTGGCCATGG GCGCCCCGCA CTGGTGGGAC CAGCTGCAGG CTGGTAGCTC 120
      GGAGGTGGAC TGGTGCAGAG ACAACTACAC CATCGTGCCT GCTATCGCCG AGTTCTACAA 180
10     CACGATCAGC AATGTCTTAT TTTTCATTTT ACCGCCATC TGCACTGTCT TGTTCGTCA 240
      GTATGCAACA TGCTTCAACA GTGGCATCTA CTTAATCTGG ACTCTTTTGG TTGTAGTGGG 300
      AATTGGATCC GTCTACTTCC ATGCAACCCCT TAGTTTCTTG GGTGAGATGC TTGATGAACT 360
      TGCAGTCCTT TGGGTTCTGA TGTGTGCTTT GSCCATGTGG TTCCCCAGAA GGTATCTACC 420
      AAAGATCTTT CGGAATGACC GGGGTAGGTT CAAGGTGGTG GTCAGTGTCC TGTCTGCGGT 480
15     TACGACGTGC CTGGCAATTG TCAAGCCTGC CATCAACAAC ATCTCTCTGA TGACCCCTGGG 540
      AGTTCCCTTG CACTGCACTGC TCATCGCAGA GCTAAAGAGG TGTGACAACA TGCGTGTGTT 600
      TAAGCTGGGC CTCTTCTCGG GCGTCTGGTG GACCCTGGCC CTGTTCTGCT GGATCAGTGA 660
      CCGAGCTTTC TGGCAGCTGC TGTCACTCCT CAACTTCCCC TACCTGCACT GCATGTGGCA 720
      CATCCTCATC TGCCCTTGCT CCACTCTGGG CIGTGTATGC TTTGCCTACT TTGATGCTGC 780
20     CTCAGAGATT CCTGAGCAAG GCGCTGTCTC CAAGTTCTGG CCCAATGAGA AATGGGCCCT 840
      CATTGGTGTG CCTTATGTGT CCGTCTGTGT TGCCAAACAG AAATCATCAG TCAAGATCAC 900
      GTGATGGCAA GATGGTGGCT GCGTCTCTGT CTATCGCCC CTCATGCAGT GGGCTTCCTT 960
      TGCTAGGAAG AGGCCCAAGG GAGTTCGAAT AGTTGGGGTG TGGGCTATCT TTTCAAAAT 1020
      CTATTGTCTG GCGCTCTTAA TTTCTTTAGT GTTCTTTGTA TGTAGGGATT TAAACTTTGT 1080
25     CATATGGTAC AAATATTCCC TGCCCCCTCG CAGTTTCCCA TTTGTCCTTC AGTATGTTAA 1140
      TATTTTGTG CCATCTGTGT TTTAACTTT CATGTTGTCA CATCTGTAA TCTTTTCTTT 1200
      AGGATTTCTG GATTTTGTGT AATTTTAA AAGTCCCTCT CCTCTCCCT AATGTGTCTG 1260
      TGGACACCTT GGATTCACAT GTACAAGGGG AAAAGTGTCT ATTCCTTTCC CAAAGATGGA 1320
      AAATGGAGGG CTTAGGGACA CTAGATGCAT CTTTCTCAGC ATCACTTCCA GATGCAGTGA 1380
30     CTTGTGGGC TGCGTCTTAT ATGGCCATGG CAGAGCAGTC CCTTGGGGGA TCCAGCCCTG 1440
      TACAATGCAT CTCTTCTG AGAAAGCTGG CCTGCTCCAG ACCCCACCAT TCCCAGGCGC 1500
      CCTGGAGTG GACTCTACTG ATGACAGACA GACCTCTGA GAGACAAGAC CCTCTGACTC 1560
      TGTGATGGAA GATGCCAGAG ATTTTCTTTT GGGGTAATTG TCCTTAAACA AAACCAACA 1620
      GATGAAACAC ACACAGGACT TGTGGCTAAA AAGGCTAGTT TTTCACTTGC ATTTCTCAAC 1680
35     TAACCCAGGT TTTACATGCA TCTGTGAATC CTTTACTTAC TACCTCTGTG GAGAGATGGA 1740
      GAGACTTCAG ATAAACCTGA AGCTAATGAG TAAAACCTTC TCTGCCAAAA CCTACACTCC 1800
      ACTTTAGGCC CTTCTGAAG ATGAGCACAA TTTTAAATA CTGAGCACAA TTTTAAATA 1860
      CTGACATCAC TTCTCTTCC CCGTCCACCC CCAGCTCAGC AGCCTCAAA CTACAGAGAA 1920
      GAAGAATTAG GGCATGAACA TTCCACAGA CCCACATCT TTAAGACTTG ACCTCTGTAA 1980
40     GTTTACAAA GGGCTCTTCA CAATGTGCT GGGGTTCTG GTTCAAAAT TGGAGCAAA 2040
      ATGAAGTTT TGGAAACGTT TTTCTATTG AAGCCTCCAG TATGCTGTAC TATTCTGGAA 2100
      ATTACCTTCA AGAGTCTCAC TTTCTTTTC TGTGTGTTT TCTGTTGGCA TCATGTTCTT 2160
      CACGCTTGCA GTAGAAGGTG CTTTCTCGGT TTCCAGAGT ATCCAACGGC TCACCTTTCT 2220
      CAAGTGTGCG CAGTAGCTAT GCACTCACGG GCTGGTTTGG GTGCTGGTG CAGCAGCGCA 2280
45     AATCTGTTG CTCTGAATT TTTCTACCT AATGTGACAC TGGTACAA GAATCTTCTC 2340
      TTTCATCGGC TGAATGAAG ATTCAAGAAC CATCTTCAAG GTGCATGGTG GGAATTATCA 2400
      ACCTCAGGGA TACTCATTTT AACTCAGGCG TGTCTGTCTT TGTAACTTC CATTGTTGGG 2460
      AGAGGGCAGG ACAGGTGTGT TCTTCTGTG GCAGGAGTCA TGTCACTGTC CTACATATGT 2520
      AAGAGTTGGG AAGGTGACGA TTTTTCACAC ATCCAGGAAC TCTTACTCTA GTTAGAATTT 2580
50     GTACCAGATC CAAGGTGAAG TTATCAAAT ATATAGGTTG TTAGAAGCA GAAACGCTGT 2640
      ACTTTATGCT ACATCTGTGG GAACCCAGT GTGTGAAGTA AATTGTATGT TATTAAATTT 2760
      TGTAGTAAGA AATCTTTGTG GAACCCAGT GTGTGAAGTA AATTGTATGT TATTAAATTT 2820
      ATTTAAGGTT AAATTTATGG CATTACTTA ATAATATATG AGGTGGTGAA AATGCAAAAT 2880
      AACAAATTGG TAATTTCCAA GGTAGAAAAA TTAGGTGTTG AATGAATGTA TATGTTGGTT 2940
55     TATTATAGTT TTATATATAT ATAGAGAGAG TGTTTTGTG TTAGAGTCAG GTCTTGCTCT 2940
      ATTACCCAGG GTGAGTGCA GTGGTGCAGT CAGTACTCAC TGTAGCCTCT GTCTCCCAGG 3000
      CTCAAGTCAT CCTCTCACCT CAGCTTCCC AGGAGCTGGG AGTACTGGTG CGTGCCTCCA 3060
      CTCCCAGCTA ATTTTGTAT TTTTTCATAG AGATGGGGTT TCACCAATTT GCCCAGGCTG 3120
      GTCTCAAACT TCTGGGCTCA AGAGATTGCG CCGCTTCCGC CTCCTCAAGT GCTGGGAATA 3180
60     GGCATGAGCC GTCACGCTGT GCGTAAAAAA TATTTTAAAA ATGATCTTTG AATTAATAT 3240
      TCGTAGAATT TCTAATGTAT CTCTTTGAGA CCTAGGAGGT TGATGGAA CA GAACTGCTGT 3300
      TAAGTCCTTT GGGTTTCAAG TCTAGAATTT TTTAAAGGCA AATATCAGCT CATTCTTATT 3360
      TTAGATTGAC CTTATCAGGC ATGGATTCTG GTCTCATCTA CTTTATGGTA TAAATGCTCC 3420
      AAGGTAGGGG GTTTGGTATA TATTTTAAGC CCGGCTTTTT TTTTTTTTTT TTTTTTTTTT 3480
65     TTTTAAATGT GAGAAGCAGA ATGTGCTTCT AGAACTGGT TTTAAAGAGA TGAGCTGAGA 3540
      AAGAAATGTG GAATGGAGTA TATTTGAGGA GGACAAAACA TAACTTCACT TTTGAACAGA 3600
      AATCACTCTA GCTTGGCCAGC ATGGGATGTA AACCAGAGA GTAGAAATAT ACCCATCTTA 3660
      TTTTAAAGTT GGTATATGTC ATCGCTCATA TATGTAAAAG CACTACAAAC TCTTTAAAGA 3720
      AAATGGGAAA ACTACAGAGA AGTCAAAGAA AAAAAAAGT AACCCATATT TCTATTGCC 3780
70     AGGTATAATC CTTGTTAATA TTTTGGTTTG GTCTCCTCTT TTTTCCCCC AATATAGTTG 3840
      TAAATAAATG ATGCTTTTCA GAGTGTACAT TTATCCTGTA GCTTGAATGG CATGTAAATG 3900
      CCAGTTGTAT ATTTTTCAT GAAGTGTAGG TTTGGAATAC ACTAGAGTTA GCTATATGCT 3960
      TGAATGCTGA TCACTGGATT CTGAGACTGA CTACTGAGTC TACCTTTTTA ATCAAGCCTA 4020
      ACATGAATGG GCTCAAAAAA GTAATGAATG TAAATGTACT TTTTGATGTG CCTCTGCACT 4080
75     TGGCTTGGTG AGTCATCTA AATAGCTGTT AAATATGTGA CTTTACAGAT TTTGATATGT 4140
      TCAGATTGTA AAAAATGAAT AGTTTATTTT ATTAATGTAT GGGCAGTCAA GAATCTCCCT 4200
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WO 03/003906

PCT/US02/21338

Seq ID NO: 22 Protein sequence:
Protein Accession #: E0S sequence

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      |      |      |      |      |      |
      MGAPHWWDQL QAGSSEVDWC EDNYTIVPAI AEFYNTISNV LFFILPPICM CLFRQYATCF 60
      NSGIYLIWTL LVVVIGISVY FHATLSFLGQ MLDELAVLWV LMCALAMWFP RRYLPKIFRN 120
      DRGRFKVVVS VLSAVTTCLA FVKPAINNIS LMTLGVPCTA LLIAELKRCD NMRVFKLGLF 180
      SGLMWTALF CNISDRAFCE LLSSFNFPYL HCMWHILICL AAYLGCVCFA YFDAASEIPE 240
10     QGPVIKFWPN EKWAFIGVPY VSLLCANKKK SVKIT
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Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: CAT cluster

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      CCAGATACGC AGGAGGACAC ATTCTTGATC GGTATTTTAT TCTATTATTI TTATTAGTTC 120
      CAATCCTTAT GACTCTGTTT AAAATGAGTA TCTGCATTAT TGTGCAAAAC CTTCTGAGAT 180
      CTCATCACAT ACCTGATCCC ATTTAACTTC AGTCTATCCC TCCATTACTT TTTGTGGAA 240
      GTGCTATCTA AGTTGGAGGT TCTGCTTGAG TATTCTTAAT TTTTCTTCTI TTTAATGCAT 300
      ACGGTGGTCA AAGTAAATAG CTRACATATT GGCATCAAAC CATTGCCTAT TGAAGCAAGC 360
      TTTGAATGAA ATTGGTTTGT CATTGACCAC TGTAAAGAAC TCATTGTGAA AGATAAATACT 420
      GAAAAACATC CTGACTCTTA TGTATGCTTG CCTGTCTCTG AACTCCACCT CTATCAGCAT 480
      ACTCAATACA TTGCCTCTTT CCAACATTTA TCTCTTAAAT CAGGAGAAAG TTTTGTGGGA 540
      CGGTCTACCA CGTTGCAAAAG ATTCAACATT TCTCTTAAAT ATAGGAGTTT CTTTATAGATA 600
      TAAGCAATGA AATTTCAAGC AACAAATATTA CTCTCTCAT GTCCCTTGCT TTTTAAAGAT 660
      CTGAACCTCA AGATTCAAAAT GGATTTTCAI TGAATTCAC CACGATCCCC TCTGCAGCTG 720
      TGGTCTGAAA GTACCAATTC TGCATTTAT TTAGCCCATG GAATAACTGT GCTGAGAAAC 780
      CACAGAGTCA ATCAGATTCA AAATGTTAAA ATCCTTCTG CTTGGAGTTT TCCGTCTTCA 840
      CATCAAGACA TTTCAATGCC GTCAGCAACT TTTTAATGCA TTTGCTCATG GTTTCAGAAA 900
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Seq ID NO: 24 DNA sequence
Nucleic Acid Accession #: E0S sequence

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35     1      11      21      31      41      51
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      GAAAGTGGTT TAGCATGCTG GAGCTGGTTT TCTGCTTGGT AGCCCTACAA CTTTGGCCCA 180
      ACTACTTGGC CTCTGGGACT CAGATTCTCT CTCTTTAAAT TGGTGCTAAT AATAGCACCC 240
      ACCCTCTGTG AGGAGGATGC TGTGAGGACA AAATGAGATC ATCCACATAA GCCGTGAACC 300
      CTGTTCTCTG TAAGCTCTCT GAAAGAAGTC TATGGATTAT ACTCAACCTA CACTCCAGTT 360
      AAAGGAACAT CTACACACAG AGGAAATGAA TAACATGAAG TGAAGTCTTC ATCTCCATTTC 420
      CCAACAGTCC CCATTCTACT TGCAGAAAGG TTGCTTACAC TGAATATCAG TTTATTTTCC 480
      CCTGGTGCAA AGAACAGTCC TTTCTCCAAA ACTGAAGCTG GAAATTATCT GAAATATCAG 540
      GTCTCCGGA AAAGGGAGCT GAAGCCCCCT TTGTAATTC TGCATTAGCG TGCTCTCCTG 600
      GCAAGCAGGA AACCTCATCA GAGAAGTCAG CCAAGGAAG TCTTTAAATG GAAATTGTGC 660
      AAACGAGGAG CAAATGCATT AAAAAGTTGC TGACGGGCAT GAAATGCTTT GATGTGAAGA 720
      CGCAAAACTC CAAGCAGGAA GGATTTTAACT ATTTTGAATC TGATTGACTC TGTGGTTTCT 780
      CAGCACAGTT ATTCCATGGG CTAAAATAAA TGCAGAAATG GTACTTTTCA ACCACAGCTG 840
      CAGAGGGGAT CGTGGTGAAT TTCAATGAAA ATCCATTTGA ATCTTGAGGT TCAGATCTTA 900
      AAAAAAGCAA GGACATGAGA GAAGTAATAT TGTGCTTGA AATTTCAATT CTTATATCTA 960
      AAAGAAATCT CTATTTTAA GAGAAATGTT GAATCTTTGC AACGTGGTAG ACGTCCCAC 1020
      AAAACTTTCT CCTGAAATAG GAGATAAATG TTGGAAGAG GCAATGIATT GAGTATGCTG 1080
      ATAGAGGTGG AGTTCAGAGA CAGGCAAGCA TACATAAGAG TCAGGATGTT TTTCAATATT 1140
      ATCTTACAA ATGAGTTTCT TACAGTGGTC AATGACAAAC CAATTTCAAT CAAAGCTTGC 1200
      TTCAATAGGC AATGGTTTGA TGCCAATATG TTAGCTATT TACTTGACCA CCGTATGCAT 1260
      TAAAAAGAAG AAAAATTAAG AATACTCAAG CAGAACCCTC AACTTAGATA GCACTTTCCA 1320
      CAAAAAGTAA TGGAGGGATA GACTGAAGTT AAATGGGATC AGGTATGTGA TGAGATCTCA 1380
      GAAGTGTGTT CACAATAATG CAGATACTCA TTTTAAACAG AGTCATAAGG ATTGGAACCTA 1440
      ATAAAAATAA TAGAATAAAA TACCGATCAA GAATGTGCTC TCCTGCGTAT CTGGGTTTGT 1500
      AATCTGGCT CCACAGAACT TGTCAGATAT ATGACATTAA AC
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Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: E0S sequence

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      AGTAGGCTCA GTAGCAGCAA CTGCAAAATC TTGAGAAGGG AAAAGTTCAG CCTTGTGCTG 120
      GAAAGTGGTT TAGCATGCTG GAGCTGGTTT TCTGCTTGGT AGCCCTACAA CTTTGGCCCA 180
      ACTACTTGGC CTCTGGGACT CAGATTCTCT CTCTTTAAAT TGGTGCTAAT AATAGCACCC 240
      ACCCTCTGTG AGGAGGATGC TGTGAGGACA AAATGAGATC ATCCACATAA GCCGTGAACC 300
      CTGTTCTCTG TAAGGAAATG AATAACATGA AGTGAAGTCT TCATCTCCAT TCCCAACAGT 360
      CCCCATTTCT CTTGCAGAAA GGTGCTTAC ACTGAAATC AGTTTATTTT CCCCTGGTGC 420
      AAAGAACAGT CGTTTCTCCA AAACCTGAAGC TGGAAATTAT CTGAAATATC AGGTCTCTCG 480
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WO 03/003906

PCT/US02/21338

	GAAAGGGAC	GTGAAGCCCC	CTTTGTAATT	TCTGCATTAG	CGTGTCTCTCC	TGGCAAGCAG	540
	GAAACCTCAT	CAGAGAAGTC	AGCCAAGGAA	AGTCTTTAAA	TGGAAATTGT	GCAAAACGAGG	600
	AGCAAAATGCA	TTAAAAAGTT	GCTGACGGGC	ATGAAATGCT	TTGATGTGAA	GACGGAAAAC	660
5	TCCAAGCAGG	AAGGATTTTA	ACATTTTGAA	TCTGATTGAC	TCTGTGTTT	CTCAGCACAG	720
	TTATTCCATG	GGCTAAAATA	AATGCAGAAA	TGGTACTTTC	AGACCACAGC	TGCAGAGGGG	780
	ATCGTGGTGA	ATTTCAATGA	AAATCCATTT	GAATCTTGAG	GTTCAGATCT	TAAAAAGCA	840
	AAGGACATGA	GAGAAGTAAT	ATTGTTGCTT	GAAATTTTCA	TGCTTATATC	TAAAAAGAAC	900
	TCCTATTTTT	AAGAGAAATG	TTGAATCTTT	GCAACGTGGT	AGACGCTCCC	ACAAAACTTT	960
10	CTCCTGAAAT	AGGAGATAAA	TGTTGGAAAG	AGGCAATGTA	TTGAGTATGC	TGATAGAGGT	1020
	GGAGTTGAGA	GACAGGCAAG	CATACATAAG	AGTCAGGATG	TTTTTCAGTA	TTATCTTTAC	1080
	AAATGAGTTT	CTTACAGTGG	TCAATGACAA	ACCAATTTCA	TTCAAAGCTT	GCTTCAATAG	1140
	GCAATGGTTT	GATGCCAATA	TGTTAGCTAT	TTACTTTGAC	CACCGTATGC	ATTAAGAAAG	1200
	AGAAAAATTA	AGAATACTCA	AGCAGAACCT	CCAACCTAGA	TAGCACTTTC	CACAAAAAGT	1260
15	AATGGAGGGA	TAGACTGAAG	TTAAATGGGA	TCAGGTATGT	GATGAGATCT	CAGAAGTGTT	1320
	TGCACAATAA	TGCAGATACT	CATTTTAAAC	AGAGTCATAA	GCATTGGAAAC	TAAATAAAAT	1380
	AATAGAATAA	AATACCGATC	AAGAATGTGT	CCTCCTGCGT	ATCTGGGTTT	TGAATTTCTGG	1440
	CTCCACAGAA	CTTGTCAGAT	ATATGACATT	AAAC			
20	Seq ID NO: 26 DNA sequence Nucleic Acid Accession #: NM_013282.2 Coding sequence: 85..2466						
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	ACCCACACGG	TGACTCTGCT	GTCCAGGCTG	ACCAAGGTGG	AGGAGCTGAG	GCGGAAGATC	180
	CAGGAGCTGT	TCCACGTGGA	GCCAGGCTG	CAGAGGCTGT	TCTACAGGGG	CAACACAGATG	240
30	GAGGACGGCC	ATACCCTCTT	CGACTACGAG	GTCCGCCTGA	ATGACACCAT	CCAGCTCCTG	300
	GTCCGCCAGG	GCCTCGTGCT	CCCCACAGC	ACCAAGGAGC	GGGACTCCGA	GCTCTCCGAC	360
	ACCGACTCCG	GCTGCTGCCT	GGGCCAGAGT	GAGTCAGACA	AGTCTCTCAC	CCACGGCGAG	420
	GCGGCCGCCG	AGACTGACAG	CAGGCCAGCC	GATGAGGACA	TGTGGGATGA	GACGGAATTG	480
	GGGCTGTACA	AGGTCAATGA	TACGTCGAT	GCTCGGGACA	CGAACATGGG	GGCGTGGTTT	540
35	GAGGCGCAGG	TGGTCAGGT	GACGCGGAAG	GCCCCCTCCC	GGGACGAGCC	CTGCACTCTC	600
	ACGTCCAGGC	CGGCGCTGGA	GGAGGACGTC	ATTTACCACG	TGAAATACGA	CGACTACCCG	660
	GAGAAAGGGG	TGGTCCAGAT	GAATCCAGG	GACGTCCGAG	CGCGCGCCCG	CACCATCATC	720
	AAAGTGGCAGG	ACTGGAGGT	GGGCCAGGTG	GTGATGCTCA	ACTACAACCC	CGACAACCCC	780
	AAAGGACGGG	GCTTCTGGTA	CGAGCGGAG	ATCTCCAGGA	AGCGCGAGAC	CAGGACGGCG	840
40	CGGGAACCT	ACGCCAACGT	GCTGCTGGG	GATGATCTC	TGAAACGACTG	TGGGATCATC	900
	TTCTGTGAGC	AAGTCTTCAA	GATTGAGCGG	CCGGGTGAAG	GGAGCCCCAT	GGTTGACAAC	960
	CCCATGAGAC	GGAGAGCGG	GCCCTCCTGC	AAGCACTGCA	AGGACGACGT	GAACAGACTC	1020
	TGCCGGGTCT	GCGCCTGCCA	CCTGTGCGGG	GGCCCGCAGG	ACCCCGACAA	GCAGCTCATG	1080
	TGCGATGAGT	GCGACATGGC	CTTCCACATC	TACTGCCTGG	ACCCGCCCTC	CAGCAGTGT	1140
45	CCGAGCGAGG	ACGAGTGGTA	CTGCCCTGAG	TGCCGGAATG	ATGCCAGCGA	GGTGGTACTG	1200
	GCGGGAGAGC	GGCTGAGAGA	GAGCAAGAAG	AAGGCGAAGA	TGGCTCTGGC	CACATCGTCC	1260
	TCACAGCGGG	ACTGGGGCAA	GGGCATGGCC	TGTGTGGGCC	GCACCAAGGA	ATGTACCATC	1320
	GTCCCGTCCA	ACCACTACGG	ACCCATCCCG	GGGATCCCGG	TGGGCACCAT	GTGGCGGTTT	1380
	CGAGTCCAGG	TCAGCGAGTC	GGGTGTCCAT	CGGCCCAACG	TGGCTGGCAT	ACACGGCCCG	1440
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	GGGAATTTTT	TCACATACAC	GCGTAGTGGT	GGTCTGAGATC	TTTCCGCAAA	CAAGGAGACC	1560
	GCGGAACAGT	CTTGTGATCA	GAAACTCACC	AACACCAACA	GGGCGCTGGC	TCTCAACTGC	1620
	TTTGTCTCCA	TCAATGACCA	AGAAGGGGCC	GAGGCCAAGG	ACTGGCGGTC	GGGGAAGCCG	1680
	GTCAGGCTGG	TGCGCAATGT	CAAGGCTGGC	AAGAATAGCA	AGTACGCCCC	CGCTGAGGGC	1740
55	AACCGCTACG	ATGGCATCTA	CAAGGTTGTG	AAATACTGGC	CCGAGAAGGG	GAAGTCCGGG	1800
	TTTCTCGTGT	GCGCTACCT	TCTGCGGAGG	GACGATGATG	AGCCTGGCCC	TTGGACGAAG	1860
	GAGGGGAAGG	ACCGGATCAA	GAAGCTGGGG	CTGACCATGC	AGTATCCAGA	AGGCTACCTG	1920
	GAAGCCCTGG	CCAACCGAGA	GCGAGAGAAG	GAGAACAGCA	AGAGGGAGGA	GGAGGAGCAG	1980
	CAGGAGGGGG	GCTTGGCGTC	CCCCAGGACG	GGCAAGGGCA	AGTGAAGCG	GAAGTCCGCA	2040
60	GGAGGTGGCC	CGAGCAGGGC	CGGGTCCCCG	CGCCGGACAT	CCAAGAAAAC	CAAGGTGGAG	2100
	CCCTACAGTC	TCACGGCCCC	GCAGAGCAGC	CTCATCAGAG	AGGACAAGAG	CAACGCCAAG	2160
	CTGTGGAATG	AGGTCTGGCC	GTCACTCAAG	GACCGGCCGG	CGAGCGGCAG	CCCGTTCCAG	2220
	TTGTCTCTTA	GTAAAGTGGG	GGAGACGTTT	CAGTGTATCT	GCTGTGAGGA	GCTGGTGTTC	2280
	CGGCCCATCA	CGACCGTGTG	CCAGCACAAC	GTGTGCAAGG	ACTGCCTGGA	CAGATCCTTT	2340
65	CGGGCACAGG	TGTTGAGCTG	CCCTGCCTGC	CGCTACGACC	TGGGCGGCAG	CTATGCCATG	2400
	CAGGTGAACC	AGCCTCTGCA	GACCGTCTCT	AACCACTCT	TCCCGGCTA	CGGCAATGGC	2460
	CGGTGATCTC	CAAGCACTTC	TCGACAGGCG	TTTTGCTGAA	AACGTGTGCG	AGGGCTCGTT	2520
	CATCGGCACT	GATTTTGTTC	TTAGTGGGCT	TAACTTAAAC	AGGTAGTGT	TCCTCCGTTT	2580
	CCTAAAAAGG	TTTGTCTTCC	TTTTTTTTTA	TTTTTTATTT	TCAATCTAT	ACATTTTCAG	2640
70	GAATTTATGT	ATTCTGGCTA	AAAGTTGGAC	TTCTCAGTAT	TGTGTTTACT	TCTTTTGAAA	2700
	CATAAAGGCC	TGCAATTTCT	CGACAAAACA	ACACAAGATT	TTTTAAAGAT	GGAATCAGAA	2760
	ACTACGTGGT	GTGGAGGCTG	TTGATGTTTC	TGGTGTCAAG	TTCTCAGAAG	TTGCTGCCAC	2820
	CAACTCTTTA	AGAAGGCGAC	AGGATCAGTC	CTTCTTAGG	GTTCTGGCCC	CCAAGGTCAG	2880
	AGCAAGCATC	TTCTTGACAG	CATTTTGTCA	TCTAAAGTCC	AGTGACATGG	TTCCCCGTGG	2940
75	TGGCCGCTGG	CAGCCCGTGG	CATGGCGTGG	CTCAGCTGTC	TGTTGAAGTT	GTTGCAAGGA	3000
	AAAGAGGAAA	CATCTCGGGC	CTAGTTCAAA	CCCTTGCCTC	AAAGCCATCC	CCCACCGAC	3060
	TGCTTAGCGT	CTGAGATCCG	CGTGAAGAGT	CCTCTGCCCA	CGAGAGCAGG	GAGTTGGGGC	3120
	CACGCAGAAA	TGGCCTCAAG	GGGACTCTGC	TCCACGTGGG	GCCAGGCGTG	TGACTGACGC	3180
	TGTCGACGGA	AGGCGGACAC	GGACGAGCGC	CAGCACACGA	AGTCACGTGC	AAGTGCCTTT	3240

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GATTCGTCC TTCCTTCTAA AGACGACAGT CTTTGTGTT AGCACTGAAT TATTGAAAAAT 3300
GTCACACGAGA TTCTAGAAAC TGGGGTCATC CAGTTCTTCC TGACACCGGA TGGGTGCTTG 3360
GGAACCGTTT GAGCCTTATA GATCATTTAC ATTCAATTTT TTTAACTCAG CAAGTGAGAA 3420
CTTACAAGAG GGTTTTTTTT TAATTTTTTT TTCTCTTAAT GAACACATTT TCTAAATGAA 3480
TTTTTTTTGT AGTTACTGTA TATGTACCAA GAAAGATATA ACGTTAGGGT TTGGTTGTTT 3540
TTGTTTTTGT ATTTTTTTTC TTTTGAAAGG GTTTGTAAAT TTTTCTAATT TTACCAAAAGT 3600
TTGCAGCCTA TACCTCAATA AAACAGGGAT ATTTAAATC ACATACCTGC AGACAAACTG 3660
GAGCAATGTT ATTTTAAAG GGTTTTTTTC ACCTCCTTAT TCTTAGATTA TTAATGTATT 3720
AGGGAAGAAT GAGACAAATT TGTGTAGGCT TTTTCTAAAG TCCAGTACTT TGTCCAGATT 3780
TTAGATTCTC AGAATAAATG TTTTTCACAG ATTGAAAAAA AAAAAAAA 3828

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Seq ID NO: 27 Protein Sequence
Protein Accession #: NP_037414.2

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1      11      21      31      41      51
|      |      |      |      |      |
MWIQVRTMDG RQHTVDSLS RLTKVEELRR KIQLFHVPE GLQRLFYRGK QMEDGHTLFD 60
YEVRLNDTIQ LLVRQSLVLP HSTKERDSEL SDTDSGCCLG QSEDSKSTH GEAAABETDSR 120
PADEDMWDET ELGLYKVNEY VDARDTNMGA WFEAQVVRVT RKAPSRDEPC SSTSRPALEE 180
DVIYHVKYDD YPENGVVQMN SRDVRARART IIKWQDLEVQ QVVMNLVNPDP NPKERGFNYD 240
AEISRKRETR TARELYANVV LGDDSLNDCR IIFVDEVFKI ERPGESEFMV DNPMMRKSGP 300
SCKHKDDVNV RLCRVACACH CCGRQDPDKQ LMCDECDMAF HIYCLDPPLS SVPSEDEWYC 360
PECRNDASEV VLAGERLRES KKKAKMASAT SSSQRDWKGK MACVQRTKEC TIVPSNHYGP 420
IPGIPVGTMM RFRVQVSESG VHRPHVAGIH GRSNDGAYSL VLAGGYEDDV DHGNFFTYTG 480
SGGRDLSGNK RTABQSCDQK LTNTNRALAL NCFAPINDQE GAEAKDWRSG KPVVRVVRNVK 540
GGKNSKYAPA EGNRYDGIYK VVKYWPEKKG SGFLVWRYLL RRDDDEPGPW TKEGKDRIKK 600
LGLTMQYPEG YLEALANRER EKENSKEREE EQEGGFASP RTGKGKWKRK SAGGSPSRAG 660
SPRRTSKKTK VEPYSTTAQQ HNVCKDCLDR SFRAQVFSCP ACRYDLGRSY AMQVNQPLQT 720
TFQCICQQLV VFRPITTVQK HNVCKDCLDR SFRAQVFSCP ACRYDLGRSY AMQVNQPLQT 780
VLNQLFPGYG NGR

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Seq ID NO: 28 DNA sequence
Nucleic Acid Accession #: NM_000756.1
Coding sequence:186..776

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GAGAGTGGGA ACAGTAAAGA GAAAGGAAGA CAACCTCCAG AGAAAGCCCC CGGAGACGTC 120
TCTCTGCAGA GAGCGCGCAG CACCCGGCTC ACCTGCGAAG CGCCTGGGAA GCGAGTGCCC 180
CTAACATGCG GCTGCCGCTG CTTGTGTCCG CGGAGTCTCT GCTGTGGGCT CTCTGCCCT 240
CGCCGCCATG CAGGCGCGTC CTGAGCCGCG GGCCGGTCCC GGGAGCTCCG CAGCGCGCGC 300
AGCACCTCTA GCCCTTGGAT TTCTTCCAGC CGCCGCCGCA GTCCGAGCAG CCCAGCAGC 360
CGCAGGCTCG GCCGTCTCTG CTCCGCATGG GAGAGGAGTA CTCTCTCCGC CTGGGGAAAC 420
TCAACAAGAG CCCGCCGCTC CCCCTTTCGC CGCCTCTCTC GCTCCTCGCC GGAGGCAGCG 480
GCAGCCGCCCC TTCGCCGGA CAGGCGACCG CCAACTTTT CCGCGTGTG CTGCAGCAGC 540
TGCTGCTGCC TCGGCGCTCG CTGCAGCAGC CCGCGGCTCT CGCGGAGGCG GCGCCTAGGA 600
ATGCCCTCGG CGGCCACCG GAGGCACCGG AGAGAGAAAG GCGGTCCGAG GAGCCTCCCA 660
TCTCCCTGGA TCTCACTTTC CACCTCTCTC GGAAGTCTT GGAATGGGCC AGGGCCGAGC 720
AGTTAGCACA GCAAGCTCAC AGCAACAGGA AACTCATGGA GATTATTGGG AAATAAAACG 780
GTGCGTTTGG CCAGAAAGAA TCTGCATTTA GCACAAAAAA AATTTAAAAA AATACAGTAT 840
TCTGTACCAT AGCGTGTCTC TTATGCCATT TGTTTATTTT TATATAGCTT GAAACATAGA 900
GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTTAGCATGC ACAAGTGTGA TTCACGTGCA 960
GCAGCAACCA AATGTTATTC GTTTTGTCTA CGTTTAGTTT CCGTTTCCAG GTGTTTATAG 1020
TGGTGTTTTA AAGAGAATGT AGACCTGTGA GAAAACGTTT TGTTTGAAA AGCAGACAGA 1080
AGTCACTCAA TTGTTTTTGT TGTGGTCTGA GCCAAAGAGA ATGCCATTCT CTTCGGTGGG 1140
TAAGACTAAA TCTGTAAGCT CTTTGAAACA ACTTCTCTT GTAAACGTTT CAGTAATAAA 1200
ACATCTTTCC AGTCCTTGGT CAGTTTGGTT GTGTAAGAGA ATGTTGAATA CTTATATTTT 1260
TAATAAAAGT TGCAGAGTT

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Seq ID NO: 29 Protein Sequence
Protein Accession #: NP_000747.1

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1      11      21      31      41      51
|      |      |      |      |      |
MRLPLVLSAG VLLVALLPCP PCRALLSRGP VPGARQAPQH PQPLDFFQPP PQSEQPQPPQ 60
ARPVLLRMGE EYFLRLGNLN KSPAAPLSPA SLLLAGSGS RPSPEQATAN FFRVLLQQLL 120
LPRRLDSPA ALAERGARN LGGHQEAPE ERRSEBPIS LDLTFHLLRE VLEMARAEQL 180
AQQAHSNRKL MEIIGK

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Seq ID NO: 30 DNA sequence
Nucleic Acid Accession #: CAT cluster

75

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1      11      21      31      41      51
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ATTTCTTGAG ATGGCTCCTC TTGGAATAT GCATCTCTCC TGATACTTGG ATGCTTTTCC 60
TCTGACTGAT GAAGATCCTG AATACCAAG AGGGCCGCTG AAAGGCTCT AGGAGTACAC 120

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CTTCTAGGAA CCCTAAGCCA GAGAGAGGCT TCACTACATC ATGCTTCTTG ACATCTCTCC 180
CTTTGAAGAG CAGTCAGACT CCTGCTTTGC TCTTCAGACT TAATTTGGGG GTTTAACAGG 240
TGAGGTTGCT GGGGGAATCT TTTTACAACA TCTCTCTGAA AGAATCCGGG CTGCCAGTTT 300
CAITTTGGTTC GGTGTGAGT AGCATGATGG AAGACAAAAA AAACACAAC TGACATCTGC 360
AGAAATGGGT TCAAAATTTA CCTGCAACTC ACCAATTCTG TGGCCTTGGT TCAGCAATTA 420
AACTCCCTAA AATTCAGTTT TTTCTTTGTA AAATGGGTTT ATGAACAGTA CCTACTTCAA 480
AATGTGTTTG TGAAGATTAA AAAAGTTAAT ATAAAGAGTT TAGAAGAGTG TCTGGCATAT 540
TGTGCTCAAT AAGTGTTTAT TTATTTATTG CTGAATAAAC CAGTAATTA ATTAGTAT

Seq ID NO: 31 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 134..1917

1 11 21 31 41 51
CACCTCAGCC CCAACCCCAA CCCAGGCGGC ATCCCTGACC CCAGCTGAGC GGTCAAAGCC 60
TCAGGAGAGT GTGGCTCTCC CCAGGCGCTA CCAGGAGGGG CAGGTCTCAG CCAGCTGGGG 120
AAACCTTTATT GCCATGGTTC TTAGAAGCCA CCCCTTCCCC AGGCAAGACA GGCCCCAAGG 180
GAGTGTCCCG AGGGCGGTTT CCGGGAGCCC CGTGGGTCCC AGCACTTCCA CACACTCTGA 240
GGACAGACAC GGCCCTCTTT CTTCACTGGG GACAGTCATA GGGACAGGTA CAGGGGGCCT 300
GGTTGAGGCT GGAGGTGAGC CACAGCCAAG AAGCTCCGAG ACCAACGGAT CGCCAGCCCC 360
AGACCTTCCC CCAGGCTTAA GAGGAGAGGG AACCAGGGAG AAAAGTCTAG ACCCGCTGCC 420
CCAAGCCCGG ATGCCCAGGG GCCCCGACCA GCGCCCGCGC CAGAGGCGCG CTGGCCCGCG 480
GGCCTCTCTC TCTGCGAGGC GCTCACAGCC GGTACCCAGC CTACGGAAC GACGACAGTG 540
CGAAATCGCC CCGAGCTCGG AGCAGGAGGT CAGGCGCGCC GCCTCGGGGG ACCCTCAAGG 600
GGAGGCGCGC GGGAGGGGGG GCAGCCCTGC CGGCCGCGAG GGGGCGCTCA CGGAAAAGCA 660
GGAGGAGGCC CGAAGCTCA TGGTGTCTCT GCAGAGGCCG GGGGCTTGGG GGGTGGTGA 720
GGGGCCCGCG AAGCCAGCT CCGGCGCCCT GGAGCCCGCC ACGGCGCGAG CCCTGCGGCG 780
GCGGCTGGAC CTGGGCACTT GCCTGGACGT GCTGGCCTTT GCCCAGCAGC ACGGAGAGCC 840
CGGCTGCGC CAGGAGACCT ACGCGCTGAT GAGCGACAAC CTGCTCGGAG TGCTGGGAGA 900
CCGCTGCTCT TACCGCGGCG TGAGCGCGGC CGACCGCGAG CGCATCTCTA GCCTGCGGAC 960
CGGCGGGGCG CGGCGGCTGC TGGGCTCCTT CGTACTGCCC AGCCTCTACC AGGGGGGCGG 1020
CTCAGGGCTC CCCAGGGGCC CTGCTGGGGA GGAGCCTCCT GCGCGCGCCC CTGTGTCCTT 1080
GCCTCTACCT GCGCACTGCG ATGTGTTCAA CCCCAGGAG AACACCTGGC GGCCCTGAC 1140
CCAGGTGCCC GAGGAGGCCG CGCTTCGGGG CTGCGGCTCT TGCAACATGC ACAACTACCT 1200
GTTTCTGGCG GGGGCGATCC GTGGCTCCGG TGCCAAAGGC GTCTGTCTCA ACGAGGTCTT 1260
CTGCTACAAC CCTCTGACCA ACATCTGGAG CCAGGTTCCG CCCATGCAGC AGGCCGAGC 1320
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CAGCATGGAG TGGTACGACC CGGGAACAGA CGCCTGGACC CCACGCGCGC CACTCCCGCG 1440
AGGCACCTTC CCTGTGGCCC ACGAGGCTGT GGCTGCCGT GGGGACATCT ACGTCAACCG 1500
GGGTCACTTC TTCTACCGCC TGCTCAGGTA CAGCCCGGTG AAGGATGCTT GGGACGAGTG 1560
CCCATACAGT GCCAGCCACC GCGGTTCCAG CGACATCGTG GCACTGGGGG GCTTCTCTGA 1620
CCGCTTGAGC CTGCTGCGGG GCGTGGGCGC CGCCTGATG CGCTACAACA CAGTGACCGG 1680
CTCCTGGAGC AGGGCTGCTT CCTTGCCCCC GCGCCCGCCC GCCCCTATGC ACTGCACCAC 1740
CCTGGGCAAC ACCATTTACT GCCTCAACCC CCAGGTCACT GCCACCTCA CGGTCTCTGG 1800
GGGGAAGTCC CAGTTCCAGG CCAAGGAGCT GCAGCCCTTC CCCTTGGGGA GCACCGGGGT 1860
CCTCAGTCCA TTCTCCCTGA CTCTGCCCCC TGAGGACCGG CTGCAGACCT CACTCTGAGT 1920
GGCAGGCAAG GAACCAAGAC TGCTTGCTGT CTCTCCAGGG AGACCTCTCT GGGATGGGCC 1980
TGAGAGGCGG GGGCTCAGG AAGGGGCTGG GATCGGAAC TCTGCTCTTT GTTCTGGAC 2040
AACTTTCCCC TTCTGCTTTA AAGGTTGTCG ATTATTTTGA AGCCCAAGCT CCCTCAGCCT 2100
CTTTCTGCCC CTCACTCCAC ACCCAGACTG TTTCTGACT CAATTCGCTA CCTACTTACA 2160
GACCTCTCA GCTTGCTGAC ACCCCCTGT CTGTGGGACT CCTATTCCC TAGAGCCAGG 2220
GACTGATGCG TCTCCACAGA CAAGGACTTG GCTCGCTGGA GCTCTGTGA GCCGAGAGAG 2280
GAGGGGGTAG AAAACATTCA CACTTCTAT GCTTCTCTAT CAGGACAGGG AGCAAAAAACG 2340
TCCCCAGGCA ACCCCTCTGC CTCTGGGACT TTCTGCTGT CTCTAAGGCTT CCCCAGGTAC 2400
CAACCCCGTA GCTATCTGGG TCTGTTTGGC ACTGTGGATT CTCAAGGGCC TAGAACCTCT 2460
GCCTCTGAAA CTGCTCGGCT GGTGCAGCCC TGCTGTCTGC AGCTCCTGCC CATACCCCCA 2520
GCCACACCA GGCAGGCGCC ACTCCGCGCT CACCACCCCT TGACGCTTG TGGGGCTCTC 2580
CCAGCCCTTC CAGAAGCCCA CCCCACTTCT CGCCAACCCC CGATCTCTAA ATGAGGCCCTG 2640
AGCGTCACCC TAGTTCTGCC CTTTTTAGC TGTGTAGACT TGGACGAGAC ATTTGACTTC 2700
CCTTTCTCT TGTCTATAAA ATGTGGACAG TGGACGCTG TCACCCAAGA GAGTTGTGGG 2760
AGACAAGATC ACAGCTATGA GCACCTCGCA CGGTGTCCAG GATGCACAGC ACAATCCATG 2820
ATGCGTTTTT TCCCTTACG CACTTTGAAA CCCATGCTAG AAAAGTGAAT ACATCTGACT 2880
GTGCTCCACT CCAACCTCCA GCCTGGATGT CCCTGTCTGG GCCCTTTTTC TGTTTTAT 2940
TCTATGTTCA GCACCACTGG CACCAATATC ATTTTAATTC ACCGAAAGCA

Seq ID NO: 32 Protein Sequence
Protein Accession #: XP_054631.1

1 11 21 31 41 51
MPRGPAQPPA QRPPGPAASS SARRSQPVPO LRKRSRCEIA PSSEQEVVPA ASGDPQGEAP 60
GEGGSPAGRS GALTQKQEEA RKLNVFLQRP GGGVVEGPR KPSSRALEPA TAAALRRRLD 120
LGSCLDVLAQ AQQHGEPGLA QETVALMSDN LLRVLDPLC YRRLSAAADRE RILSLRTGRG 180
RAVLQVILVLP SLYGGGRSGL PRGPRGEEPP AAAPVSLPLP AILHVENPRE NTRPLTQVP 240
EEAPLRGCGL CTMHNLYFLA GGIRGSGAKA VCSNEVFCYN PLTNISQVR PMQQAQQLK 300
LVALDGLLYA TGGECLYSME CYDPRTDWT PRAPLPAGTF PVAHEAVACR GDLYVTGGHL 360
FYRLRLSPV KDAWDECPYS ASHRRSDIV ALGGFLYRFD LLRGVGAAMV RYNTVTGSWS 420

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RAASLPLPAP APLHCTTLGN TIYCLNPQVT ATFTVSGGTA QFQAKELQPF PLGSTGVLSP 480
FILTLPPEDR LQTSL

Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: CAT cluster

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    AATCCCCTTG CAGACTTTAC AAACAGAGTG TTTCCCTAACT GCTCTATGAA CAGAAAGGTT 120
    AAACCTCTGTG AGTTGAACCA ACACATCACA ACGCAGTTTG TGGGAATGAT TCTGTCTAGT 180
    TTTGAAACGA AGATATTTCC TTTTCTGCCG TTGACCTTAA AGCGCTTGAA ATCTACACTT 240
    GCAAAATTGCA CAAATAGAGT GTTTCAAATC TGCTCTGTCT AAGGGAACGT TCAACTCTGT 300
    GAGTTGAATG CACACAACAC AAGGAAGTTA CTGGGAATTC TTCTGTCTAG CCTTACATGA 360
    AAGAAAACCC GTTCCCAACG AAGGCCTCTA AGTGGTCAAA ATATCCACGT GCAGACTTTA 420
    CAAACAGAGT GTTTCACAA TGTGSAATGA AAAGAAAAGT AAACCTCTGAG AGTTGAACGC 480
    ACACATCGCA GAGCAGTTTC TGAGAAATGAT TCTGTCTAGT TTTTATACGA AGATATTTCC 540
    TTTTCTGCTT TGGCCTCTCA AGCGCTTGAA ATCTCCACTT GCAAAATCCA CAAAAAGAGT 600
    GTTTCAAATC TGTCTGTCTT AAGGAAGGT TCAACTCTGT GAGTTGAATA CACACAACAC 660
    20  AAAGAAGTTA CTGAGAAATC TTTCTGTCTG CATTATATGA AGAAATCCCG TTTCCAACGA 720
    AGGCATCTAA GAGGTCCAAA TATCCACTTG CAGACTTTAC AAACAGAGGG TTTCCAGAAT 780
    GGCTGTATGA AAAGAAAGT TAAACTCTGT GAGTTAAACA CACA
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Seq ID NO: 34 DNA sequence
Nucleic Acid Accession #: AF011468.1
Coding sequence: 257..1468

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    ATCTCAGTGG CGGACGAGGA CGCGCGGGAC AAGGGCGCGC TGGTCGGAGT GGCGGAGCGT 120
    CAAGTCCCCT GTCCGTCTCT CGTCCCTGTA GTGTCTTGG CGCTGCCTTG TGCCCGCCCA 180
    GCGCCTTTGC GGCCTCTCTT GCGCACCGAG GCGCCCTGTA GGATACTGCT TGTACTTAT 240
    35  TACAGCTAGA GGCATCATGG ACCGATCTAA AGAAAATGCG ATTTGAGGAC CTGTTAAGGC 300
    TACAGCTCCA GTTGGAGGTC CAAAACGCTGT TCTCGTGA CTGCAAAATTC CTGTGTCAGAA 360
    TCCATTACCT GTAAATAGTG GCCAGGCTCA GCGGGTCTTG TGTCTCTCAA ATTTCTCCCA 420
    GCGCGTTCTT TTGCAAGCAC AAAAGCTTGT CTCCAGTCAC AAGCCGGTTC AGAATCAGAA 480
    GCAGAAGCAA TTGCAAGCAA CCAGTGTAAC TCATCTCTGC TCCAGGCCAC TGAATAACAC 540
    CCAAAAGAGC AAGCAGCCCC TGCCATCGGC ACCTGAAAAT AATCTGAGG AGGAACTGGC 600
    40  ATCAAAACAG AAAATGAAG AATCAAAAAA GAGGCAGTGG GCTTTGGAAG ACITTTGAAAT 660
    TGGTCCGCCCT CTGGGTAAAG GAAAGTTTGG TAATGTTTAT TTGGCAAGAG AAAAGCAAAG 720
    CAAGTTTATT CTGGCTCTTA AAGTGTATT TAAAGCTCAG CTGGAGAAAG CCGGAGTGGA 780
    GCATCAGCTC AGAAGAGAAG TAGAAATACA GTCCCACCTT CGGCATCCTA ATATTCTTAG 840
    ACTGTAATGGT TATTTCCATG ATGCTACCAG AGTCTACCTA ATTTCTGGAAT ATGCACCACT 900
    45  TGAACAGTTT TATAGAGAAC TTCAAGAACT TTCAAAGTTT GATGAGCAGA GAACTGTCTAC 960
    TTATATAACA GAATTTGGCA ATGCCCTGTC TTAAGTCTAT TCGAAGAGAG TTATTCATAG 1020
    AGACATTAAG CCAGAGAACT TACTTCTTGG ATCAGCTGGA GAGCTTAAAA TTGCAGATTT 1080
    TGGGTGGTCA GTACATGCTC CATCTTCCAG GAGGACCACT CTCTGTGGCA CCCTGGACTA 1140
    CCTGCCCCCT GAAATGATTG AAGGTGCGAT GCATGATGAG AAGGTGGATC TCTGGAGCCT 1200
    50  TGGAGTTCTT TGCTATGAAT TTTAGTTTGG GAAGCCTCCT TTTGAGGCAA ACACATACCA 1260
    AGAGACCTTAC AAAAGAATAT CACGGGTGGA ATTCAATTC CCTGACTTTG TAACAGAGGG 1320
    AGCCAGGGAC CTCATTTCAA GACTGTTGAA GCATAATCCC AGCCAGAGGC CAATGCTCAG 1380
    AGAAGTACTT GAACCCCTCT GGATCACAGC AAATTCATCA AAACCATCAA ATTGCCAAAA 1440
    CAAAGAACTCA GCTAGCAAA CAGTCTAGGA ATCGTGCAGG GGGAGAAATC CTGAGCCAG 1500
    55  GGCTGCCATA TAACCTGACA GGAACATGCT ACTGAAGTTT ATTTTACCAT TGACTGTCTC 1560
    CCTCAATCTA GAACGCTACA CAAGAAATAT TTGTTTACT CAGCAGGTGT GCCTTAACCT 1620
    CCCTATTACG AAAGCTCCAC ATCAATAAAC ATGACACTCT GAAGTGAAAG TAGCCACGAG 1680
    AATTGTGCTA CTTATACIGG TTCATAATCT GGAGGCAAGG TTCGACTGCA GCGGCCCCGT 1740
    60  AGTGACCACT CTGCCCTGAC CCCGATCAGT TAAGGAGCTG TGCAATAACC TTCTTAGTAT 1800
    CTGAGTGAGT GTGTAACCTA TTGGGTTGGC GAAGCCTGTT AAAGCTGTTG GAATGAGTAT 1860
    GTGATTCTTT TTAAGTATGA AAATAAAGAT ATATGTACAG ACTTGTATTT TTTCTCTGTT 1920
    GGCATTCCTT TAGGAATGCT GTGTGTCTGT CCGGCACCCC GGTAGGCTTG ATTGGGTTTC 2040
    65  TAGTCTCTCT TAACCACTTA TCTCCATAT GAGAGTGTGA AAAATAGGAA CACGTGCTCT 2100
    ACCTCCATTT AGGGAATTGC TTGGGATACA GAAGAGGCCA TGTGTCTCAG AGCTGTATAAG 2160
    GGCTTATTTT TTTAAACAT TGGAGTCATA GCATGTGTGT AAACCTTTAA TATGCAATA 2220
    AATAAGTATC TATGTCTAAA AAAAAAATAA AAA
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Seq ID NO: 35 Protein Sequence
Protein Accession #: AAC63902.1

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    AQKLVSSHKP VQNKQKQQLQ ATSVPHPVSR PLNNTQKSKQ PLPSAPENNP EEBELASKQKN 120
    EESKKRWAL EDFFIGRLG KGFNGVYLA REKQSKFILA LKVLFKAQLE KAGVEHQLRR 180
    EVEIQSHLRH PNILRLYGYF HDATRVYLIL EYAPLGTVYR ELQKLSKFDE QRTATYITEL 240
    ANALSYCHSK RVIHRDIKPE NLLGSSAGEL KIADFGWSVH APSSRRTTLC GTLDYLPPEM 300
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IEGRNHDEKV DLWSLGLVCY EFLVGKPPFE ANTYQETYKR ISRVEFTFPD FVTEGARDLI 360
SRLKKNPSQ REMPLREVLEH PWITANSSKP SNQNKESAS KQS

5 Seq ID NO: 36 DNA sequence
Nucleic Acid Accession #: NM_016267
Coding sequence: 67..843

10 1 11 21 31 41 51
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AGCGTAGTGG ATGAACACTT CTCCAGAGCT CTGAGCAATA TCAAGAGCCC CCAGGAATTG 240
ACCCCTCGA GTCAAGAGTA AGGTGTGATG CTGAAAAACG ATGATAGCAT GTCTCCAAAT 300
15 CAGTGGCGTT ACTCTCTCC ATGGACAAAG CCACAACGAG AAGTACCTGT CACAAACCGT 360
GCCGCCAACT GCAACTTGCA TGTGCCTGGT CCCATGGCTG TGAATCAGTT CTCACCGTCC 420
CTGGCTAGGA GGGCCTCTGT TCGGCCTGGG GAGCTGTGGC ATTTCTCCTC CCTGGCGGGC 480
ACCACTCCTT TAGAGCCTGG CTACTCTCAT CCCTTCCCGG CTCGGCACCT GGTTCAGAG 540
CCCCAGCCTG ATGGGAAACG TGAGCCTCTC CTAAGTCTCC TCCAGCAAGA CAGATGCCTA 600
20 GCGCGTCCTC AGGAATCTCG CGCCAGGGAG AATGGCAACC CTGGCCAGAT AGCTGGAAGC 660
ACAGGGTTGC TCTTCAACCT GCCTCCCGGC TCAGTTCAC TAAAGAACT ATATGTATCT 720
CTGGATCTG CCAGTACACG CCTTCCAAAT GAAACTCTT CAGAGTTAGA GACACCTGGG 780
AATACTCAC TTACACCAAC AAACCACTGG GGCCACCCAC ATCGATACCT GCAGCATCTT 840
TAGTCAAGTT GGAGGAGAAA GACAACACTT GGTCTAAGAC ACGGCAGCAA GACATCCCTG 900
25 CATATGTGTC CAGATAAAAA TGAAGCTGC TCACACCCAC TTGCCTCCCC AATCTGTTAA 960
ACAGCTTCGT GTCTAGTATG AGCTCAGTAC TTGCGCTGTG AAAATCCAG AAGCCCCCGC 1020
TGTCATGTT CCCATCCAC ACCCTGCTTG CTCTGTGTA ACAGCTCAGA TGATGAATAA 1080
TAATAAACT GTACTTTTTT GGAATAAAAA AAAAAAAAAA AAAAAA

30 Seq ID NO: 37 Protein Sequence
Protein Accession #: NP_057351.1

35 1 11 21 31 41 51
MEEMKKAIR LPKGKQKPIK TEWNSRCVLF TYFQGDISSV VDEHPSRALS NIKSPQELTP 60
PSSQSEGVM LKNDDSMSPNQ WRYSSPWTKP QPEVPTNRA ANCLHVP GP MAVNQFSPSL 120
AARRASVRFP ELWHFSSLAG TSSLEPGYSH PFPARHLVPE PQPDGKREPL LSLQLQDRCL 180
ARRPQESAPR ENGNPQIAG STGLLFLNLP GSVHYKKLYV SRGSASTSLP NETLSELETP 240
40 GKYYSLTPPN HWGHPHYRLQ HL

Seq ID NO: 38 DNA sequence
Nucleic Acid Accession #: AK058088.1
Coding sequence: 252..1772

45 1 11 21 31 41 51
AGGAAACCAA GGCAAGCTCC CCCTGTCAAA GCACCTTGGC CCATAAGAAG AAAAGGGGGA 60
GCCCCAGATG TGATGAGCGC TTCCAGGCTT CAGGCTCAGA AGGCGCCCCC AGCTCTCCTG 120
TAACCTCAGG GCCAGTGTGA TGGGAGTTCC TCCACTCAGC ACACTTCCCC TGTAAACACG 180
50 CCTGTGTGGG GCAAAAGGGC TTGGAACGG TTGCTGTCT TTTCTCTCCT GCGTAATTTT 240
CACTTTTCATT CATGATAATG TCGAACCGC ACAAGCTCG GCTGGAACGC CGGGTCACTG 300
GCTCAACCAA CCGGTGGCGT TTGCCCAAAC AGCCTTTCTC TGGGGACCTG CTCTCACTTT 360
CCCAGATGTG CAAGGCTCTG AGCATAGACT TTGAGGAAGC TTTGAGGAAC CCAGACAGGT 420
TATGCATTTT ACAATCCAG AAGTTTTTCT TTGAGAATTT CAAGAACAAG GACATCCAAA 480
55 GTGGGGAAGC AGATGTGATT CTCGAGTGCC TGGGCTTCAA ATGGGAGCTC CATCAGCCCC 540
GGCTTTTTCA GTCTGAGACC TTGGCCAAGC TCTACCTGAA AGCCCTGGCG CAGGGCACCA 600
CACACCCCTT GAGGGAGCTG GAGGAGCTTC TGCGAGCTCA ATCACCTAAG AAGACCAAAG 660
AAAAATCCCC TGCAAGAGG ATCATCATTT CCTTGAAGAT CAATGACCCA CTGGTCACTA 720
AAGTCGCTACT CGCCACGGCC CTGAAGAACC TCTACATGAG TGAGGTGGAG ATTAACCTGG 780
60 AAGACCTACT GGGAGTGTG GCTTCCGCCC ACATCCTCCA GTTCAGTGGC CTGTTTCAAA 840
GGTGCCTGGA TGTGATGATA GCCAGACTCA AGCCAAGCAC CATCAAGAAA TTCTACGAGG 900
CGGGCTGCAA GTACAAGGAA GAGCAGCTCA CCACCGGCTG CGAGAAGTGG CTGGAATGA 960
ACTTGGTTCC TCTAGGGGGG ACGCAGATCC ACCTCCACAA AATCCACAG GACCTGCTCC 1020
ACAAAGTGCT GAAGTCCCCC AGGTTATTTA CCTTTAGTGA ATTCCATCTT CTGAAAACAA 1080
65 TGCTTTTGTG GGTCTTCTTG CAACCTGAAT ACAAGATTCA GGCAATTCAG ACTTATGAAA 1140
CGTGATGAC ATTTTAAAG AGCTTTCCTG AGAACTGTTG CTTTCTGGAC CGGGACATAG 1200
GACGGAGCTT GAGGCCGCTC TTCTCTGCTG TGCTCTGCA CGGCATCACC AAAGGCAAGG 1260
ATCTGGAGGT GTGCGGCAC CTTAACTTCT TCCCAGATC ATGGCTCGAC CAGGTTACAG 1320
70 TCAACCATTA CCACGCACTG GAGAATGGGG GCGACATGGT CCACCTGAAA GATCTTAACA 1380
CCACGGCTGT GAGATTTTGG CTGCTCTTTA ACCAGGAGAA TACAACCTAT TCGAAAAACGA 1440
TTGCTCTATA TGGATTCTTC TTTAAGATAA AGGGACTCAA ACATGATACT ACCCTCTATA 1500
GTTTTTACAT CGAGAGAATA AAGCACACAG ACCTGGAATC TCCTCTGCG GTCTACGAGC 1560
ACAACCCAGT CAGCCTGCGA GCGCACGCCC TGGTGAAGTA TGAGATCAGA GCAGAGGCC 1620
75 TGGTTGACGG CAAGTGGCAG GAGTTCAGGA CAAACCAAGT TGTGGGCATC CCAATCTATG 1680
CCACGTCACT CTGCAAAAGC CATACCTTGA AAATCCAAAC TGTGGGCATC CCAATCTATG 1740
TAAGTTTTCG ATTCATCTTC CCAGCATCTT GACAGTTTCC AGAAGAATCT ATGGGATTTT 1800
CCCCCACTG GTCTGCATAA AAGAAAATAA AATGACATAA AAGGGAGC

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Seq ID NO: 39 Protein Sequence
Protein Accession #: BAB71658.1

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5      1      11      21      31      41      51
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QIQKFFPFNF KNKDIQSSEA DVILECLGPK WELHQPRLFQ SETLAKLYLK ALAQGITHTPL 120
RELEELLRAQ SPKKTKEKSP AKRIISLKI NDPLVTKVAF ATALKNLYMS EVEINLEDDL 180
GVLASAHILQ FSGLFQRCDV VMARLKPEST IKKFYEAGCK YKEEQLTITGC EKWLENNLVP 240
10    LGGTQIHLHK IPQDLLHKVL KSPRLFTFSE FHLLKTMLLW VFLQLNYKIQ AIPTYETVMT 300
PFKSFPENCC FLDRDIGRSL RPLFLCLRHL GITKGKDLEV LRHLNFPFES WLDQVTVNHV 360
HALENGGDMV HLDKDLNTQAV RPLGLFNQEN TTYSKTIALY GFFPKIKGLK HDTTSYSFYM 420
QRIKHTDLES PSAVYEHNVH SLRAARLVKY EIRAEALVDG KWQEFRTNQI KQKFGILTSS 480
15    CKSHTLKIQT VGPIYVSFA FIPPAS
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Seq ID NO: 40 DNA sequence
Nucleic Acid Accession #: NM_032899.1
Coding sequence: 186..1070

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CTTGGGAGCA GCGCGCTCC CCGGGGTGCG GAGCCCCAC TCCTCCGTGG TGTGTTCCAT 120
TTGCTTCCCA CATCTGGAGG AGCTGACGTG CCAGCTCCCC CCAGCACAC CCAGGAGCGG 180
25    GAGGCATGAG CCGTCAAGG CACCTGGGCA AAATCCGGAA GCGTCTGGAA GATGTCAAGA 240
GCCAGTGGGT CCGGCCAGCC AGGGCTGACT TTAGTGACAA CGAGAGTGCC CGGCTGGCCA 300
CGGACGCCCT CTGGATGGG GGTTCGTGAAG CCTACTGGCG GGTGCTCAGC CAGGAAGCGG 360
AGGTGGAGCT CTGTCTCTCG GTGGAGGCC AGTACATCCA GGGCAGGCC AGGGAGCCCC 420
CGTGTCCCCC AGACACCTCG GGAGGGGCGG AAGCAGGCC TAAGGGACTG GACTCCAGCT 480
30    CCTACAGTC CCGCACCTAC TTCCCTGTGG CCTCAGAGGG CAGCGAGCCG GCCCTACTGC 540
ACAGCTGGGC CTAGCTGAG AAGCCCTACC TGAAGGAAAA ATCCAGCGCC ACTGTGTA 600
TCCAGACCGT CAAGCAACAC AACATCAGAG ACCTCGTCCG CCGCTGCATC ACCCGGACTA 660
GCCAGAACAT TTCATCCCGG AGTGTGGAAG GAGAGATATA CTGTGCCAAG TCAGGCAGGA 720
AATCACTGG CCAAAATCCG GAGAAAGTTCA TCATCTCGGA CTGGAGATT GTCTGTCTG 780
35    GATCTTACAG CTTCACCTGG CTCTGCGGAC ACGTGCACCG GAACATCCTC TCCAAGTTCA 840
CAGGCCAGGC GGTGGAGCTG TTTGACGAGG AGTTCGGCCA CCTCTACGCC TCCTCCAAGC 900
CTGTGATGG CCTGAAGTCC CCGCGGTCTG TCGCCCCCGT CCGCCCCGGA GCAGCCCCGG 960
CCAAATGGCG CCTTAGCAGC AGCAGTGGCT CCGCCAGTGA CCGCACGTCC TCAAACCCCT 1020
40    TCAGCGCGCG CTGCGCAGGC AGCCACCCCG GTACCCGAAC TGACGGCTGA GATGAGGTTA 1080
GAATGACTGG GCCCGGCTGA ACATTCCTAA TTGATTTC AATCTGCTG AGAAAGTTTA 1140
AGGAAGGCAA AGCTTGCCAG GTACAGAGA CTCCAAAGCC AACCTGCAGG CAGGAACAAG 1200
CCTGTGCGCT TGTGAGCTC AGTCCCTGGG GATAGGGGAG AACTGCAGG CAGGAACAAG 1260
CCCCCTACT CCTGACCACC CTCCATCAGC AGTCTCCCT CCGTGGTCTG CTCTGTGAC 1320
45    AAAGGTGCAG TTTCTCTCT CTGGGCACC TGTAAACATGT GATGCGCTGC CTGCTGGGAG 1380
GTTAGGTCGG GGCTGCCCCG GCGAGTGGAG CATGAGCAGA ACCGCGAGG GTCACTTCTG 1440
GGCAGAGCT TTGAGAGCT GGGTCCAGGT TGCCACATAG AAGCAGCTCT CCAAGTTGAA 1500
CCTCTCTCTG CCAGCTGGG GTCCTAAGCG ATGAGCAGAA TCCCCACTC CCACCCACC 1560
AACCACAAT GGATATGTAG TGAGCAAGAA ATAAACCTTT GTGTGTTAAA AAAAAAAAAA 1620
50    AAAAAAA
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Seq ID NO: 41 Protein Sequence
Protein Accession #: NP_116288.1

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55      1      11      21      31      41      51
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DFLSSVEAQY IQAQAREPPC PBDTLGGAEA GPKGLDSSSL QSGTYFPVAS EGSEPALHLS 120
WASAEKPYLK EKSSATVYFQ TVKHNNIRDL VRCIIRTSQ NISIRSVGE IYCAKSGRKF 180
60    TQIREFKFI SDWRFLVSGS YSFTWLCGHV HRNLSKFTG QAVELPDEEF RHLVASSKPV 240
MGLKSPRLVA PVPPGAAPAN GRLSSSSGSA SDRSSSNPFS GRGAGSHPGT RTDG
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Seq ID NO: 42 DNA sequence
Nucleic Acid Accession #: NM_000782.2
Coding sequence: 405..1946

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CCCCGTGGCT CCAGCAAGCC CTAGAGGTCA GCCTTGCGGA CCAACAGGAG GACTCCCAGC 120
70    TTTCCTTTT CAAGAGGTAC CCCAGACACC GGCCACCTCT TCCAGCCCC TGCGGCCAGT 180
GCAAGGAGGC ACCAATGCTC TGAGGCTGTC GCGTGTGCA GCGTCGAGCA TCCTCGCCGA 240
GTCTTCTGTC TGCTGTCCC GCCTCACCCC GCTCCATCAC ACCAGCTGGC CCTCTTGCT 300
TCCTTTTCCC AGAATCGTTA AGCCCCGACT CCACTAGCA CCTGTACCA ACCTCGCCCC 360
ACCCATCTCT CTGCTTCC CGCGCTCCGG TGTCCCCCGT TGCCATGAGC TCCCCATCA 420
75    GCAAGAGCCC CTCGCTGGC GCCTTCTGTC AGCAGCTGCG CAGTCCGAGG CAGCCCCGA 480
GACTGGTGAC ATCTACGGCG TACAGTCCC CTCAGCCGCG AGAGGTGCCA GTCTGCCCGC 540
TGACAGCTGG TGCGGAGACT CAGAACGCG CCGCCCTGCC GGGCCCCACC AGCTGGCCAC 600
TGCTGCGGAG CCTGCTGAG ATTCTCTGGA AAGGGGTCT CAAGAAACAG CACGACACC 660
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TGGTGGAGTA CCACAAGAAG TATGGCAAGA TTTTCCGCAT GAAGTTGGGT TCCTTTGAGT 720
CGGTGCACTT GGGCTCGCCA TGCCTGCTGG AAGCGCTGTA CCGCACCGAG AGCGTACCCC 780
AGCGGCTGGA GATCAAACCG TGGAAAGCCCT ATCGCGACTA CCGCAAAGAA GGCTACGGGC 840
TGCTGATCCT GGAAGGGGAA GACTGGCAGC GGGTCCGGAG TGCCTTTCAA AAGAACTAA 900
TGAAACCAGG GGAAGTGATG AAGCTGGACA ACAAAATCAA TGAGGTCTTG GCCGATTTTA 960
TGGGCAGAAT AGATGAGCTC TGTGATGAAA GAGGCCACGT CGAAGACTTG TACAGCGAAC 1020
TGAACAAATG GTCGTTTGAA AGTATCTGCC TCGTGTGTA TGAGAAGAGA TTTGGGCTTC 1080
TCCAGAAGAA TGCAGGGGAT GAAGCTGTGA ACTTCATCAT GGCCATCAAA ACAATGATGA 1140
GCACGTTTGG GAGGATGATG GTCACTCCAG TCGAGCTGCA CAAGAGCCTC AACACCAAG 1200
TCTGGCAGGG ACACACTCTG GCCTGGGACA CCATTTTCAA ATCAGTCAAA GCTTGATCG 1260
ACAACCGGTT AGAGAAGTAT TCTCAGCAGC CTAGTGCAAG TTTCTTTGT GACATTTATC 1320
ACCAGAAATG GCTTTCAAAG AAAGAATTGT ATGCTGCTGT CACAGAGCTC CAGCTGGCTG 1380
CGGTGGAAAC GACAGCAAAC AGTCTAATGT GGATTTCTTA CAATTTATCC CGTAATCCCC 1440
AAGTGCAACA AAAAGTCTCTT AAGGAAATTC AAGTGTATT ACCTGAGAAT CAGAGGCCAC 1500
GGGAGGAAGA TTTGAGGAAT ATGCCGTATT TAAAAGCCTG TCTGAAAGAA TCTATGAGGC 1560
TTACCCCGGG TGTACCATTT ACAACTC3GA CTCTTGACAA GGCAACAGTT CTGGGTGAAT 1620
ATGCTTTTACC CAAAGGAAAC GTGCTCATGC TAAATACCCA GGTGTTGGGA TCCAGTGAAG 1680
ACAAATTTTGA AGATTCAAGT CAGTTTAGAC CTGAACGTTG GCTTCAGGAG AAGGAAAAAA 1740
TTAATCCITT TGGCATCTTT CCATTTGGCG TTGAAAAAAG AATGTGCATT GGTGCGCAT 1800
TAGCAGAGCT TCAACTGCAT TTGGCTCTTT GTTGGATTGT CCGCAAAATC GACATCCAGG 1860
CCACAGACAA TGAGCCTGTT GAGATGCTAC ACTCAGGCAC CCTGGTCCCC AGCCGGGAAC 1920
TCCCCATCGC GTTTTGCCAG CGATAATACG CCI CAGATGG TGGTATTGTC TAACATCATA 1980
TCCAATCGAG GGAAGCGGAC TGAGTGTCTGG GATCCAAGGC ATTCTACAGG GTTCACTGCT 2040
GGTTTACACT TCACCTGTGT CAGCAACATC TTCAGGTGCT TAGAATGGCC TGGGAGCCTG 2100
TTCTGCTCTG CATCTTCCAT GACATGAAAG GGAGGCTGGC ACTTGTCACT CAGGTAGAGG 2160
TTACAAACCG TTTACGGCCC TGCTACCACA TTCACTGTTT GAATCTTTAA TTCCCAAGAA 2220
TAAGTTTACA TTTCACAATG AATGACCIAC AACAGCTAAA TTTTCTGGGG CTGGGAGTAA 2280
TACTGACAAAT CCATTTACTG TAGCTCTGCT TAATGTACTA CTTAGGAAAA TGTCCTGCT 2340
TAATAATGTA AGCCAAGCTA AATGATGTTT AAAGTTATCA GGCCTCCCAT GAAATTCGCT 2400
TCTTCTCGCA TTGAATATAA AACATTATTG GGAAACTAGA GAACACCTCT ATTTTAAAA 2460
GGACTTTAAG GAAGTCAAAC AACTTCTAAG ACTAGTCATT CACTGGGGCA TTATTGTTA 2520
GAGGACCTTA AAATTGTTTA TTTTAAAT GTGATTCCTT TATGGCATT GGTAAAGAT 2580
GAAGCAATAA TTTTAAAT GTGATGTGC ATATGAAGCA CAGACATGCA TGTGTGTGTG 2640
TGTCTGTGTG TGTGTGTGCG TGTATGTGTG TGTGGTCTCT AATGTAATT TGCCTCAGTC 2700
ATTTTTTAA TATTGTCAGT ACTTGATTTA GGATCTGTGG TGCAGGGCAT GTTTCAGAGT 2760
TTAGTCACAG CTTAAAACAT TTCAGTGTGA CTTTAAATTT ATAAATGAT TTCCCATGCC 2820
ATAATTTTTC TGTCTATTA AATGGACAAG TGTAAAGCAT GCAAAAGTTA GAGATCTGTT 2880
ATATAACATT TGTTTTGTGA TTTGAATCC TAGGAAAAAT ATGATTTTCA AAATGTAAAA 2940
TGACACAGAA TGCAATGCAAT ACTTATAAGA CTTAAAAATT GTGTTTACAG ATGTTTATT 3000
TGTGCATATT TTTACTACTG CTTTTCCTAA ATGCATACGT TATATAATTC TGTGTATTG 3060
ATAAATATT CTCTCATACAT TATAATTTTA GAATATTTC GAAATATACA TTTATGCTCT 3120
TATATTGTAA TAAATATGTA CATATCTAGG TATATGCTTT CTCTCTGCTG TGAATATTAT 3180
TTTAGAATTA TAATTCACGT CTTGTCATAT TTCACTGTA TACCTTCAAA TTCTCTGAAA 3240
GTAAAAATAA AAGTTTTTAA ATATT

Seq ID NO: 43 Protein Sequence
Protein Accession #: NP_000773.1

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55
60

1 11 21 31 41 51
MSSPISKSRs LAAPLQQLRS PRQPPRLVIS TAYTSFQPRE VVPCPLTAGG ETQNAALPG 60
PTSWPLLASL LQILWKGGLK KQHDTLVEYH KKYGKIFRMK LGSFESVHLG SPCLLEALYR 120
TESVPORLEI KPWKAYRDYR KEGYGLLILE GEDWQVRSA FQKKLMKPGE VMKLDNKINE 180
VLADFMGRID ELCDERHVE DLYSELNKS FESICLVLYE KRFGLLQKNA GDEAVNFIMA 240
IKTMMSTFGR MNVTPVELHK SLNTKVMQGH TLAWDTIFKS VKACIDNRLE KYSQQPSADF 300
LCDIYHQNRL SKKELYAAVT ELQLAAVETT ANSLMWILYN LSRNPQVQOK LLKEIQSVLP 360
ENQRPREEDL RNMPYLKACL KESMRLTFGV PFTTRTLDKA TVLGEYALPK GTVLMMLNTQV 420
LGSSDNEFED SSQFRPERWL QEKEKINPFA HLPFGVGKRM CIGRRLAELQ LHLALCWIVR 480
KYDIQATDNE PVEMLHSGTL VPSRELPIAF QQR

Seq ID NO: 44 DNA sequence
Nucleic Acid Accession #: NM_007000.2
Coding sequence: 1-777

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1 11 21 31 41 51
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GTTGTGGGCA ATATCATTAT TCTGCTGTCA GGCCTGTCCC TGTGTTGCTGA GACCATATGG 120
GTGACAGCCG ACCAGTACCG TGTATACCCA CTGATGGGAG TCTCAGGCAA GGATGACGTC 180
TTCGCTGGTG CCTGGATTGC CATCTTCTGC GGCCTTCTCT TCTTCATGGT AGCCAGTTTT 240
GGTGTGGGTG CCGCACTCTG CCGCCGCGCG TCCATGGTCC TCACGTACCT GGTGCTCATG 300
CTCATGCTCT ACATCTTCCA GTGCGCCTCC TGCAATCAGT CCTACACCCA CCGTGACTAC 360
ATGGTGTCCA ACCCATCCCT GATCAACCAAG CAGATGCTGA CCTTCTACAG CGCGGACACC 420
GACCAAGGCC AGGAGCTGAC CCGCCTCTGG GACCGCGTCA TGATTGAGCA AGAATGCTGT 480
GGCACATCTG GTCCCATGGA CTGGGTGAAC TTCACGTGAG CCTTCCGGGC GGCCACTCCG 540
GAGGTGGTGT TCCCTGGGCC CCCACTGTGC TGTGCGCGGA CGGGAAACTT CATCCCCCTC 600
AACGAGGAGG GCTGCCCCCT GGGGCACATG GACTACCTGT TCACCAAGGG CTGCTTCGAA 660
CACATGAGCC ACGCCATCGA CAGCTACACG TGGGGTATCT CGTGGTTTGG GTTTGCCATC 720

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CTGATGTGGA CGCTCCCGGT CATGCTGATA GCCATGTATT TCTACACCAT GCTCTGAGGG 780
 ACAGGAGGGG AAGGCAACAT ACACACCCCG GACTCCTCCG CATCCTCTTC CTGCTTCCTC 840
 CGCTGGGCGT GATGGGCTGC CTCACCTCTC ACCTCCCAAC GTCCCTAGCC CTTACGTCCT 900
 TOCACTTCCA AGATCTTTT CCAGGTTCTT GAGCCCTACT GTGTCTCAGG TGTGCCCTGA 960
 AACCCAGGG CTGTGTGCA CATATCCTTA GCCCATCTTT CAAGGGACCT CTCCATGATC 1020
 CCACCTCCCA TTCACAGATA CCTCTCTGT AGCTCTCTGA CCTCCTCTT CATGGCAGGC 1080
 ATCGCATTC TTGCTGAACC GTTTGTGATT GCCATTTGAG CTCTGGAAGC CTCTATTGCC 1140
 ATGAGAGTTC TGTACCGGTC ACTTTACTGT CCCCATCATC ACCCAGCAG GGGCTAAGCA 1200
 TATACTAGAT AGTCAATAAA TAA

Seq ID NO: 45 Protein sequence:
 Protein Accession #: NP_008931.1

1 11 21 31 41 51
 MASAAAAEAE KGSPVVVGLL VVGNIILLS GLSLFAETIW VTADQYRVYP LMGVSGKDDV 60
 FAGANIAIFC GFSFFMVASF GVGAALCRRR SMVLTYLVLM LIVYIFECAS CITSYTHRDY 120
 MYSNPSLITK QMLTFYSADT DQGQELTRLW DRVMIEQECC GTSGPMDWVN PTAFAFRATP 180
 EVVFPWPPLC CRRIGNFIPL NEEGCRLGHM DYLFYTKGCFE HIGHAIDSYT WGISWFGFAI 240
 LMWTLFVMLI AMYFYTML

Seq ID NO: 46 DNA sequence
 Nucleic Acid Accession #: NM_006760.1
 Coding sequence: 39..593

1 11 21 31 41 51
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 ACATCTCAAG CCTCTCTGGT CTGCTGTCCC CGGCGCTAAC GGAGAGCCTG CTGGTTGCCT 180
 TGGCCCGCTG TCACCTCACA GGAGGCAATG CCACACTGAT GGTCCGAGAG GCCAATGACA 240
 GCAAAGTGGT GACGTCCAGC TTTGTGGTGC CTCCTGTCCG TGGCGCAGG GAACTGGTGA 300
 GTGTGGTGGG CAGTGGTGTG GGCTTCACAG TCACTCGGCT CAGTGCATAC CAGGTGACAA 360
 ACCTCGTGCC AGGAACCAAA TTCTACATT CTACCTAGT GAAGAAGGGG ACAGCCACTG 420
 AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCCTCGAAG GAACATGGAA TCATTGGGC 480
 TGGGTATGGC CCGCACAGGG GGCATGGTGG TCATCAGGT GCTGCTCTCT CTCGCCATGT 540
 TCCTGCTGGT GCTGGGCTTC ATCATTTGCC TGGCACTGGG CTCCCGCAAG TAAGGAGGTC 600
 TGCCCGGAGC AGCAGCTTCT CCAGGAAGCC CAGGCGACCA TCACGCTCCC CAGCCCACTT 660
 GCTCCGAGGC CCGAGGCTGT TGGCTCCCTT GGTGCCCTCG CCTCCTCTC CTGCCCTCTT 720
 CTCCCCTAGA GCCTCTCTCT CCTCTGTGCC CTCTCCTTGC CCCAGTGC TCACCTTCCA 780
 ACACCTCATT ATTCCTCTCA CCCCACTCCT GTCAGAGTIG ACTTTCCTCC CATTTTACCA 840
 CTITAAACAC CCCCAATAA ATTCCCAT CTTTCAGTGA ACTAAGTCCC TATAATAAAG 900
 GCTGAGGCTG CATCTGCCAA AAAAAAAAAA AA

Seq ID NO: 47 Protein Sequence
 Protein Accession #: NP_006751.1

1 11 21 31 41 51
 MAPLLPIRTL FLILILLALL SPGAADFNIS SLGGLLSPAL TESLLVALPP CHLTGGNATL 60
 MVRRANDSKV VTSSFVVPPC RGRRELVSIV DSGAGFTVTR LSAYQVNLV PGTKFYISVL 120
 VKKGATIESS REIPMSTLPR RNMESIGLGM ARTGGMVVIT VLLSVAMFLV VLGFIIALAL 180
 GSRK

Seq ID NO: 48 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 200-2932

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 ATTGCTGATG GATCAGTGAG CCTGTGTTCA TGCCAGTGAG CTGCTGTGGC TCAGATACTG 60
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 TCCTCGAGT TCTGGTGTGA AGAGATAAAT CACCAGTCAC AGACTATGCA CCCGACTGCT 180
 GCTGTTCACT CCAGGGAATA TGAAAGTTGG AGTGCTGTGG CTCACTTCTT TCTTCACTT 240
 CACTGACGGC CACGGTGGCT TCCTGGGGAA AAATGATGGC ATCAAAACAA AAAAAAGACT 300
 CATGTGAAAT AAGAAAAAAC ATCTAGGCCC AGTCGAAGAA TATCAGCTGC TGCTTCAGGT 360
 GACCTATAGA GATTCCAAAG AGAAAAGAGA TTTGAGAAAT TTTCTGAAGC TCTTGAAGCC 420
 TCCATTATTA TGGTCACATG GGCTAATTAG AATTATCAGA GCAAAGGCTA CCACAGACTG 480
 CAACAGCCTG AATGGAGTCC TGCACTGTAC CTGTGAAGAC AGCTACACCT GGTTCCTCTC 540
 CTCATGCTT GATCCCCAGA ACTGCTACCT TCACACGGCT GGAGCACTCC CAAGCTGTGA 600
 ATGTCACTC AACAACCTCA GCCAGAGTGT CAATTCTCTG GAGAGAACAA AGATTTGGGG 660
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 CTCCAAATAT GCAAATGGAA TTGAAATTCA ACTTAAAAA GCATATGAAA GAATTCGAAG 780
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 TAAGACAGCC CTTCACAGC TGTTCCTATT AGAAGACGGC TCTTCAGAG TGTTCGGAAA 960
 AGCCCACTGT AATGACATTG TCTTTTGATT TGGGTCCAGG TATGATGAAT ATACCTGACC 1020
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TGTAGGCAAT GCCACTGAGG CAGCTGTGTC ATCCTTCGTG CAAAATCTTT CTGTATCAT 1200
TCGGCAAAAC CCATCAACCA CAGTGGGGAA TCTGGCTTCG GTGGTGTGCA TTCTGAGCAA 1260
TATTTCTATCT CTGTCACTGG CCAGCCATTT CAGGGTGTCC AATTCAACAA TGGAGGATGT 1320
CATCAGTATA GCTGACAATA TCCTTAATTC AGCCTCAGTA ACCAACTGGA CAGTCTTACT 1380
GCGGGAAGAA AAGATATGCCA GCTCACGGTT ACTAGAGACA TTAGAAAACA TCAGCACTCT 1440
GGTGCCCTCCG ACAGCTCTTC CTCTGAATTT TTCTCGGAAA TTCATTGACT GGAAGGGGAT 1500
TCCAGTGAAC AAAAGCCCAAC TCAAAAGGGG TTACAGCTAT CAGATTAAAA TGTGTCCCCA 1560
AAATACATCT ATTCCCATCA GAGGCGTGT GTTAATTGGG TCAGACCAAT TCCAGAGATC 1620
CCTTCCAGAA ACTATTATCA GCATGGCCTC GTTGACTCTG GGGAACTTC TACCCGTTTC 1680
CAAAAATGGA AATGCTCAGG TCAATGGACC TGTGATATCC ACGGTATTTC AAAACTATTTC 1740
CATAAATGAA GTTTTCTTAT TTTTTCCTCA GATAGAGTCA AACCTGAGCC AGCCTCATTTG 1800
TGTGTTTTGG GATTTTCAGTC ATTTGCAGTG GAACGATGCA GGCTGCCACC TAGTGAATGA 1860
AACTCAAGAC ATCGTGACGT GCCAATGTAC TCACCTGACC TCCTTCTCCA TATTGATGTC 1920
ACCTTTTGTCT CCTCTTACAA TCTTCCCGT TGTAAAATGG ATCACCTATG TGGAGCTGGG 1980
TATCTCCATT GGAAGTCTCA TTTTATGCTT GATCATCGAG GCTTTGTGTT GGAAGCAGAT 2040
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CCAGCATTTG ATGATGGCTG TTGGATTITG CCTGGGTATG GGGTGCCCTC TCATTATATC 2340
TGTCATTACC ATGTCTGTCA CGCAACCTAG CAAACCTAC AAAAGGAAAG ATGTGTGTTG 2400
GCTTAACTGG TCCAATGGAA GCAAACTACT CCTGGCTTTT GTTGTGCTCT CACTGGCTAT 2460
TGTGGCTGTG AACTTCTGTT TGCTGTCTCT AGTTCTCACA AAGCTCTGGA GGCCGACTGT 2520
TGGGGAAGA CTGAGTCGGG ATGACAAGGC CACCATCATC CGCGTGGGGA AGAGCCTCCT 2580
CATTCGTACC CCTCTGCTAG GGCTCACCTG GGGCTTTGGA ATAGGAACAA TAGTGGACAG 2640
CCAGAATCTG GCTTGGCATG TTATTTTTCG TTTACTCAAT GCATTCCAGG GATTTTITAT 2700
CTTATCTCTT GGAATACTCT TGGACAGTAA GCTGCGACAA CTCTCTGTCA ACAAGTTGTC 2760
TGCTTTAAGT TCTTGAAGC AAACAGAAAA GCAAAACTCA TCAGATTATC CTGCCAAACC 2820
CAAAATCTCA AAGCCTTTCA ACCCACTGCA AAACAAAGGC CATTATGATC TTCTCATAC 2880
TGGAGATTCC TCCGACAACA TCATGCTAAC TCAGTTTGTG TCAAAATGAAT AAGGCAAGGA 2940
ATCATAAAAT CAAGAAAAAA TTTCCAGAAC AACTTGACAT TTAGAGACAA ATGTCAATGA 3000
AGAAATATG CTCAGTATTC GATCGGGTTT TCTGATTAG GGGTCTGGGA ATAAACAAAG 3060
AATGTCTCAG TGGCTTCA

Seq ID NO: 49 Protein sequence:
Protein Accession #: EOS sequence

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1 11 21 31 41 51
MKVGVWLWIS FFTFTDGHGG FLGKNDGIKT KKEILVNKKK HLGFEVEEYQL LLQVTVRDSK 60
EKRLRLNFKL LKPPLLWISH GLIRIIRAKA TTDNSLNGV LQCTCEDSYT WFPFSCLDPQ 120
NCYLHTAGAL PSCECHLWNL SQSVNFCERT KIWGTFKINE RFTNDLNSG SAIYSKYANG 180
IEIQLKKAYE RIQGFESVQV TQFRNGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALHK 240
LFPLEDGSFR VFGKACNDI VPGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV 300
LSLLEELNKN FSMIVGNATE AAVSSFVQNL SVIIRQNPST TVGNLASVVS ILSNISLSL 360
ASHFRVSNST MEDVISIADN ILNSASVTNW TVLLREEKYA SSRLLLETLEN ISTLVPPPTAL 420
PLNFSRKPID WKGIIVNKSQ LKRGYSYQIK MCPONTISIP RGRVLIGSDQ QRSPLPETII 480
SMASLTIGNI LPVSRNGNAQ VNGFVISTVI QNYSINEVFL FFSKIESNLS OPHCVWFDFS 540
HLQWNDAGNI LVNETQDITV CQCHLTSFSS ILMSPFVPST IFFVVKWITY VGLGISIGSL 600
ILCLIEALF WKQIKKSQTS HTRRICMVNI ALSLLIADVW FIVGATVDTT VNPSPGVCTAA 660
VFFTHFFYLS LFFWMLMLGI LLAYRIILVF HHMAQHLMMV VGFCLGYGCP LIISVITIAV 720
TQPSNTYKRR DVCWLNWSNG SKPLLAFFVVP ALAIVAVNFV VVLLVLTKLW RPTVGERLSR 780
DDKATILRVG KSLLLLTPLL GUTWFGIGT IVDSONLAWH VIPALLNAPQ GFFILCFGLL 840
LDSKLRLQLF NKLSALSSWK QTEKQNSSDL SAKPKFSKPF NPLQNKGHYA PSHTGDSNDN 900
IMLTQFVSNE

Seq ID NO: 50 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 63-3224

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1 11 21 31 41 51
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AGCAGCAGCC GCAGCAGCAG ACCCCGGAGT TTGCAGATGC GGCCCCAGCG GCGCCCGCGG 180
CGGGGAGGCT GGGTGTCTCA GTGAACCACC CAGGGRATGA CGAGGTGCGG AGTGAGGATG 240
AAGCCACAGT AAAGCGGCTT CGTGGGAGG AGACGCACGT CTGTGAGAAA TGCTGTGCGG 300
AGTTCTTCAG CATCTCTGAG TTCTTGAAC ATAGAAAAA TTGCACTAAA AATCCACCTG 360
TCCTCATCAT GAATGACAGC GAGGGGCTTG TGCTTTCAGA AGACTTCTCC GGAGCTGTAC 420
TGAGCCACCA GCCCACCAGT CCGGCAGTA AGGACTGTCA CAGGGAGAAT GGCGGCAGCT 480
CAGAGGACAT GAAGGAGAG CCGGATGCGG AGTCTGTGGT GTACCTAAAG ACAGAGACAG 540
CCTTGCCACC CACCCCCAGG GACATAAGCT ATTTAGCCAA AGGCAAAGTG GCCAACACTA 600
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CACTCCCTGC CCCCGTGCCT GTGCGCAACA GCATCCCGTG GGTCTCTGAG CAGATCTTGT 720
GTCTGCAGCA GCAGCAGCTA CAGCAGATCC AGCTCACCGA GCAGATCCGC ATCCAGGTGA 780
ACATGTGGGC CTCGCCAGCC CTCCTACTCA GCGGGGCAGG GGCCGACACT CTGAAGACCT 840
TGGCAGCCA CATGTCTCAG CAGTTTCTG CAGCTGTGCG TTTGCTCAGC CAGAAAGCTG 900

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GAAGCCAAAG TCTGTCTCTG GATGCTTGA AACAAAGCAA GCTACCTCAC GCCAACATCC 960
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TGCTGCAGCA ACATATTCGG ATGCACATGG GCGGTACAGT TCCCAACACG CCCCTGCCAG 2040
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CTCTGTAGG TACGAGCGGA AAAAGAGTCT CAGAATCTT TCCCAAGGAA ATCTTGCCCC 2940
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TGGCCGTGAA GACCAATGAG ATCTCTGTGA TCCAGAGTGG GGGGTTTCTT ACCCTCCCGG 3060
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AGTCGGGTAT CAGTGCAGAT GTGGAATAAC CAAGTGCTAC TGACGGCGTT CCCAAACACC 3180
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45 Seq ID NO: 51 Protein sequence:
Protein Accession #: NP_065169.1

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1 11 21 31 41 51
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SHQPTSPGSK DCHRENGGSS EDMKEKPDAA SVVYLKTETA LPPTPQDISY LAKGKVANTN 180
VTLQALRGTK VAVNQRSADA LPAPVPGANS IPWVLEQILC LQQQLQQLI LTEQIRIQVN 240
MWASHALHSS GAGADTLKTL GSHMSQQVSA AVALLSQKAG SGLSLDLALK QAKLPHANIP 300
SATSSLSPLG APFTLKPDGT RVLPNVMSRL PSALLPQAPG SVLFQSFST VALDTSKKGK 360
GKPPNISAVD VKPKDEAALY KHKCKYCSKV PGTSSSLQIH LRSHTGERPF VCSVCGHRT 420
TKGNLKVHFH RHPQVKANPQ LFAEFQDKVA AGNIPYALS VPDPIDEPSL SLDSKPVLT 480
TSVGLPQNLS SGTNPKDLTG GSLPGDLQPG PSPESEGGPT LPGAAGPNYS PRAGGFQSG 540
TPEPGSETLK LQQLVENIDK ATTDNECLI CHRVLSCQSS LKMHYRHTG ERPFQCKICG 600
RAFSTKGNLK THLGVRHTNT SIKTQHSCTP CQKFTNAVM LQQHIRMHM GGIPNTLPE 660
NPCDFTGSEP MTVGENGSTG AICHDDVIES IDVEEVSSQE APSSSSKVPF PLPSIHSASP 720
TLGFAMMASL DAPGKVPAP FNLQRQGSRE NGSVESDGLT NDSSSLMGDQ EYQSRSPDIL 780
ETTSFQALSP ANSQAESIKS KSPDAGSKAE SSENSRTEME GRSSLPTFI RAPPTYVKVE 840
VPGTFVGPST LSPGMTPLLA AQPRRQAKQH GCTRCGNFS SASALQIHER THTGKPFVVC 900
NICGRAFTTK GNLKVHYMTH GANNNSARRG RKLAIENTMA LLGTDGKRV EIFPKELAP 960
SVNVDPVVWN QYISMLNGL AVKTNELSVI QSGGVPTLPV SLGATSVVNN ATVSKMDGSQ 1020
SGISADVEKP SATDGVPKHQ FPFLEENKI AVS

70 Seq ID NO: 52 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1 11 21 31 41 51
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TCTGTGAGTT GAAGGCACAC ATCACAAGT AGTTTCTGAG AATGATTCTG TCTAGTTTTT 180
ATTTGAAGAT ATTTCTCTTT CTACTGTGAG CATCAATCG CTGAAATCT CCACTTGCAA 240
ATTCCACAAA AAGAGTGTTT CAAATCTGCT CTGTCTAAAG GGACGTTCCA CTCTGTGAGT 300
TGAATACACA CAACACAAGG AAGTTACTGA GAATTTCTCT GTCTAGCATG ATATGAAGAA 360

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ATCCCGTTTC CAACGAAGGC CTCAATGAGG TCTATATATC CACTTGCAGA CTTTACAAAC 420
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CATCACAAAA GGAGTTTCTG AGAATCATTC TGCTAGTTT TTTTAGGAAG ATATTTCCTT 540
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Seq ID NO: 53 DNA sequence
Nucleic Acid Accession #: NM_001910.1
Coding sequence: 50..1240

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CCCCTCTGTG TACTGCACTA GCCCAGCCTG CAAGACGCAC AGCAGGTTCC AGCCTTCCCA 420
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GATGGCTCAG AACCTGGTGG ACTTGGCGAT GTTTCTGTG TACATGAGCA GTAACCCAGA 720
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GGTGGGAGGC ACTGTTAIGT TCTGCTCCGA GGGCTGCCAG GCCATTGTGG ACACAGGGAC 900
TTCCCTCATC ACTGGCCCTT CCGACAAGAT TAAGCAGCTG CAAPACGCCA TTGGGGCAGC 960
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TGGGAATAAC CTTGTGGGAC TGGCCCCAGC AGTCCCTTAA GGGAGGGGCT TGTGTCTGTG 1260
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CTGTTTTTGT AGTTGGATTG TTTGTATTAG GATTCAAGCA AGGCCCATAT ATTGCATTTA 1860
TTTGAAATGT CTGTAGTCT CTTTCCATCT ACAGAGTTTA GCACATTGTA ACGTTGCTGG 1920
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Seq ID NO: 54 Protein Sequence
Protein Accession #: NP_001901.1

1 11 21 31 41 51
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QPSQSSTYSQ PQSFSFIQYG TGSLSGIIGA DQVSVEGLTV VLGQFGEVST EPGQTFVDAE 180
FDGILGLGYP SLAVGGVTPV FDNMNAQNLV DLPMSFVYMS SNEEGGAGSE LIPGGYDHS 240
FSGSLNWVPEV TKQAYWQIAL DNIQVGGIVM FCSEGOQAIV DTGTSITGTP SDKIKQLQNA 300
IGAAPVDGEY AVECANLNMV PDVTFITNGV PYTLSPATYAT LLDFVDGMQF CSSGFQGLDI 360
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Seq ID NO: 55 DNA sequence
Nucleic Acid Accession #: NM_018058.1
Coding sequence: 319..1575

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AACTTCTTTC TCCACAACCG GGGCGATGGC ACCTTTGTGG ACGCTGCGGC CAGTGTCTGT 540
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Seq ID NO: 56 Protein Sequence
 Protein Accession #: NP_060528.1

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1 11 21 31 41 51
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FRDIASPKFS MPSPVRTVIT ADFDNDQBLE IFNNNIAYRS SSANRLPRVI RREHGDPLIE 180
ELNFGDALEP EGRGTGGVVT DFDGDGMLDL ILSHGESMAQ PLSVFRGNQG FNNNWLRRVP 240
RTRVGAFARG AKVVLYTKKS GAHLRIIDGG SGVLCEMEFPV AHFGLGKDEA SSVVETNPDG 300
KMVSRNVASG EMNSVLEILY PRDEDTLQDP APLETPMNAS SSHSCALETS PYVSTPMEAT 360
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Seq ID NO: 57 DNA sequence
 Nucleic Acid Accession #: AJ279016.1
 Coding sequence: 1..1962

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TTTGAGATCG TCGTGCGGGG GTACAAATGGA CCCAACCTGG TTCTGAAGTA TGACCGGGCC 240
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GACCGGACAG GGAACGCCAT CGGGGTCACA GCCTGCGACA TCGACGGGGA CGGCCGGGAG 360
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CGTGGTGTGG CCAGCCTCTT TGCCGACGCG TCTGTGGCCT GTGTGGACAG AAAGGGCTCT 540
GGACGCTACT CTATCTACAT TGCCCAATTAC GCCTACGGTA ATGTGGGCCC TGATGCCCTC 600
ATTGAAATGG ACCCTGAGGC CAGTGACCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG 660
GCTGCTGAGG CTGGGCTCAG CAAATATACA GGGGGCCGAG GCGTCAGCGT GGGCCCCATC 720
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CACAAACCGG GCGATGGCAC CTTTGTGCAC GCTGCGGCAA GTGCTGGTGT GGACGACCCC 840
CACCAGCATG GGCAGGTGTG CCCCCTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC 900
GTCTATGGCA ACTGGAATGG CCCCCACCGC CTCTATCTGC AAATGAGCAC CCATGGGAAG 960
GTCCGCTTCC GGGACATCGC CTCACCCAAG TTCTCCATGC CCTCCCTGT CCGCACGGTC 1020
ATCACGCGCG ACTTTGACAA TGACCAGGAG CTGGAGATCT TCTTCAACAA CATIGCCTAC 1080
CGCAGCTCCT CAGCCAACCG CTTCTTCCGC GTCATCCGTA GAGAGCACGG AGACCCCTC 1140
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GTGACCGACT TCGACGGAGA CGGGATGCTG GACCTCATCT TGTCCCATGG AGAGTCCATG 1260
GCTCAGCCGC TGTCCGTCTT CCGGGGCAAT CAGGGCTTCA ACAACAACCT GCTGCGAGTG 1320
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CCC GTGGCAC ACTTTGGCCT GGGGAAGGAT GAAGCCAGCA GTGTGGAGGT GACGTGGCCA 1500
GATGGCAAGA TGGTGAACCG GAACGTGGCC AGCGGGGAGA TGAACCTAGT GCTGGAGATC 1560
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Protein Accession #: CAC08451.1

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Seq ID NO: 59 DNA sequence
Nucleic Acid Accession #: FGENESH
Coding sequence: 1..4794

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Protein Accession #: FGENESH

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 TCAACTATGA TGTACAGTGC TAATTTCCAA GAAATGTTAC ATGTGAGAAG TCTTTGAAAT 4080
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 35 GCTTGGTAAA TAATTTTTT TTTCTTTTGA GACAGAGTCT GGCTCTGTCA TCCAGGCTAG 4200
 AGTGTAGTG

Seq ID NO: 64 Protein sequence:
 Protein Accession #: NP_036338.1

40 1 11 21 31 41 51 60
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 SLEIVPPKVT IPTIVTVPVT VTTVRTSTTV PTTTVPVPTT VPTTMSIPTT TTVPTTMTVS 180
 45 TTTSVPTTTS TPTTTSVPVT TTVSTFVPPM PLPRQNHPEV ATSPSSQPEA ETHPTTLQGA 240
 IRREPTSSPL YSYTTDNDT VTESSDGLWN NNQTQLFLEH SLLTAMTTKG IYAGVCISVL 300
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Seq ID NO: 65 DNA sequence
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 60 GACCTGAAGT ACCAGCCCCC AGAGGGCGCT ACTGGAGCCT GGTGAGAGGA GGACTTTGGG 300
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Seq ID NO: 66 Protein sequence:

Protein Accession #: EOS sequence

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PVFLGRALAA PRVKLMEDPY QRPELQFFPL RKGPPWAAGEL IAAFLQIELD YSGRLEPSVP 180
SEVEPQDLAP LVEPHSGRLS LPPNVCPLVR EFRVEVLFWG LRGLGRVHLL EVEQPQVVL 240
VAGQGVSEV LASYRESFNF TELVRHLTVV FKDTAPLFHP QDLPEQPYLQ PPLSLVIER 300
RAFGHIVLVG SHIVPHMLRF TFRGHEDPPE EBGEMEETGD MPMKGFQGQK SLDPLAEAG 360
ISRQLLKHNF DEDEMDDPGD SDGVNLISMV GEIQDQGEAE VKGTVSPKKA VATLKIYNRS 420
LKBEFPHNFD WLVNVPFLYRG QGGQDGGGEE EGSGLVKGK KGSFLIYPS EAVLFSEPI 480
SRGIPQNRPI KLLVRYVYVVK ATNLAPADPN GKADPYVVVS AGRERQDTKE RYIPKQLNPI 540
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Seq ID NO: 67 DNA sequence

Nucleic Acid Accession #: NM_002449.2

Coding sequence: 223..1026

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Seq ID NO: 68 Protein Sequence
Protein Accession #: NP_002440.1

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 TCGAGTGACT ATTCTTTGTC TCAGTTCOGA TATCTGCAGA GGCTACTGCT GGTGCATGGC 2820
 CGATGGTCTT ACATAGGAT GTGCAAGTTC CTACGATACT TCTTTTACAA AAACCTTGGC 2880
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 75 GAGGATTGGT TCATCACCT CTACAACGTG CTGTACACCA GCCTGCCCGT GCTCCTCATG 3000
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 GTCTTAACAT CGATGATCT CTCTTCTATA CCTCTTGGAG CTTATCTGCA AACGATAGG 3180
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Seq ID NO: 70 Protein Sequence
Protein Accession #: NP_005594.1

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ECTWQVKAND RKVHEQPHFM NTKFLCIKES KYANNAIKTY KYNAPT FIPM NLFEQFKRAA 120
NLYFLALIL QAVPQISTIA WYTLVPLLV VLGVTAIKDL VDDVARHKMD KEINNRTCEV 180
IKDGRFKVAK WKEIQVGDVI RLKKNDFVPA DILLSSSEP NSLCYVETAE LDGENTLKF 240
MSLEITDQYL QREDTLATFD GFIECEEPNN RLDKFTGTLF WRNTSFPLDA DKILLRGCVI 300
RMTDFCHGLV IFAGADTKIM KNSGKTRFKR TKIDYLMNYM VYTIFFVLIL LSAGLAIGHA 360
YWEAQVGNSS WYLYDGEDDT PSYRGFLIFW GYIIVLNTMV PISLYVSVEV IRLGQSHFIN 420
WDLQMYAEK DTPAKARTTT LNEQLGQIHY IFSDKTGTLT QNIMTFKKCC INGQIYGDHR 480
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IEBKFEETWN KKFMAASVAS TNRDEALDKV YEBIEKDLIL LGATAIEDKL QDGVPTISK 720
LAKADIKIWW LTGDKKETAE NIGFACELLT EDTTICYGED INSLHARME NQRNRGGVYA 780
KFAPPVQESF FPPGGRNALI ITGSWLNEL LEKKTKRNI LKLKPPRTEE ERMRTQSKR 840
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IKTAHIGVGI SGQSGMQAVM SSDYSFAQFR YLQRLLLVHG RWSYIRMKCF LRYFFYKNFA 960
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VITVNFQIGL DTSYWTFVNA FSIFGSIALY FGIMFDFHSA GIHVLFPFSAF QFTGTASNAL 1140
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Seq ID NO: 71 DNA sequence
Nucleic Acid Accession #: NM_138784.1
Coding sequence: 334-816

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Seq ID NO: 72 Protein sequence:
Protein Accession #: NP_620139.1

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QSVRKHPDFS INQOWDVVVE TEEKQETLVF DGVLVCSGHH TDPVLPLOQS PGIEKFEGCY 120
FHSREYKSPS DFGSKRIIVI GIGNSGV DIA VELSRAVAKI
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	CGTCTCGGCA	CCATGGACC	AGAGAGACGT	ATCTTTATTT	AGGATGCCAT	TAAGTATTTCT	180
10	AAGGAAAAAG	TAGACACACA	GAATCTGCTA	CTCTCTGTGA	CTGATAATGA	GGCCTGGGAA	240
	GGATTCTGTG	CTGCTGCTGA	ACTGCCACAG	AATGAGGCAG	ATGAGCTCCG	TAAAGCTCTG	300
	GACAACCTTG	CAAGACAAAT	GATCATGAAA	CAAGAAAAAT	GGCAGCATTA	ACGCCAGTCG	360
	TACAGCAATG	GGTTTCTGAA	AGAGTTTCTT	CGGTTGAAAA	GTGAGCTTTG	GGATAACATA	420
15	AAGAGGCTCC	GTGCCCCTGC	AGATGGGGTT	CAGAAGGTCC	ACAAAGGCAC	CACCATCGCC	480
	AATGTGGTGT	CTGGCTCTCT	CAGCATTTTC	CTGCGATCTC	TGACCTCTGT	GGCGATGGGT	540
	CTGGCCACCT	TACACAGGGG	AGAGAGCCCT	GTACTCTTGG	AACCTGGGAT	GGAGTTGGGA	600
	ATCACAGCCG	CTTTGACCGG	GATTACAGCG	AGTACCATTG	ACTACGGAAA	GAAGTGGTGG	660
	ACACAGAGCC	ACGCCACGGA	CTTGGTCACT	AAAGCCCTTG	ACAAATTGAA	GGAGTGGAGG	720
20	GAGT'TTTTGG	GTGAGAACAT	ATCCAACTTT	CTTCTCTTAG	CTGCGAATCA	TATCAACACT	780
	ACACAGAGCA	TTGGGAAGGA	CTCCCGTGCC	CTCAGACGAG	CCAGAGGCCA	TCTTCAGTCA	840
	GTACGCGATG	CCTCAGCCTC	ACGCCCCCGG	GTCTCATGAC	CAATCTCAGC	TGAAAGCGGT	900
	GAACAGCGTG	AGAGGGTTAA	TGAAACCAGC	ATCTCTGGAA	TGAGCAGAGG	AGTCAAGCTC	960
	ACGGATGTGG	CCCGGTGAAG	CTTCTTTCTT	GTGCTGGATG	TAGTCTACCT	CGTGTACGAA	1020
25	TCAAAGCACT	TACATGAGGG	GGCAAAGTCA	GAGACAGCTG	AGGAGCTGAA	GAAAGTGGCT	1080
	CAGGAGCTGG	GAGGAAGAGCT	AAACATTCTC	AAACAATAATT	ATAAGATTCT	CGAGCGCGAC	1140
	CAGAACACTG	GA					

Protein Accession #: NP_003652.1

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35	YRNWFLKEFF	RLKSELEDNI	RLRLAALADGV	QKVHKGTTIA	NVVSGLSLIS	SGILTVWGMG	180
	LAPPTIEGSSL	VLLPEGMVEL	ITAAALTGITS	STMDYVGKKWN	TQAQAHDLVI	KSLEDKLKEVR	240
	EPLGNISNLF	LSLAGNTYQL	TRIGIKDIRA	LRRARANLQS	VPHASASRPR	VTPEPISAESG	300
	EQVERVNEPS	ILEMSRGVKL	TDVAPVSFFL	VLDVVVLYVE	SKHLHEGAKS	ETAEELKKVA	360
	OBLEEKLNIL	NNNYKILQAD	QEL				

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	ATGGGGACCT	CTCCGAGCAG	CAGCACCGCC	CTCGCCTCCT	GCAGCGGCAT	CGCCCCCGCA	60
	GCACAGGCCA	CGATGATCGC	GGGCTCCCTT	CTCCTGCTTG	GATTCCTTAG	CACCCACACA	120
	CTCGCAGGCC	AACGAGAAGC	CTCGAATCTC	ATTGGGCACAT	ACCGCATGTG	TGACGCTGCC	180
50	AGCCCGCAGG	TGCTAACCTT	TGCACAGTGT	CCAGCAGGAA	CCTATGTCTC	TGAGCATTTG	240
	ACCAACACAA	GGCTGCGCGT	CTGCGACGAT	TGGCCCTGTGG	GGACCTTTAC	CAGGCATGAG	300
	AATGGCATAG	AGAAATTGCCA	TGACTGTAGT	CAGCCATGCC	CATGGCCCAAT	GATTGAGAAA	360
	TTACCTTTGT	TCGCCTTGAC	TGACCGAGAA	TGCACTTGCC	CACCTGGCAT	GTPTCCAGTT	420
55	AACGCTACCT	TGTGCCCCCCA	TACGGTGTGT	CTCTGTGGTT	GGGGTGTGCG	GAAGAAGAGG	480
	CAGAGACTGT	AGGATGTGGG	GTGTAAACAG	TGTGCTCGGG	GTACCTTCTC	AGATGTGCCT	540
	TCTAGTGTGA	TGAAATGCAA	AGCATACACA	GACTGTCTGA	CTGACAACCT	CTTGCTGTATC	600
	AAGCGCGGGG	CCAAGGAGAC	AGACAACCTG	TGTGGCACAC	TCCCGTCTTT	GTCCAGCTCC	660
	ACCTCACCTT	CCCTTGGCAC	AGGCCATCTT	CCACGCGCTG	AGCACATGGA	AACCCATGAA	720
60	GTCCCTTCTT	CCACTTATGT	TCCCAAAGCG	ATGAACCTCA	CAGAAATCCA	CTCTTCTGCC	780
	TCTGTTAGAC	CAAAGGTACT	GAGTAGCATC	CAGGAAGGGA	CAGTCCCTGA	CAACACAGC	840
	TCAGCAAGGG	GGAAGGAAGA	CGTGAACAAC	ACCTCCCCAA	ACCTTCAGST	AGTCACCAAC	900
	CAGCAGAGCT	CCCACCACAG	CACATCCCTG	AAGCTCTGCG	CGTCCATGGA	GGCCATCTGG	960
	GGCGAGAAGT	CCAGCAGGCC	CCCAAGAGGG	CCCAAGAGGG	GACATCCTAG	ACAGAACTTA	1020
65	CAGCAGCATT	TGTACATCAA	TGAGCATTTG	CTCGTGATGA	TTGTGCTTTT	CTCGCTGCTT	1080
	TGCTTTGTGT	TGATTGTGGT	TGTCAGTATG	CGGAAAAGCT	CGAGGACTCT	GAAAAAGGGG	1140
	CCCCGCGAGG	ATCCCACTGC	CATTGTGGAA	AAGCGAGGGC	TGAAGAAATC	CATGACTCCA	1200
	ACCAGCAACC	GGGAGAAATG	GATCTACTAC	TGCAATGGCC	ATCAGTTTCT	TTGCAATGCC	1260
	CTTGTAGACG	CCCAAGTGGG	GAATCAGTGG	AAAGATATCT	ATCAGTTTCT	TTGCAATGCC	1320
70	AGTGAGAGGG	AGGTTGCTGC	TTTCTCCAAT	GGGTACACAG	CCGACACAGA	GCGGGCCCTC	1380
	GCAGCTCTCG	AGCACTGGAC	TCTCCGAGGC	CCGAGAGCCA	GCCTCGCCCA	CTCAATTAGC	1440
	GCCTTGGGCC	AGCACCGGAG	AAACGATGTT	GTGGAGAAGA	TCTTGGGGCT	GATGGAAGAC	1500
	ACCACCAATC	TGGAACCTGA	CAAACTAGCT	CTCCCGATGA	CCGAGAGGCC	GGTTAGCCCG	1560
	AGCCCATACG	CCAGCCCCAA	CGCGAAACTT	GAGAAATTCG	CTCTCCTGAC	GGTGGAGCCT	1620
75	TCCCAACAGG	ACAGAACAAC	GGGCTTCTTC	TGTGATGAGT	CGGAGCCCTT	TCTCCGCTGT	1680
	GACTCTACAT	CCAGCGGCTC	CTCGCGGCTC	AGCAGGAACG	TTCTCTTTAT	TACCAAGAAA	1740
	AAGAAGGAACA	CAGTGTTCGG	GCAGGTACGC	CTGGACCCCT	GTGACTTTGA	GCTTACTCTT	1800
	GATGACATGC	TCCACTTTCT	AAATCTCTGAG	GGAGCTCGGG	TGATTGAGAA	GATTTCCCGA	1860
	CTCGAGGACA	AACTAGACCG	GCTATTCTGAA	ATTATTGGAG	TCAAGAGCCA	GGAAGCCAGC	1920

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CAGACCTCC TGGACTCTGT TTATAGCCAT CTTCTGACC TGCTGTAG

Seq ID NO: 76 Protein Sequence
Protein Accession #: NP_055267.1

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LPCAALTDRE	CTCPPGMFQS	NATCAPHTVC	PVGNVVRKKG	TETEDVRCKQ	CARGTFSDDP	180
SSVMKCKAYT	DCLSQNLVVI	KPGTKETDNV	CGTLPSFSSS	TSPPSGTAIF	PRPEHMETHE	240
VPSSITYVPKG	MNSTESNSSA	SVRPKVLSSI	QEGTVPDNTS	SARGKEDVNK	TLPNLQVVNH	300
QQGPHRRHIL	KLFSMEATG	GEKSSTPIKG	PKRGHPRQNL	HKHFDINEHL	PWMIVLFLLL	360
VLVVIVVCSI	RKSRTLKKG	PRQDPSAIVE	KAGLKSMTPT	TQNRKWKIYY	CNGHGIDILK	420
LVAAQVGSQW	KDIYQFLCNA	SEREVAAPSN	GYTADHERAY	AALQHWITIRG	PEASLAQLIS	480
ALRQHRRNDV	VEKIRGLMED	TTQLETDKLA	LPMSFPSPLSP	SPISPSNAKL	ENSALLTVEP	540
SPQDKKNGFF	VDESEPLLRC	DSTSSGSAL	SRNGSFITKE	KKDITVLRQVR	LDPCDLQPIF	600
DDMLHFLNPE	ELRVIEIIPQ	AEDKLDRLF	IIGVKSQEAS	QTLDSVSYSH	LPDLL	

Seq ID NO: 77 DNA sequence
Nucleic Acid Accession #: NM_003105.3
Coding sequence: 123..6767

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ACATGGCGAC	ACGGAGCAGC	AGGAGGGAGT	CGCGACTCCC	GTTCCATATC	ACCCTGGTCG	180
CAGTCTGTCC	GCCCGGAGCT	CTCTGCGAAG	TCTGGACGCA	GAGGCTGCAC	GGCGGCACCG	240
CGCCCTTGCC	CCAGGACCGG	GGCTTCCTCG	TGGTGCAGGG	CGACCCGCGC	GAGCTGCGGC	300
TGTGGGCGCG	CGGGGATGCC	AGGGGGGCGA	GCCGCGCGGA	CGAGAAGCCG	CTCCGGAGGA	360
AACGGAGCGC	TGCCCTGCAG	CCCGAGCCCA	TCAAGGTGTA	CGGACAGGTT	AGTCTGAATG	420
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TGGCCCGAGA	TAGCCTGGCA	TTGGCGAGGC	CCAAGAGCAG	TGATGTGTAC	GTGTCTTAGC	540
ACTATGGAAA	ATCATTCAAG	AAATTTTCAG	ACAAGTTAAA	CTTTGGCTTG	GGAAATAGGA	600
GTGAAGCTGT	TATCCGCCAG	TCTACACACA	GCCCTGCGGA	CAACAAGCGG	TACATCTTTG	660
CAGACGCTTA	TGCCCAGTAC	CTCTGGATCA	CGTTTGACTT	CTGCAACACT	CTTCAAGGCT	720
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AGCAGTTGCC	TCTCACCGBG	CTACGGGCAG	CAGTGGCCCT	GGACTTTGAC	TATGAGCACA	2460
ACTGTTTGTA	TTGGTCCGAC	CTGGCCTTGG	ACGTTCATCCA	GCGCCTCTGT	TTGAATGGAA	2520
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AACCCCTCAG	CCAGCTGCTT	TACTGGGTAG	ATGCAGGCTT	CAAAAAGATT	GAGGTAGCTA	2640
ATCCAGATGG	CGACTTCCGA	CTCACAAATC	TCAATTCCTC	TGTGCTTGAT	CGTCCAGGGG	2700
CTCTGGTCTC	CGTCCCCCAA	GAGGGGGTGA	TGTTCTGGAC	AGACTGGGGA	GACCTGAAGC	2760
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Seq ID NO: 78 Protein Sequence
Protein Accession #: NP_003096.1

70
75

1 11 21 31 41 51
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ARDSLALARP KSSDVVYSYD YGKSFKKISD KLNFG LGNRS EAVIAQFYHS PADNKRYIFA 180
DAYAQYLVIT FDFCNTLQGF SIPFRAADLL LHSKASNLLL GFDRSHPNKQ LWSDDDFGQT 240
WIMIQBHVKS FSWGIDPYDK PNTIYIERHE PSGYSTVFRS TDFQFSREBQ EVILEEVDRF 300
QLRDKYMFAT KVVHLLGSEQ QSSVQLWVSF GRKPMRAAQF VTRHPINEYY IADASEDQVF 360
VCVSHNNRRT NLYISEAEGF KFSLSLENVL YSPGAGSD TLVRYFANEP FADFHRVEGL 420
QGVYIATLIN GSMNEENMRS VITFDKGGTW EFLQAPAFGT YGEKINCELS QGCSLHLAQR 480
LSQLLNLQLR RMPILSKESA PGLIATGTSV GKNLASKTNV YISSAGARW REALPGPHY 540

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5 TWGDHGGIIT AIAQGMETNE LKYSTNEGET WKTFFIFSEKP VFVYGLLTPEP GEKSTVFTIF 600
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 10 QLPPLTGLRAA VALDFDYBHN CLYWSDLALD VIORLCLNGS TGQEVIIINSQ LETVEALAFE 840
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 20 CIPNRWKCRR ENDCGDSDE KDCGDSHILP FSTPGFSTCL PNYRCSSTG CVMDTWVCDG 1440
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 30 DYVVVKMIPD SRLPPRHLLV VHTGKTSVVI KWESPYDSPD QDLYIAIAVK DLIRKTDTSY 1980
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30 Seq ID NO: 79 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 120-755

35 1 11 21 31 41 51
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 40 TCTCTGSGTG GAGGGGCCCA CGCTTCGGGG CCTCCTGTCC TTCAAGAAC TCCAGGTCTA 240
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 CTCACGGCAG CCTGCTCAAC CTGAAGGCCA TGGTGGAGGC CGTCACAGGG AGGAGCGCCA 360
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75 Seq ID NO: 80 Protein sequence:
 Protein Accession #: Eos sequence

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1 11 21 31 41 51
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 5 GCHPYVDHYD HTIENNTEIV CSDLNKTECD KQTCMCDKNM VLCLMNQTYR EEYRGFLNVY 180
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Seq ID NO: 81 DNA sequence
 Nucleic Acid Accession #: NM_018136.1
 Coding sequence: 38..2218

1 11 21 31 41 51
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 20 TGCCCTACGG ATTCAGTTCCT TCCTTCAGAT GGCTGTGTAT CGGAGAAGAT TTGTTACAGCA 360
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 25 TCAGGCTATG TGGAGGAGAT ATAGAGCCAA GAAATATTTA TGTAAGTGA AAGCTGCCTG 660
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 30 TTATAGAGGA TATAAAGGAA GGCAGGTCTC TCTTCGGCAG AAATCTGCTG CTTTGATCAT 960
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 35 GCAGGTTAAT TCAGTCATCT GTATTAGAG ATGGTTTCGA GCAAGATTAC AAGAAAAGAG 1260
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 45 AGAAAATTGT ATAGATATAC TATTGGAGCT TTTGCAGATA TACCAGAGAA AGCCTGTTAA 1860
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 AAAGTGATTT TTGCTCTCTG TGTACAACTT TTAATACTG ACTTTGTTTT AAAAAACAT 2340
 55 AAACGTTCAT TTACATTCTT CATTTTATC ATTTATAGTT TTAGCATGT AATAAACTAA 2400
 TATGTCATAA GATG

Seq ID NO: 82 Protein Sequence
 Protein Accession #: NP_060606.1

1 11 21 31 41 51
 60 MKVRQKLKNV SEEKMAAIVN QSALCCYRSK TQYBAVQSEB VMIQEWYKAS GLACSQBAEY 60
 HSQSRAAVTI QKAFCRMVTR KLETQKCAAL RIQFFLQMAV YRRRFVQQRK AAITLQHYFR 120
 TWQTRKQPLL YRKAADVVLON HYRAFLSAKH QRQVYLQIRS SVIIQARSK GFIIQKRKFQE 180
 65 IKNSTIKIQA MWRRYRAKKY LCKVKAACKI QAWYRCWRAH KEYLAVLKAV KIIQGCIFYTK 240
 LERTRELVNR ASALIIQKRW RAILPAKIAH EHFLMIKRHR AACLIQAHYR GYKGRQVSLR 300
 QKSAALIIQK YIRAREAGKH ERIKYIEFKK STVILQALVR GWLVKRFLE QRAKIRLLHF 360
 TAAAYYHLNA VRIQRAYKLY LAVKNANKQV NSVICIQRFW RARLQEKRFI QKYHSIKKIE 420
 HEGQECLSQR NRAASVIQKA VRHFLLRKKQ EKFTSGIIKI QALWRGYSWR KKNDCIKKIA 480
 70 IRLSLQVVRN EIREBNKLYK RTALALHYLL TYKHLSAILE ALKHLLEVVR LSPLCCENMA 540
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 IYREKPGNKV ADKGGISIFTK TCCLLAILLK TTNRASDVRS RSKVVDRIYS LYKLTAKHKH 660
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 TLGIPY

Seq ID NO: 83 DNA sequence
 Nucleic Acid Accession #: NM_000612.2
 Coding sequence: 553..1095

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1 11 21 31 41 51
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5 TTCTGTTTCT CTCGCTGCTG TTCTCTCCCG CTGTGCGCCT GCCCGCCTCT CGCTGCTCTC 180
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15 TGGGTGGACA CCTTCCAGTT CGTCTGTGGG GACCGCGGCT TCTACTTCAG CAGGCCCGCA 720
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20 CGCGGGGTC ACCTGCTCGC CAAGAGCTC GAGGCGTCA GGGAGGCCAA ACCTCACCT 1020
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25 CCTCGGCCCC CTCATCGGG CTGAGGAAGC ACAGCAGCAT CTTCAAACAT GTACAAAATC 1320
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Seq ID NO: 84 Protein Sequence
Protein Accession #: NP_000603.1

30 1 11 21 31 41 51
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35 QSTQRLRRGL PALLRARRGH VLAKLEAFR EAKRHRPLIA LPTQDPAHGG APPEMASNRK 180

Seq ID NO: 85 DNA sequence
Nucleic Acid Accession #: XM_092643.1
Coding sequence: 1-5352

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CGGAAGACCC TGGCCTCGGT GATAATCATG GAGAAGGCCA CCACTGAGCC TTCTGTAGTG 240
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50 CAGAGGCTGG TGGCCATTGC CTCCAAGGAG ATGAGGGAGA TCCAGAGAT GGAGGGCTAT 420
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60 ATCTCGGAAC TGTCAGTCA CACCAACACC CCGTCTCCCC AAATGCAGCT ACACACCAT 1020
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70 CTGTGTACAC TCATGGAGAC AGACTACGTG CAAGCTTTGA CTCCTATCTG TATCAGCTC 1620
ACAAACCTGG CAGAACACCA GCTCCATGGC CAGGATGTGG ATGTACAGCT GCTGGCAAG 1680
AGCAGGCAAG TGGACCTGCC TGACCTCAG AAGCTGTGCG CCCGTCTCCT GGTGCTGATG 1740
TCATCACCTT ACRAAGGGGA GGTCTGTGGG ATAGCCATGC TCAACCTCTT GAGGACCTG 1800
AGCCAGAGCA TCGCACCTCC CATGGCCGAC ATGTGGGAGC TGGAGATTGC GCTACTGGTC 1860
CGGTACTCTG AAGAACATAC TGAGTTCACT TGGGATCAGA AAGCCTGGGA ACACAGCTG 1920
75 ATTCAATTTT TGGCAAACTC CCTCAAGAAG ACCCGGGGCT CTAGCTGGAG CTTGCGCTTG 1980
AGTAAAGAGC TGAACRACCA GATTGCGAGC TTTGACAGCC CCTCTCTGGA GAAGGGCTTT 2040
CTGTACCGGG CCTTGGGCTT CACTTGGCC ACAGGCTTGG AGGCCAGCAA GGTGGAGGTG 2100
CTGCTGTTGG AGCTGCTGTA CAAGACGGAC TACAGCAATG ACTTTGACAG CGAGGGTGTG 2160

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ATTATGTGCT TTGGCCTGTG TGCCCGGGGC CAGGTAAAAA CGGTGCTGAA TGTGCTTCAT 2220
GACTTCGAGG AGAGGATCCA GGAGTCAGAG CAGTCCTGGC AGATCAGTGC TTGCCGGAAG 2280
GACCATCCCT GCGAGCGGGA GACAGTGAAA AGTGCCCTCA TGGTGATGTA TAGCTGCGTG 2340
GCCTCCTACT GCCACCCCCA GTTGCTCCTC AACCTCGTGG ACAGCCCCAT CACCGCTAAG 2400
ATCATTCAAC ATTATGTCAG CAGCTGCCAG GACATCTGTC TCAAAATGGC CTTTCATGAAG 2460
AGTGTGTGTC AGGTIACCAA GGCCATCAAC AACATCAAGG ACCTGGAGGA CTTTCACTTT 2520
GCCCAGAGA CGACTCTTAC CAGCATTATA GTGGCGGTCA TCAAGGCAGA ACCGACTGAC 2580
AACCTGGTTT CTCAGTGGC AGCCTTGGCG ATGGAGGCC TCTCGCACCT GAGCAAGCTG 2640
AAGCCTTTCT ACTCCACAGA GGAACACAGT GAGCTGATGG ATATCAGCAT ACATTCTGTA 2700
ATTTCCTCTC AACTCCCAGG AGAGGACAAAT GAGTCCATTA AGACCCCTGTA TGCAAAATGCC 2760
CTGAGCTCCC TGGAGCAGCT GATGGAGAGC CTCTGCAGAG GGCAGCTGGA CCCCAAGGGG 2820
CTGCAGGAGA TGGTGACGCT CCTGGAAAAG TGGATCTTGT CGGAGAAAGA ATGGGAGCGG 2880
GAAAAGGCCG TGAGCTCCA TCTCTATCTC ATGTGGATT ATGTCCACAG CACTGCTGTC 2940
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TGTGATGCCC ATCAAGAAGC CCGCATGGCC TCAATGAATG TCCTGTCCAG CCTGCTAGAT 3060
CTTCACGCAA GCCCAGCTG CTCTTTGTGG GGCCCTTCCA AGCAGAAGGA GCTTGAGAAA 3120
TGTAAGGGGG ACCTCCAGAG CACAGATGTC GAGAAGATCT TCTGTGCATC CTCCAGAATC 3180
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GTGCCCATGG AGAGCCACCT GGCAGAGGTG TGGCTGGCAG TGTGAGAGAA CGTGCCCTTC 3540
CGCCCGGACCA TGCTCCACAG CCTGATGGGC CGGCTGCAGT CAOGCTCAG CCCAGAATC 3600
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CCTGACCTCA TCTACACCTT CCTGCTGCAG CTTGGAAGCA GCCACCGACC AGAGGCCGCC 3780
CCGCCGTCTT TGAAGATGTG GAAGCTGGTC CACACCACTC CTCTGCCGGA GGAGATGAAC 3840
CTGCAAAAGT GCTCTCGAGG GCGGTCACCT ATCAAGTCCA TGCAGCTCTT GTTCAAGAGA 3900
GTCAAGAGCC AGCACTGGC ACATACCTCG GACGAGCAGG CAGTGTGGGA CCTCTGCAG 3960
GACGGCGGGA CTTCTCTGGA GGTGTGAGC CTGCTGGCCA GGCTGTGCAT GCAGCACGTG 4020
GAGGGCCACA CGCAGAGGCT GGCCGAGCTG GTGCTCAGGG GCATGGACTC AGAAGTCTCT 4080
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CTGGGCGCCC CCAAGAAGCT GAAGCAGTAC CGAAAGGTCT TGCTGGAGAA GTGCGTGGGC 4320
CCCTGAGGG AGCCCGTGAG CAACAGCGTG ACTGCCGAGG GCATGGAGGC CTGACCAAG 4380
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GGAAAGCTGG CAAGGCTGGT CGGGATGTCC AAGAAGCATT TCTTCAAAGG GGAGGTGAAG 4560
AAGGCCGTGA TCCCTCTCAT GCTGCACTCC CAGGACCCCT GCTCCATGTC AGCCCAAGTA 4620
AGATACATCC TGGGCTTTGT GTCCAGTCT GGGGCCCGCT GTTCCCGGAG GAACAGGTC 4680
CTTGGGTCTG CTGGCTCGGC CTGTATGGCT ACCATGTTTC AGTGTGTGCA CTCTGGGGC 4740
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GGCCCAAAGG GTCGGAACCT ACCTTTGTGT CTTCACTCGG AGTTTATCCA CACGATGCT 5100
GACAGCGTGC CTAAGGCCAG GCACTGTGCC AAGCCAGCAG GTAAACGAGG ACTTCCAAAC 5160
TGTTCCAGT CCAACTGCCA AAGGAATTCA CCATCCGGGG TCCCATCAAC AGGAGAGAGC 5220
TGCTATAGCT TCCAAATCC AACCCGTGCT AAAGCCTTCT CTGGAACAGT GGTCTTCAAA 5280
CTGTTTTGTG GAGCAATAGG TGACTTGATT TCCTGCCCAG TGATAAAGAG TATTGCTGCT 5340
AAACAAGCTT GA
  
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Seq ID NO: 86 Protein sequence:
 Protein Accession #: XP_092643.1

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1 11 21 31 41 51
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RKTLASVIIM EKATTEPSVV INTLIRCLQV PEISTQRKVN IYNILODIIQ QEGELEEQCV 120
QRLVAIASKE MREIPEMEGY MKAEVASDTL VALSRNHFSL VMYELQHHLK PLNLNDEFVI 180
ITLAKLANGN VFEPFYMGI TLATIFTMLR LANEAKIRQA ICSAMETPCE TVQFYLKHLE 240
ESVYVPMTEE EFALKVFPYI RYFVTVWLRH YNPEVKLGVI KSLKPMGLLL LPNDDLREQV 300
YDYIPELLAE YQGSLEVLRL ILELGVTTNT PVPQMLHTI FTELHVQVCN KAPAQHOYSS 360
QNLMEMVHCF VALARSYPKE LMKFFFSQME TNKEAVRVGT LNLIRAIKVA DEPRMSIRAI 420
YLAIRVVKNT ISDTRSKVRM AILHIIGQLA LCGYQERIKG WGLKYLVSQV TLSTYKLTNR 480
REKFYQRDLE ERMVHKVTMD TVKIITSSVS GMTTEFWVRL LCYIMETDVI EALTPIICISL 540
TNLABHQHLHG QDVVSVAGK SRQVDLPAPQ KLLARLLVLM SSPYKGEGRG IAMLNLLRTL 600
SQSIAPSMAD MWELEIALLV RYLBEEHTEFT WDQKAWEDKL IQFLRNSLKK TRGSSWSLRL 660
SKELNNQIAS FDSPLERKGF LYRALGFTLA TGLEASKVEV LLELLLYKTD YSNDFDSEGV 720
IMCFGLCARG QVKTVLNLVH DFEERIQESE QSWQISAWRK DHPWRRETVK SALMVMVYSCV 780
ASYCHPQLLL NLVDSPTAK IHHYVSSCO DICLKMAFMK SVVQVTKAIN NIKDLEDFHF 840
AQKTTLSII VAIKAEPTD NLVSPVRALA MEALSHLSKL KPFYSTEENS ELMDISHSV 900
ISLQLPGEDN ESIKTLYANA LSSLEQLMES LLQRLDPKG LQEMVQLLEK WILSEKEWER 960
EKAIVSLHLYL MWIYVHSTAV CIHLKLQQFG TMVGLIAPCT CDAHQRTMA SMNVLSLLD 1020
LHASQTCSLW GPSKQKELEK CKGDLQSTDV EKIFCASSRI AKVVCMFESC DEVVSLIQKL 1080
  
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CENTGAMNLO HDKASVTWIA FFLQMRAKEL EDKVABEILSA ILVHLPVVDH PEVRRLLIDG 1140
 ILLLAHHHQE TILTSLLRQP LPMESHAEV WLAVSENVVF ARTMLHSLMG RLQSRLSPRI 1200
 SATSKADIWR LAAVDPLMTL CTIHLIQKL DENDKLPDFL PDLIYTLLLQ LGSSHRPEAA 1260
 PPVLKMWKLV HTTPLEEMN LQRCRGRVT IKSMQLLFKR VKSQHLAHTL DEQAVWDLQ 1320
 DGGTFLEGVLS LLARLCMQHV EGHQRRLAEL VLRGMDSEVL SCRISSTAVC VEMRHRFMSG 1380
 PVLVQEKLLK PAALLLEKGA DQEEDEALRV LSLRALGNMA LGAPKKVKQY RKVLEKCLG 1440
 PLREPVSNSV TABGMEALTK ILAELREGDV GSSFDAMSEQ CRIFFDNESE LLRLKAFILF 1500
 GKLARVVGMS KKHFFKGEVK KAWIPLMLHS QDPCSNAQV RYILGFVSQS GARCSPRKQV 1560
 LGSAGSACMA TMFQCVHFVG WKSLEHPSGP SDTATDDKMT VFQTTMCSIL TRKKPAVLYR 1620
 FLLETMAYVK NNLSRIRIAA CNLAGIIMKQ MSHYLLKLD FPALRNSLQE LQLDPPGPPT 1680
 GPKGRKLALC LHSEFHTHA DSVPKARHCA KRAGKPGLEN CSQSNQQRNS PSGVPSTGES 1740
 CYAVQNPTRA KAPSGTVVFK LFCGANGDLI SCPVIKSIAA KQA

Seq ID NO: 87 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 CACTTCTCCC TCTCCTTAGT TCTCCGGTAA CCAAACCTTC TCTCGTTATA TACCCCAATGA 60
 TAAAACCAAA GTAATGTGT ACAGGTAAAG GATTCAAAC AAACCATAGC AACTGAAACA 120
 GGGTATCAGG ACGCAATGC TTGGCTGGAA TGGATTAAAC ATTCTGTGC AGGCTAAACA 180
 AAAGCGCTG TTAACATTGT GTGACAGGCA GGCCAGAGAC CCAAAATTGTT CCCTTTCCAC 240
 TTGGGTGGTC CTCTCACAGA CCGGGCATGA GCTGTGTGGT AGCTCTCTTC CAGAACCCCA 300
 CAGCCTGGGG TGGTGAAGTCA TGCAAGACTC TTTCACTGCT GTTCCCTGAG GTCAAGAGCC 360
 CTGCAGGTCA GCCCTGAGGA CTATCCGGCC TCCAGCCCT GATGTTAACT TCACCTCATG 420
 CCTTTCACGG CAGGGGGAAA AGTTAGCATT CCTTGGAGAC TTAACAGGCT GCAGTGAAC 480
 CAGGCCCTTT GAAGAGCTTA CCAATCAGTC TGCCCTTGTT CATCCCCGAG CAGATGTGTG 540
 GTGGTATTGC TGGGGACTAC TGCTGGGTAC TCTGCCAAGT AATTAGAGCA GCACTCATGC 600
 TCTAGTCCAA CTGGCCATCC CTTTCACCT AGCATTCTGT CAATATGATA AAAAAAATG 660
 TAAAGAAAGT CCTCAGTGG GTCCTTGACC CCCATGTTA TATAAACT ATTGGGTCT 720
 ATGAGGAGAA CCCGATGA

Seq ID NO: 88 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..759

1 11 21 31 41 51
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 GTAACCTCTGT GCACAGACCC AGAAGAAAGT AGAAAAATAA GTTTTGGAGG AAACCTCATT 120
 GTGAACACAC CTCACCAAGT CAGAACTATC CTAAGTCAGA AAGCAGAAAG GTGGCTTACT 180
 GACTCCAGAA TCTTAAAGTA TGAGGCTATT CTCTTAGAAA AAGATCATTT AACATTAACC 240
 ACTGATAATT CACTTAACCC AGCAGGTTTC CTAACAGGGG ATCTATATCA AAAGAGAGAG 300
 CACACATGTT TAGTTTAAAT TAATTACCAT ACAAAGGTCC GACCAGACCT AGGAGAAACT 360
 CCCTTCAGGA CCGGACAAACA CTTTATAGAT GGTTCTCTCC AGTGATAGA GGGAAAAAGA 420
 TACAATGGGT ATTCAGTAAT TGATAGAGAA ACTCTGTAG AAATAGAGTT AGGAAATTTG 480
 CCTAATAATT GGTCTGCTCA AACATGTGAG CTGTTTGAC TCAGCCAAGC CTTAAAGGAC 540
 TTACAGAAAC AGGAAGGAAC CATCTATACA GATTCTAAGT ACGCCTTTGG AGTGGCTCAT 600
 ACATTTGGAA AAATTTGGAC TGAACGAGGT CTTATTAATA GCAAAAGCCA AGACTTGGTC 660
 CATAAGGAAT TAATCACCCA AGTATTAAC TACCTTCAGC TGCCAAAGA AACAGCTATT 720
 GACCATGTCC CCGGACACCA AAAAGCCCT TCTTTTAA

Seq ID NO: 89 Protein Sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 MQEETGWQLG ERILTYHGDQ VILCTDPEES RKISFGGNLI VNTPHQVRTI LSQKAERWLT 60
 DSRILKYEAI LLEKDDLTLT TDNSLNPAFG LTGDLYQKRE HTCLVLINXH TKVRPDLGET 120
 PFRITGQHFID GSSOVIEGKR YNGYSVIDRE TLVEIELGKL PNNWSAQTC LFALSOALKD 180
 LQNQEGTIYT DSKYAFGVAH TFGKIWTERG LINSKQDLV HKELITQVLT NLQLPKETAI 240
 DHVPHQKSL SF

Seq ID NO: 90 DNA sequence
 Nucleic Acid Accession #: NM_000756.1
 Coding sequence: 186..776

1 11 21 31 41 51
 AGAAACTCAG AGACCAAGTC CATTGAGAGA CTGAGGGGAA AGAGAGGAGA GAAAGAAAAA 60
 GAGAGTGGGA ACAGTAAAGA GAAAGGAAGA CAACCTCCAG AGAAAGCCCC CGGAGACGTC 120
 TCTCTGCAGA GAGCGGGCAG CACCCGGCTC ACCTGCCAAG CGCCTGGGAA GCGAGTGCCC 180
 CTAACATGCG GCTGCCGCTG CTGTGTCCG CGGGAGTCTT GCTGGTGGCT CTCCTGCCCT 240
 GCCCGCCATG CAGGGCGCTC CTGAGCCGGG GGCCGGTCCC GGGAGCTCGG CAGGCGCCGC 300
 AGCACCCCTCA GCCCTTGGAT TTCTTCCAGC CGCGCCGCGA GTCCGAGCAG CCCAGCAGC 360
 CGCAGGCTCG GCGGTCCTG CTCCGATGAG GAGAGGAGTA CTTCCTCGCG CTGGGGAACC 420
 TCAACAAGAG CCGCGCGCTC CCGCTTTCG CCGCTCTCTC GCTCCTCGCG GGAGGCAGCG 480
 GCAGCGCGCC TTCGCGCGAA CAGCGACCG CCAACTTTTT CCGCGTGTG CTGCAGCAGC 540

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TGCTGCTGCC TCGGCGCTCG CTCGACAGCC CCGCGGCTCT CGCGGAGCGC GGCGCTAGGA 600
ATGCCCTCGG CGGCCACCAG GAGGCACCGG AGAGAGAAAG GCGGTCCGAG GAGCCTCCCA 660
TCTCCCTGGA TCTCACCTTC CACCTCCTCC GGGAACTCTT GGAAATGGCC AGGGCCGAGC 720
AGTTAGACCA GCAAGCTCAC AGCAACAGGA AACTCATGGA GATTATTGGG AAATAAAACG 780
GTGCGTTTGG CCAAAAAGAA TCTGCATTTA GCACAAAAAA AATTAAAAAA AATACAGTAT 840
TCTGTACCAT AGCGCTGCTC TTATGCCATT TGTTTATTTT TATATAGCTT GAAACATAGA 900
GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTTAGCATGC ACAAGTGTGA TTCACGTGCA 960
GCAGCAACAC AATGTTATTTC GTTTGTCTA CGTTTAGTTT CCGTTTCCAG GTGTTTATAG 1020
TGGTGTTTAA AAGAGAATGT AGACCTGTGA GAAACGTTT TGTTTGAAAA AGCAGACAGA 1080
AGTCACTCAA TTGTTTTTGT TGTGGTCTGA GCCAAAGAGA ATGCCATTCT CTTGGGTGGG 1140
TAAGACTAAA TCTGTAAGCT CTTTGAACA ACTTCTCTT GTAAACGTTT CAGTAATAAA 1200
ACATCTTCC AGTCCTTGGT CAGTTTGGT GTGTAAGAGA ATGTTGAATA CTTATATTTT 1260
TAATAAAAGT TGCAAGGT

Seq ID NO: 91 Protein Sequence
Protein Accession #: NP_000747.1

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1 11 21 31 41 51
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ARPVLLRMGE EYFLRLGNLN KSPAAPLSPA SLLLAGSGS RPSPEQATAN FFRVLLQQLL 120
LPRRLDSPA ALAERGANA LGGHQEPER ERRSEEPPI SLDLTFHLLRE VLEMARAEQL 180
AQAHSNRKL MEIIGK

25

Seq ID NO: 92 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092

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1 11 21 31 41 51
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GCCAGAAAGG AGAACTCCTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG 120
AGCACCTGCG CCAGCGAGGT CCTCCGGAAA GAGCCTGTCA CCCCATCTGC ACTTGTCTCT 180
ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCTGCGC AGAAGTGAT GGAGAATAGC 240
AGTGGACAC CCGACATCTT AACCGCGCAC TTCACAAATG ATGACTTTGA GATTGGCGGT 300
CCTCTGGGCA AAGGCAAGTT TCGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360
ATCGTGGCGC TCAAGGTCTC CTTCAAGTCC CAGATACAGA AGGAGGCGGT GGAGCATCAG 420
CTGCGCAGAG AGATCGAAAT CCAGGCCAC CAGCACCATC CCAACATCCT CGCTCTCTAC 480
AACTATTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG 540
CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTGACGAGC AGCGAACAGC CACGATCATG 600
GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTCAATCA CAGAGACATA 660
AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTGCGCTGG 720
TCTGTGATG CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCTGGA CTACCTGCCC 780
CCAGAGATGA TTGAGGGGCG CATGCACAAT GAGAAGGTGG ATCTGTGTG CATTGGAGTG 840
CTTTGCTATG AGCTGCTGGT GGGGAACCCA CCCTTTGAGA GTGCATCACA CAACGAGACC 900
TATCGCCGCA TCGTCAAGGT GGACCTAAG TTCCCGCTT CTGTGCCAC GGGAGCCGAG 960
GACCTCATCT CCAAACTGCT CAGGCATAAC CCCTCGAAC GGCTGCCCT GGGCCAGGTC 1020
TCAGCCACCT CTTGGGTCG GGGCAACTCT CGGAGGGTGC TGCTCTCTC TCCCTTTCAA 1080
TCTGTGCGCT GATGGTCCCT CTCATTCACT CGGTGCGTG TGTGTGTATG TCTGTGTATG 1140
TATAGGGGAA AGAAGGGATC CCTAATCTGT CCCTTATCTG TTTTCTACCT CCTCTTTGT 1200
TTAATAAAG CTGAAGCTTT TTGT

Seq ID NO: 93 Protein Sequence
Protein Accession #: NP_004208

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1 11 21 31 41 51
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QLRREIEIQA HLHHPNILLR YNYFYDRRI YLILEYAPRG ELYKELQKSC TFDQRTATI 180
MEELADALMY CHGKKVIHRD IKPENLLLGL KGELKIADFG WSVHAPSLRR KTMCGTLDYL 240
PPMIEGRMH NEKVDLWCIG VLCYELLVGN PPFESASHNE TYRRIVKVDL KFPASVPTGA 300
QDLISKLLRH NPSERLPLAQ VSAHPWVRAN SRRVLPPSAL QSVA

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Seq ID NO: 94 DNA sequence
Nucleic Acid Accession #: NM_007019.1
Coding sequence: 41..580

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1 11 21 31 41 51
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CCCAGCGCCG ACTAGCGTGC CCGCCGCCCC TAAAGGAGCT GAGCCGAGCG GGGGCGCCGC 120
CCGGGTCCG GTGGGCAAAA GGCTACAGCA GGAGCTGATG ACCCTCATGA TGTCTGGCGA 180
TAAAGGATT TCTGCTCTCC CTGAATCAGA CAACCTTTT AAATGGGTAG GGACCATCCA 240
TGSAGCAGCT GGAACAGTAT ATGAAGACCT GAGGTATAAG CTCTCGCTAG AGTTCCCGAG 300
TGGTACCTT TACAATGCGC CCACAGTGAA GTTCTCTCAG CCTGCTATC ACCCCAAAGT 360
GGACACCGAG GGTAAACATAT GCCTGGACAT CCTGAAGGAA AAGTGGTCTG CCTGTATGA 420
TGTCAGGACC ATTCTGCTCT CCATCCAGAG CCTTCTAGGA GAACCCAACA TTGATAGTCC 480

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CTTGAACACA CATGCTGCCG AGCTCTGGAA AAACCCACACA GCTTTTAAGA AGTACCTGCA 540
AGAAACCTAC TCAAAGCAGG TCACCAGCCA GGAGCCCTGA CCCAGGCTGC CCAGCCTGTC 600
CTTGTCTCGT CTTTCTAATT TTTCCTTAGA TGGTCTGTCC TTTTGTGTAT TTCTGTATAG 660
GACTCTTTAT CTTGAGCTGT GGTATTTTGG TTTTGTTTTT GTCTTTTAAA TTAAGCCTCG 720
5 GTTGAGCCCT TGTATATTAA ATAAATGCAT TTTTGTCCCT TTTTAAAAAA AAAAAAAA 780
AAA

Seq ID NO: 95 Protein Sequence
Protein Accession #: NP_008950.1

1 11 21 31 41 51
MASQNRDPAA TSVAAARKGA EPSGGAARGP VGKRLQQBELM TLMMSGDKGI SAPPESDNLF 60
KLVGTIHHGA GIVYEDLRYK LSLEFFSGYP YNAPT VKFLT PCYHPNVDTQ GNICLDILKE 120
15 KWSALYDVRT ILLSIQSLLG EPMIDSPLNT HAAELWNKNT AFRKYLQETY SKQVTSQEP 179

Seq ID NO: 96 DNA sequence
Nucleic Acid Accession #: AK055663
Coding sequence: 38..1423

1 11 21 31 41 51
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25 AAAACCCCAA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA 120
CCGAAGSTCC TGGAGATAC TGCTCTTTGG TGAATAAAC TTGATATGTA CTGGCTTCCT 180
GCTTATGTGG TGCAGTTCTA CTAATAGTAT AGCTTTAACT GCCTATACCT ACCTGACCAT 240
TTTTGATCTT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAACAT TGAGGAAACC 300
TAGCCCTGTC TATTCATTTG GGTITGAAAG ATTAGAAGTC CTGGCTCTAT TTGCTCCAC 360
AGTCTTGGCA CAGTTGGGAG CTCTCTTTAT ATTAAAAGAA AGTGCAGAAC GCTTTTGGGA 420
30 ACAGCCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTTGTGGCTC TTTGTTTCAA 480
CCTGTTCAAG ATGCTTTCTA TTGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG 540
TACGAGCTGG TCTCAAGAGC ATGTTGCAGA TCTTAGTCGA AGCTTGTGTG GAATTATTCC 600
GGGACTTAGC AGTATCTTCC TTCCCCGAAT GAATCCATTT GTTTTGATTG ATCTTGCTGG 660
AGCATTTGCT CTTTGTATTA CATATATGCT CATTGAAATT AATAATTATT TTGCCGTAGA 720
35 CACTGCCTCT GCTATAGCTA TTGCCTTGAT GACATTTGGC ACTATGTATC CCATGAGTGT 780
GTACAGTGGG AAAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATTGGTC AGTTGGACAA 840
ATCATCAGA GAGGTATCTA CCTTAGATGG AGTTTTACAA GTCCGAATG AACATTTTGG 900
GACCCTAGGT TTTGGCTCAT TGGCTGGATC AGTGCATGTA AGAATTCGAC GAGATGCCAA 960
40 TGAACAAATG GTTCTTGCTC ATGTGACCAA CAGGCTGTAC ACTCTAGTGT CTACTCTAAC 1020
TGTTCAAATT TTCAAGATG ACTGGATTAG GCCTGCCTTA TTGCTGGGCG CTGTTGCAGC 1080
CAATGTCCTA AACTTTTCAG ATCATCACGT AATCCCAATG CCTCTTTTAA AGGGTACTGA 1140
TGATTTGAAC CCAGTTACAT CAACTCCAGC TAAACCTAGT AGTCCACCTC CAGAATTTTC 1200
ATTTAACACT CCTGGGAAAA ATGTGAACCC AGTTATTCCT CTAACACACG AAACAAGGCC 1260
45 TTATGTTTTT GGTCTCAATC ATGGACACAC ACCTTACAGC AGCATGCTTA ATCAAGGACT 1320
TGGAGTTCCA GGAATTTGGAG CAACTCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG 1380
TAGATATGGA ACTAATAATA GAATTTGGACA ACCAAGACCA TGATAGACTC TAACTTATTT 1440
TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTTAG TAACTCAACT TTGCATTGAC 1500
TGTTTAATCA TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCAACAT TCATGAAACC 1560
50 TATGAACTA TATTTTGTGA AGAATATGTT TTTCTTTAAA TTTGGATTTT GGTATCTTTG 1620
GCTTTAAATA GGCTTCCTTT AGAAAAATGT TTTCTTTAAA TTTGGATTTT GGTATCTTTG 1680
GTTTGTAGT TGACTGCACT GTGATGTGAC CTACCTTTTA TAAGAGCCAC TTGATGGAGT 1740
AGATCTGTCA CATTACTAAG ATACGATATT TCTTTTTTTT TCCGAGACGG AGTCTTGCTC 1800
TGCCACTGTG CCCGCCCAAT ACATTATTAT TAACTTAAAG CTGTACTTTA TTAAGGCTTC 1860
CTTAGTTTTT GTTTTGTTTT GTTTTGTGAG ATGGAGTCTC ACTCTGTGCG CCAGGCTGGA 1920
55 ATGCACTGGC ATGATCTCAG CTCACTGCAA CCTCTGCCTC CTGAGTTCAA ATGATTCTCC 1980
TGCCCTCAGC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCAAGCCC AGCTAATTTT 2040
TCTATTTTGA GTAAAGACGG GGGATTTCAC CATGTTGGCC AGGCTGGTCT TGAACCTCTG 2100
ACCTCATGAT CCACCCACCT TAGCCTCCCA AAGTGCTGGG ATTAGGTGTG AGCCACCCGA 2160
60 CCTGGCCGGT ATTTCTTTTA ATGAAATTTA TAAATATGCT TCTTGAATAA TACACATTTT 2220
GGGAAAGGGA AAAATGCTGT TTCAAAAAGT AAAGGTCTCT TTTATAGCTT TTCCAAACIT 2280
AATTGCTAAA TTTTCTTTTG AGTTCTCCTT GAATTATGTC TTACAACTA AAAGCAAAAA 2340
TTTTTAGCAG AAATTTTGGG ATACATTCTA TCTAGCACAA TTTGAATTTT TAATTATCAA 2400
GATTTTGTGT AAAGTTTCTC TCCTTTTAAA ATTTTAGTAC ATTTGTAAT

Seq ID NO: 97 Protein Sequence
Protein Accession #: BAB70980.1

1 11 21 31 41 51
MGIHLFRKP QRSFFGKLLR EFRLVAADRR SWKILLFQVI NLICTGFLLM WCSSTNSIAL 60
70 TAYTYLTIFD LFLSLMCLIS YWVTLRKPSV VYSFGFERLE VLAVFASTVL AQLGALFILK 120
ESAERFLBEP EIHTGRLLVG TFVALCFNLF TMLSRNKP AVVSEAASTS WLQEHVADLS 180
RSLCGIIPGL SSIFLPRMNP FVLIDLAGAF ALCITYMLIE IMNYFAVDTA SAIAIALMTF 240
75 GTMYPMVSVS GKVLQQTTPP HVIGQLDKLI REVSTLDGVL EVRNEHFWTL GFGLAGSVH 300
VRIRRDANEQ MVLAHVTNRL YTLVSTLTVO IFKDDWIRPA LLSGPVAANV LNFSDHVTIP 360
MPLLKGTDDL NPVTSTPAKP SSPPEPFSFN TPGKNVNPVI LLNTQTRPYG FGLNHGHTPY 420
SSMLNGGLGV PGIGATQGLR TGFTNTPSRY GTNNRIGQPR P

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TCCACCCTAA CCCCAGTCT GCACTCAACG AGGAGGCGGG CCGCCTGCTC TTGGAGAACT 480
ACGAGGAGTA TGGCGCTCGG GCCCGTCTGC TCACAGAGAT CCACGGGGGC GCCGGCGGGC 540
CCAGCGGCAG GGGCGAAGCC GGTCCGCCCC TGGCCAGTGG CACTGAAGCT TCCTCCACCG 600
ACCTTGGGGC CCCAGGGGGC CCGGGAGGGG CTGAGGGTCC CATGGCCAAG AAGCATGCTG 660
GCGAGCGGCA TAAGAAGCTG GCGGCCAAGA AAAAGACGGA CAAGAAGCGG GCGCTGCGGG 720
CGCTGCGGCG GCTGTAGTGG GCTCTCTTCC TCCTTCACCC GTGACCCCAA CCTCTCCTGT 780
CCCTCCCTC CAATCTGTCT TCTAAGTTAT TTAAATTATG GCTGGGGTCG GGGAGGGTAC 840
AGGGGGCACT GGGACCTGGA TTTGTTTTTC TAAATAAAGT TGGAAAAGCA

Seq ID NO: 104 Protein Sequence
Protein Accession #: NP_055316.1

1 11 21 31 41 51
MNSNVENLPP HIIRLVYKEV TTLTADPPDG IKVFPNEEDL TDLQVTIEGP EGTPYAGGLF 60
RMKLLLGKDF PASPPKGYFL TKIFHPNVGA NGEICVNVLK RDWTAEGLIR HVLLTIKCLL 120
IHPNPESALN EEAGRLLEN YEYAAARAL LTEIHGGAGG PSGRAEAGRA LASGTEASST 180
DPGAPGGPOG AEGPMAKKHA GERDKKLAAK KKTDKKRALR ALRRL

Seq ID NO: 105 DNA sequence
Nucleic Acid Accession #: NM_005101
Coding sequence: 76..573

1 11 21 31 41 51
CGGCTGAGAG GCAGCGAACT CATCTTTGCC AGTACAGGAG CTGTGCGCGT GGCCACAGC 60
CCACAGCCCA CAGCCATGGG CTGGGACCTG ACGGTGAAGA TGCTGGCGGG CAACGAATTC 120
CAGGTGTCCC TGAGCAGCTC CATGTGCGTG TCAGAGCTGA AGCGGCAGAT CACCCAGAAG 180
ATTGGCGTCC ACGCCTTCCA GCAGCGTCTG GCTGTCCACC CGAGCGGTGT GCGCTGCAG 240
GACAGGCTCC CCTTGCAG GCAGGCGCTG GCGCCTGGCA GCACGGTCTT GCTGGTGGTG 300
GACAAATGCG ACGAACCTCT GAGCATCTGT GTGAGGAATA ACAAGGCGCG CAGCAGCACC 360
TACGAGGTCC CGCTACGCCA GACCGTGGCC CACCTGAAGC AGCAAGTGAG CCGGCTGGAG 420
GGTGTGCAGG ACGACCTGTT CTGGCTGACC TTCCAGGGGA AGCCCTTGGG GGACAGCTC 480
CCGCTGGGGG AGTACGGCCT CAAGCCCTGT AGCACCCTGT TCATGAATCT GCGCTGCGGG 540
GGAGGCGGCA CAGAGCCTGG CCGGCGGAGC TAAGGGCCTC CACCAGCATC CGAGCAGGAT 600
CAAGGCGCGG AAATAAAGGC TGTGTGAAGA GAAT

Seq ID NO: 106 Protein Sequence
Protein Accession #: NP_005092

1 11 21 31 41 51
MGWDLTVKML AGNEFQVSL SSMVSVELKA QITQKIGVHA FQORLAVHPS GVALQDRVPL 60
AQQLGPGST VLLVVDKDE PLSILVRNNK GRSSTYEVRL TQTVAHLKQQ VSGLEGVQDD 120
LFWLTFBCKP LEDQLPLGEY GLKPLSTVFM NLRRLGGGTE PGGRS

Seq ID NO: 107 DNA sequence
Nucleic Acid Accession #: NM_006018
Coding sequence: 1..1161

1 11 21 31 41 51
ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAATAG ACAAGAAGAA CTGCTGTGTG 60
TTCCGAGATG ACTTCATTGC CAAGGTGTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTT 120
GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCTCGGAAA 180
TCCAGCCGGA TTTTCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 240
CGCTTGTGTA TGGACTACTA TGTGCGCGGT TCAGACTGGA ACTTTGSGGA CATCCCTTSC 300
GCGCTGGTGC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 360
GTGGCGGTAG ACAGGTATTT CCGCGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420
AATTGGACAG CAGCCATCAT CTCTTGCCCT CTGTGGGGCA TCACTGTGTG CCTAACAGTC 480
CACCTCCTGA AGAAGAAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 540
AGCATCTGCC ATACCTCCG GTGGCAGCAA GCTATGTTCC TCCTGGAGTT CCTCCTGCCC 600
CTGGGCATCA TCCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660
GACCCGCATG CCAAGATCAA GAGAGCCATC ACCTTTCATCA TGCTGTTGGC CATCGTCTTT 720
GTCACTGCT TCCTTCCAG CGTGTTGTG CCGATCCGCA TCTTCTGGCT CCTGCACACT 780
TCGGGCAAGC AGAATTGTGA AGTGACCGC TCGGTGGACC TGGCTTCTT TATCACTCTC 840
AGCTTCACCT ACATGAACAG CATGCTGGAC CCGCTGGTGT ACTACTTCTC CAGCCCTCC 900
TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGAAAGAT GACAGGTGAG 960
CCAGATAATA ACCGACAGAC GAGGTCGAG CTCACAGGGG ACCCCAACAA AACCAAGAGG 1020
GCTCCAGAGG CTTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1080
ACCTCAAATA ACCATTCCAA GAAGGACAT TGTACCAAG AACCCAGCATC TCTGGAGAAA 1140
CAGTTGGGAT GTTGCATCGA G

Seq ID NO: 108 Protein Sequence
Protein Accession #: NP_006009.1

1 11 21 31 41 51

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MNRHHLQDHF	LEIDKKNCCV	FRDDFIAKVL	PPVLGLEPIF	GLLGNGLALW	IFCFHLKSWK	60
SSRIFLFNLA	VADFLLIICL	PFVMDYYVRR	SDWKFGDIPC	RLVLFMFAMN	RQGSIIFLT	120
VAVDRYFRV	HPHHALNKIS	NWTAIIISCL	LWGITVGLTV	HLLKKLLIQ	NGPANVCISF	180
SICHTFRWHE	AMFLEFLLP	LGIIIFCSAR	IWSLRQRQM	DRHAKIKRAI	TFIMVVAIVF	240
VICFLPSVVV	RIRIFWLLHT	SGTQNCVYR	SVDLAFFITL	SFTYMNSMLD	PVVVYFSSPS	300
PFNFSTLIN	RCLQRKMTGE	PNNRSTSV	LTGDPNKTRG	APBALMANSG	EPWSPSYLGP	360
TSNNHKKGH	CHQEPASLEK	QLGCCIE				

Seq ID NO: 109 DNA sequence
Nucleic Acid Accession #: NM_005030.2
Coding sequence: 63..1874

1	11	21	31	41	51	
GGCAGGAGGG	AGCGGTGCGG	AGGCTCTGCT	CGGATCGAGG	TCTGCAGCGC	AGCTTCGGGA	60
GCATGAGTGC	TGCAGTGACT	GCAGGGAAGC	TGGCACGGGC	ACCGGCCGAC	CCTGGGAAAG	120
CGGGGTCCCC	CGAGATTGCA	GCTCCCGGAG	CTCCGGCGGC	GGCTCCACCG	CGGAAAGAGA	180
TCCCAGGAGT	CCTAGTGGAC	CCACGCAGCC	GGCGGCGCTA	TGTGCGGGGC	CGCTTTTGG	240
GCAAGGGCGG	CTTGCCCAAG	TGCTTCGAGA	TCTCGGACGC	GGACACCAAG	GAGGTGTTCG	300
CGGGCAAGAT	TGTGCCTAAG	TCTCTGCTGC	TCAAGCCGCA	CCAGAGGGAG	AAGATGTCCA	360
TGGAATATC	CATTACCCGC	AGCCTCGCCC	ACCAGCACGT	CGTAGGATTC	CACGGCTTTT	420
TCGAGGACAA	CGACTTCGTG	TTCGTGCTGT	TGGAGCTCTG	CGCGCGGAGG	TCTCTCCTGG	480
AGCTGCACAA	GAGGAGGAAA	GCCCTGACTG	AGCCTGAGGC	CCGATACTAC	CTACGGCAAA	540
TTGTGCTTGG	CTGCCAGTAC	CTGCACCGAA	ACCGAGTTAT	TCATCGAGAC	CTCAAGCTGG	600
GCAACCTTTT	CCTGAATGAA	GATCTGGAGG	TGAAAAATAGG	GGATTTTGA	CTGGCAACCA	660
AAGTCGAATA	TGACGGGAG	AGGAAGAAGA	CCCTGTGTGG	GACTCCTAAT	TACATAGCTC	720
CCGAGGTGCT	GAGCAAGAAA	GGGCACAGTT	TCGAGGTGGA	TGTGTGGTCC	ATTGGGTGTA	780
TCATGTATAC	CTTGTTAGTG	GGCAAAACCAC	CTTTTGAGAC	TTCTTGCCTA	AAAGAGACCT	840
ACCTCCGGAT	CAAGAAGAA	GAATACAGTA	TTCCTCAAGCA	CATCAACCCC	GTGGCCGCCT	900
CCCTCATCCA	CAAGATGCTT	CAGACAGATC	CCACTGCCCG	CCCAACCAT	AACGAGCTGC	960
TTAATGACGA	GTTCTTTACT	TCTGGCTATA	TCCCTGCCCG	TCTCCCCATC	ACCTGCCTGA	1020
CCATTCCACC	AAGGTTTTCG	ATTGCTCCCA	GCAGCCTGGA	CCCCAGCAAC	CGGAAGCCCC	1080
TCACAGTCTC	CAATAAAGGC	TTGGAGAACC	CCCTGCCCTGA	CGCTCCCCGG	GAAAAAGAG	1140
AACCAAGTGT	TCGAGAGACA	GSTGAGTGG	TCGACTGCCA	CCTCAGTGAC	ATGCTGCAGC	1200
AGCTGCACAG	TGTCAATGCC	TCCAAGCCCT	CGGAGCGTGG	GCTGGTCAGG	CAAGAGGAGG	1260
CTGAGGATCC	TGCCTGCATC	CCCATCTTCT	GGGTCAGCAA	GTGGGTGGAC	TATTCGGACA	1320
AGTACGCGCT	TGGGTATCAG	CTCTGTGATA	ACAGCGTGGG	GGTGCTCTTC	AATGACTCAA	1380
CACGCTCAT	CCTCTACAAT	GATGGTGACA	GCCTGCAGTA	CATAGAGCGT	GACGGCACTG	1440
AGTCCTACCT	CACCGTGAGT	TCCCATCCCA	ACTCCTTGAT	GAAGAAGATC	ACCCTCCTTA	1500
AATATTTCCG	CAATTACATG	AGCGACCACT	TGCTGAAGGC	AGGTGCCAAC	ATCACGCCGC	1560
GGGAAGGTGA	TGAGCTCGCC	CGGCTGCCCT	ACCTACGGAC	CTGCTTCCGC	ACCCGCGAGG	1620
CCATCATCCT	GCACCTCAGC	AACGCGACGG	TGCAGATCAA	CTTCTTCCAG	GATCACACCA	1680
AGCTCATCTT	GTGCCCACTG	ATGGCAGCGG	TGACCTACAT	CGACGAGAAG	CGGGACTTCC	1740
GCACATACCG	CCTGAGTCTC	CTGGAGGAGT	ACGGCTGCTG	CAAGGAGCTG	GCCAGCCGGC	1800
TCGGCTACCG	CCGCACTATG	GTGGACAAGC	TGCTGAGCTC	ACGCTCGGCC	AGCAACCGTC	1860
TCAAGGCCTC	CTAATAGCTG	CCCTCCCTCC	CGGACTGGTG	CCCTCCTCAC	TCCCACCTGC	1920
ATCTGGGGCC	CATCTGGTTT	GGCTCCCGCG	GTCCCATGTC	TGCAGTGTGC	CCCCAGGCC	1980
CGGTGGCTGG	GCAGAGCTGC	ATCATCCTTG	CAGGTGGGGG	TTGCTGTGTA	AGTTATTTTT	2040
GTACATGTTT	GGGTGTGGGT	TCTACAGCCT	TGTCCTCCCT	CCCTCAACC	CCACCATATG	2100
AATTGTACAG	AATATTTCTA	TTGAATTCGG	AACTGTCTCT	TCCTTGGCTT	TATGCACATT	2160
AAACAGATGT	GAATATTCAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAA	

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Seq ID NO: 110 Protein Sequence
Protein Accession #: NP_005021.2

1	11	21	31	41	51	
MSAAVTAGKL	ARAPADPGKA	GVPGVAAPGA	PAAAPPAKEI	PEVLVDPRSR	RRYVRGRFLG	60
KGGFAKCFEI	SDADTKEVFA	GKIVPKSLLL	KPHQREKMSM	EISIHRS LAH	QHVVGFGHFF	120
EDNDFVFFVL	ELCRRRSLL	LHKRRKALTE	FEARYVLRQI	VLGCQYLRHN	RVIHRDLKLG	180
NLFNLNEDLEV	KIGDFGLATK	VEYDGERKKT	LCGTPNYIAP	EVLSSKKGHSF	EVDVWSIGCI	240
MYTLVLVGKPP	FETSCLKETY	LRIKNEYYSI	PKHINPVAAS	LIQKMLQTDN	TARPTINELL	300
NDEFFTSGYI	PARLPITCLT	IPPRFSIAPS	SLDPSNRKPL	TVLNKGLENP	LPERPREKEE	360
PVVRETGEVV	DCHLSMDLQQ	LHSVNASKPS	ERGLVROEEA	EDPACIPIFW	VSKMVDYSDK	420
YGLGYQLCDN	SVGVLPNDST	RLILYNDGDS	LQYIERDGTE	SYLTVSSHNP	SLMKKITLLK	480
YFRNYMSEHL	LKAGANITPR	EGDELARLPY	LRTWFRTRSA	IILHLSNGSV	QINFFQDHTK	540
LILCPLMAAV	TYIDEKRDFR	TYRLSLLEBY	GCCKELASRL	RYARTMVDKL	LSSRSASNRL	600
KAS						

Seq ID NO: 111 DNA sequence
Nucleic Acid Accession #: NM_005409.3
Coding sequence: 94..378

1	11	21	31	41	51	
TTCTTTTCAT	GTTTCAGCATT	TCTACTCCTT	CCAAGAAGAG	CAGCAAAGCT	GAAGTAGCAG	60

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CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGACGACGC 180
TGCTTTTGA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAAT 300
AAAGGACAAC GATGCTTAAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT 360
GAAAAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGGAAGAAG GCATCTGAAA 420
AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
AGACTTTTCT ATGGTTTTGT GACTTTCAAC TTTGTACAG TTATGTGAAG GATGAAAGGT 540
GGGTGAAAG ACCAAAAACA GAAATACAGT CTTCTGAAT GAATGACAAT CAGAATTCCA 600
CTGCCCAAAG GAGTCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
GGTTACCATC GGAGTTTACA AAGTGCTTTC ACGTCTTAC TTGTTGTATT ATACATTCTAT 720
GCATTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
CATCTATGTG TCGTAAAGCA TTCCTCAAAC ATTTTTTCAT GCAAAATACAC ACTTCTTTCC 960
CCAAATATCA CAATATGTAG GGAACATTC TTATGCATCA TTTGGTTTGT 1020
TTTATAACCA ATTCAATTA TGTAAATCTA AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
TGGGATACTG GCAACAGTGC ACATATTCA TAACCAAAAT AGCAGCACCG GTCTTAATTT 1140
GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
TGACTTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGGAC ACATTTGAAA 1260
TACAAATGT TTTTGTCTAC CAAGAAAAA TGTGAAAAA TAAGCAAAAT TATACCTAGC 1320
AATCACTTTT ACTTTTGTG ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
TTGTTTCATG CTATATACTG TAAATTTTAA GTATACTCA GACTAGTTTA AAGAATCAAA 1440
GTCTTTTCTT TCTCTAATAA ACTACACAAA CCTTCTTTT TTAACAAAAA AAA

Seq ID NO: 112 Protein Sequence
Protein Accession #: NP_005400.1

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1 11 21 31 41 51
MSVKGMALAL AVILCATVVQ GFPMPKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60
EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF

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Seq ID NO: 113 DNA sequence
Nucleic Acid Accession #: NM_001110.1
Coding sequence: 470..2716

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1 11 21 31 41 51
GAATTCGAGG ATCCGGGTAC CATGGCGCGC GGCAGGCCTA GCAGCAGCGG AACCGTCCCC 60
CGCGCGCATG CGCGCGCCCC TGAAGCGCCT GGGGACGGG TATGGCGGG AGGTAGGGGC 120
CGCGCTCCCG GTGCCAGTTG GGTGCCCCGC CGTCACGTGG TGAGGAAGGA GCGGAGGGTC 180
TGAGTTTCGA GGGAGGGGGG GAGAGAAGAG GGAACGAGCA AGGGAAGGAA AGCGGGGAAA 240
GGAGGAAGGA AACGAACGAG GGGGAGGGAG GTCCCTGTTT TGGAGGAGCT AGGAGCGTTG 300
CCGCGCCCTG AAGTGGAGCG AGAGGGAGGT GCTTCGCGGT TTCTCTGCGC AGGGGAGGTC 360
CCGGCTTCCC GTGGAGGCTC CGGACCAAGC CCCTTCAGCT TCTCCCTCCG GATCGATGTG 420
CTGCTGTAA CCCGTGAGGA GCGCGCGCGC GCGGCAGCGG CAGCGGAAGA TGGTGTGTGT 480
CAGAGTGTTA ATTCGTCTCC TCTCCTGGGC GCGGGGATG GGAGCTCAGT ATGGGAATCC 540
TTTAAATAAA TATATCAGAC ATTATGAAGG ATTATCTTAC AATGTGGATT CATTACACCA 600
AAAACACCGG CGTGCCAAAA GAGCAGTCTC ACATGAAGAC CAATTTTAC GTCTAGATTT 660
CCATGCCCAT GGAAGACATT TCAACCTACG AATGAAGAGG GACACTTCCC TTTTCAGTGA 720
TGAATTTAAA GTAGAACAT CAAATAAAGT ACTTGATTAT GATACCTCTC ATATTTACAC 780
TGGACATATT TATGGTGAAG AAGCAAGTTT TAGCCATGGG TCTGTTATTG ATGGAAGATT 840
TGAAGGATTC ATCCAGACTC GTGGTGGCAC ATTTTATGTT GAGCCAGCAG AGAGATATAT 900
TAAAGACCGA ACTCTGCCAT TTCACTCTGT CATTATCAT GAAGATGATA TTAACATATC 960
CCATAAATAC GGTCTCTCAG GGGGCTGTGC AGATCATTTCA GTATTTGAAA GAATGAGGAA 1020
ATACCAGATG ACTGGTGTAG AGGAAGTAA ACAGATACCT CAAGAAGAAC ATGCTGCTAA 1080
TGCTCCAGAA CTTCTGAGGA AAAAAAGTAA AACTTCAGCT GAAAAAATA CTTGTCTAGT 1140
TTATATTGAG ACTGATGATT TGTTCCTTAA ATATTACGGA ACACGAGAAG CTGTGATTGC 1200
CCAGATATCC AGTCATGTTA AAGCGATTGA TACAATTTAC CAGACCACAG ACTTCTCCGG 1260
AATCCGTAA ATCAGTTTCA TGGTGAAACG CATAAGAATC AATACAACCT CTGATGAGAA 1320
GGACCTTACA AATCCTTTCC GTTTCCTAAA TATTGGTGTG GAGAAGTTTC TGAATTTGAA 1380
TTCTGAGCAG AATCATGATG ACTACTGTTT GGCCTATGTC TTCACAGACC GAGATTTTGA 1440
TGATGGCGTA CTTGGTCTGG CTTGGGTGG AGCACCTTCA GGAAGCTCTG GAGGAATATG 1500
TGAAAAAGT AAACCTATT CAGATGGTAA GAAGAAGTCC TTAACACTG GAATTTATAC 1560
TGTTTCAAGC TATGGGTCTC ATGTACCTCC CAAAGTCTCT CACATTACTT TTGCTCACGA 1620
AGTTGGACAT AACTTTGGAT CCCACATGA TTCTGGAACA GAGTGCACAC CAGGAGATC 1680
TAAGAAATTT GGTCAAAAAG AAAATGGCAA TTACATCATG TATGCAAGAG CAACATCTGG 1740
GGCAAACTT AACAACAATA AATTCTCACT CTGTAGTATT AGAAATATAA GCCAAGTTCT 1800
TGAGAAGAAG AGAAACAAC GTTTTGTGTA ATCTGGCCAA CCTATTTGTG GAAATGGAAT 1860
GGTAGAACAA GGTGAAGAAT GTGATTGTGG CTATAGTGAC CAGTGTAAAG ATGAATGCTG 1920
CTTCGATGCA AATCAACCG AGGGAAGAAA ATGCAAACTG AAACCTGGGA AACAGTGCAG 1980
TCCAGTCAA GGTCTTGTG GTACAGCACA GTGTGCATTC AAGTCAAAGT CTGAGAAGTG 2040
TCGGCATGAT TCAGACTGTG CAAGGGAAGG AATATGTAAT GGCCTCACAG CTCTCTGCC 2100
AGCATCTGAC CCTAAACCAA ACTTCACAGA CTGTAATAGG CATACACAAG TGTGCATTAA 2160
TGGGCAATGT GCAGGTCTTA TCTGTGAGAA ATATCCCTTA GAGGAGTGTA CGTGTGCCAG 2220
TTCTGATGGC AAAGATGATA AAGATTATG CCATGTATGC TGTATGAAGA AAATGGACCC 2280

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ATCAACTTGT GCCAGTACAG GGTCTGTGCA GTGGAGTAGG CACTTCAGTG GTCGAACCAT 2340
CACCCGTCGA CCTGGATCCC CTTCGCAACGA TTTTAGAGGT TACTGTGATG TTTTCATGCG 2400
GTGCAGATTG GTAGATGCTG ATGGTCCTCT AGCTAGGCTT AAAAAAGCAA TTTTAGTCC 2460
AGAGCTCTAT GAAAAATGTG CTGAATGGAT TGTGGCTCAT TGGTGGGCG TATTACTTAT 2520
GGGAATTGCT CTGATCATGC TAATGGCTGG ATTTATTAAG ATATGCAGTG TTCATACTCC 2580
AAGTAGTAAT CCAAGTTGCG CTCTCTCTAA ACCACTTCCA GGCACCTTAA AGAGGAGGAG 2640
ACCTCCACAG CCCATTTCAGC AACCCCGAGCG TCAGCGGCGCC CGAGAGAGTT ATCAAATGGG 2700
ACACATGAGA CGCTAACTGC AGCTTTTGGC TTGGTTCTTC CTAGTGCCTA CAATGGGAAA 2760
ACTTCACTCC AAAAGAGAAC CTATTAAGTC ATCATCTCCA AACTAAACCC TCACAAGTAA 2820
CAGTTGAAGA AAAAATGGCA AGAGATCATA TCCTCAGACC AGGTGGAATT ACTTAAATTT 2880
TAAAGCCTGA AAATCCAAT TTGGGGTGG GAGGTGGAAG AGGACCCAA TTTTCTTATG 2940
AACAGATATT TTTAACTTAA TGGCACAAG TCTTAGAATA TTATTATGTG CCCCGTGTTC 3000
CCTGTTCTTC GTTGCTGCAT TTTCTTCACT TGCAGGCAAA CTGGGCTCTC AATAAACTTT 3060
TACCACAAAT TGAATAAAT ATATTTTTT CAACGTCCAA TCAGGGCTAG GAGGCTCGAC 3120
CACCTCAACA TTGGAGACAT CACTTGCCAA TGTACATACT TTGTTATATG CAGACATGTA 3180
TTTCTTACGT ACACGTACT TCTGTGTGCA ATTGTAAACA GAAATTGCAA TATGGATGTT 3240
TCTTTGTATT ATAAAAATTT TCCGCTCTTA ATTAATAAAT ACTGTTTAA TGCATATCTC 3300
AGGATAACAG AGAATGGTGG TATTCAGTGG TCCAGGATTC TGTAAATGCTT TACACAGGCA 3360
GTTTTGAAT GAAATCAAT TTACCCCATG GTACCCCGAT CCTCGAATTC

Seq ID NO: 114 Protein Sequence
Protein Accession #: NP_001101.1

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1 11 21 31 41 51
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MVLRLVILL LSWAAGMGGO YGNFLNKYIR HYEGLSYNVD SLHQKHQRAK RAVSHEDQFL 60
RLDFHAHGRH FNLRMKRDTS LFSDEFKIVET SNKVLDDYDTS HIYTGHIYGE EGSFSGHSGVI 120
DGRFEGFIQT RGGTFYVEPA ERYIKDRITLP FHSVIYHEDD INYPHYKGPQ GGCADHSVFE 180
RMRKYQMTGV BEVTQIPQEE HAANGPELLR KKRTTSAEKN TCQLYIQDTH LFFKYVGTRE 240
AVIAQISSHV KAITDIYQTT DFGSIRNISP MVKRIIRINTT ADEKDPNTNP RFPNIGVEKF 300
LELNSBQNH DYLAVVFTD RFDGDLVGL AWVGAPSGSS GGICEKSKLY SDCKKSLNT 360
GIITVQNYGS HVPPKVSHTT FAHEVGHNF SPHDSGTCT PGESKNLQOK ENGNVIMYAR 420
ATSGDKLNN KFLSCSIRNI SQVLEKKRNN CFVESGQPIC GNGMVEQGEE CDGYSDDQCK 480
DECCFDANQP RGRCKLKPQ KQCSFSGGPP CTAQCAFPSK SEKCRDSDC ARBICNGFT 540
ALCPASDPKP NFTDCNRHTQ VCINGQCAGS ICEKYGLEEC TCASDSDGDD KELCHVCMK 600
KMDPSTCAST GSVQWSRHFS GRTITLQPGS PCNDFRGYCD VFMRCLVDA DGPLARLKA 660
IFSPELYENI AEWIVAHWMA VLLMGIALIM LMAGFIKICS VHTPSSNPKL PPKPLPGL 720
KRRRPQPIQ QPQRPRPRES YQMGMHMR

Seq ID NO: 115 DNA sequence
Nucleic Acid Accession #: NM_000577.2
Coding sequence: 41..520

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1 11 21 31 41 51
| | | | |
GGCAGGAGGG GAAGACCTCC TGTCTATCA GGCCCTCCCC ATGGCTTTAG AGACGATCTG 60
CCGACCTCTT GGGAGAAAAA CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAACCA 120
GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAAAATG 180
CAATTTAGAA GAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
CCATGGAGGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
GGAGCGAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT 360
CATCCGCTCA GACAGTGGCC CCACCACCAG TTTTGAGTCT GCCGCTGCC CCGTTGGTT 420
CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
CGTCATGGTC ACGAAATTT ACTTCCAGGA GGACGAGTAG TACTGCCAG GCCTGCCTGT 540
TCCCATTCTT GCCATGGCAAG GACTGCAGG ACTGCCAGTC CCCCTGCCCC AGGGCTCCCG 600
GCTATGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACACAA 660
CCTGGTCACA GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAATG 720
GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTGCA CAAAGCCCTT CCATGTGCGC 780
TCTGCATTCA GGATCAAAAC CCGACCACT GCGCAACTG CTCTCTCTT GCCACTGCCT 840
CTTCTCTCCT CATTCACCT TCCCATGCC TGGATCCATC ACGGCACTTG ATGACCCCA 900
ACCAAGTGGC TCCACACCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
TTTAAAGGTT TGTGGAATAA GAAAAATAGG ATTTCATGAT TTTTTTTTT CAGTCCCGT 1020
GAAGGAGAGC CTTTCATTG GAGATTATGT TCTTTCGGG AGAGGCTGAG GACTTAAAT 1080
ATTCTGTAT TTGTGAAATG ATGGTGAAG TAAGTGGTAG CTTTTCCTT CTTTTCTTC 1140
TTTTTTTGTG ATGTCCCAAC TTGTAAAAAT TAAAGTTAT GGTACTATGT TAGCCCCATA 1200
ATTTTTTTT TCTTTTAA ACACCTCCAT AATCTGGACT CCTCTGTCCA GGCAGTGTG 1260
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TCCATCAGA AGTTTCTCAG CTCCCAGGC TCTGAGCAAA TGTGCTCCT GGGGTTCTT 1380
TCTTCTCTG CTGAAGGAAT AATTTGCTCC TTGACATTGT AGAGCTTGT CACTTTGAG 1440
ACTGTATGA AAGATGGCTG TGCCTCTGCC TGTCTCCCC ACCAGGCTGG GAGCTCTGCA 1500
GAGCAGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAAG CTAAGCCTCG 1560
CTCTGGCAG GTACTCAGCG AATGAATGCT GTATATGTT GGTGCAAGT TCCCTACTTC 1620
CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAAAA GCCTAAAAA AAAAAAAA 1680
AAAAAAA AAAAAAAA AAAAAAAA AAAAAA

Seq ID NO: 116 Protein Sequence
Protein Accession #: NP_000568.1

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PCT/US02/21338

1 11 21 31 41 51
MALETICRPS GRKSSKMQAF RINDVNQKTF YLRNNQLVAG YLQGNVNVLE EKIDVVPPIEP 60
5 HALFLGIHGG KMCLSCVKSG DETRLQLEAV NITDLSENK QDKRFAPIRS DSGPTTSFES 120
AACPGWFLCT AMEADQPVSL TNMPDEGVMV TKFYFQEDE

Seq ID NO: 117 DNA sequence
Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
GCACTTTAGC TCAGTGATGG ATTTTAAGAA GGATTACACC TGTGCGCTGT GGTCTGACTC 60
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15 CATCAATGGT TCCTTTTCGT CGCTTGGCTT TATTCATGAG GCTCAGGTCT GGGAAAGACT 180
GATGGTCCAC TGTGACAGCA AGACAGGTAA TGCAAAATACG GATTTTCATCT GGGTGGGTCC 240
AGATAACAGA CTGCTAGAGC CGGATAAAGA GATGGAAGAC TTTTACGTGT TTCACAATGG 300
AAGTCTGTGT ATAGAAAGCC CTGTTTTGA GGATGCTGGA GTGTATTCTT GTATCGCAAT 360
CAATAAGCAA CGCTGTATA ATGAAACGTG GGACGTACCA ATAAATGTGA GCAATTTTCA 420
20 TGTAAAGCAGA TCCCATGTCT ATGAGGCATT TAACACAGCT TTTACCACCT TTGCTGTCTG 480
CGTGGCCAGT ATCGTTTTGG TACTTTTGTG CCTCTATCTG ACTCCATGCC CTGCAAGTGG 540
TAAACCAAG AGACAGAAAA ATATGCTACA CCAAGCAAT GCCATTTCAT CGATTCTCAG 600
TCCTGGCCCG GACTAGTAGG CCTCGCTGA TGAACGGAAG GCAGGTGCAG GTAAAAGAGT 660
GGTGTTTTTG GAACCCCTGA AGGATACTGC AGCAGGGCAG AACGGGAAG TCAGGCTCTT 720
25 TCCAGCGAG GCAGTGATG CTGAGGGCAT CCTAAAGTCC ACGAGGGGGA AATCTGACTC 780
AGATTCAGTC AATTCAGTCT TTTCTGACAC ACCTTTTGTG GGTCCACTT AA

Seq ID NO: 118 DNA sequence
Nucleic Acid Accession #: AB032989.1
Coding sequence: 1..1316

1 11 21 31 41 51
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35 TGGGGGCCGA GTGGACCCCG AGCGCCCTGA CCCAACTGCA CTCCCTGCTG CTGAGCCACA 120
ACCACCTGAA CTTCATCTCC TCTGAGGCTT TTTCCCGGT ACCCAACCTG CGTACCTGG 180
ACCTCTCCTC CAACCAAGCTG CGTACACTGG ATGAGTTCCT GTTCAGTGAC CTGCAAGTAC 240
TGGAGGTGCT GCTGCTCTAC AATAACCACA TCATGGCGGT GGACCGGTGC GCCTTCGATG 300
40 ACATGGCCCA GCTGCAGAAA CTCTACTTGA GCCAGAACA GATCTCTCGC TTCCCTCTGG 360
AACTGGTCAA GGAAGGAGCC AAGTACCCA AACTAACGCT CCTGGATCTC TCTTCTAACA 420
AGCTGAAGAA CTGCGCATTG CCTGACCTGC AGAAGCTGCC GGCTGGATC AAGAATGGGC 480
TGTACCTACA TAACAACCCC CTGAACCTGG ACTGTGAGCT CTACCAGCTG TTTTCACACT 540
GGCAGTATCG GCAGCTGAGC TCCGTGATGG ACTTTCAAGA GGATCTGTAC TGCATGAAT 600
45 CCAAGAAGCT GCACAATGTC TTCAACCTGA GTTTCCTCAA CTGTGGCGAG TACAAGGAGC 660
GTGCGCTGGA GCGCCACCTG GGTGACACT TGATCATCAA GTGTGACACC AAGCAGCAAG 720
GGATGACCAA GGTGTGGGTG ACACCAAGTA ATGAACGGGT GCTAGATGAG GTGACCAATG 780
GCACAGTGAG TGTGTCTAAG GATGGCAGTC TTCTTTTCCA GCAGGTGCAG GTGACGAGC 840
GTGGTGTGTA TACCTGCTAT GCCATGGAG AGACTTTCAA TGAGACACTG TCTGTGGAAT 900
TGAAAGTGCA CAATTTCACC TTGCAAGGAC ACCATGACAC CCTCAACACA GCCTATACCA 960
50 CCCTAGTGGG CTGTATCCTT AGTGTGTGCC TGTCTCTCAT ATACCTATAC CTCACCCCTT 1020
GCCGCTGCTG GTGCCGGGGT GTAGAGAAGC CTTCAGGCCA TCAAGGAGAC AGCCTCAGCT 1080
CTTCCATGCT TAGTACCACA CCAACCATG ATCCTATGGC TGGTGGGGAC AAAGATGATG 1140
GTTTTCACCG GCGGTGGCT TTCTGTGAAC CTGCTGGACC TGGCAGGGT CAAAACGGCA 1200
AGCTCAAGCC AGGCAACACC GTGCCAGTGC CTGAGGCCAC AGGCAAGGGC CAAAGGAGGA 1260
55 TGTCCGATCC AGAATCAGTC AGCTCGGTCT TCTCTGATAC GCCCATTTGT GTGTGAGCAG 1320
GATGGGTGG TGGGGAGATT CTGCCCGAG AGAGGTAATG CACCCCTGAA GGATATGAGG 1380
GGATGGAGA GAGGGCTGGC TGCCCCAAGG AATGGATTCC TCCTGACCTC AAGGGAATTG 1440
GTCCCAGGTA CAACAGAGAG CAAGACCCCA AACAGGGCGT GGCTGCCACG ATTTTCAAAT 1500
GGGGGTATAT TAATCCTCAG GCAATTGCTA CACCCGTACC CAAAGCCCTG CCAATTCTCA 1560
60 GTGTGGTAGA GGAAGAGAAG CATGTCTGAG TTGGATGGGA ATGAGGAAGG AGTGAGGGGA 1620
AGAACAGATT CCTTAAACTT TCATGAGGTC ATCCCTAGCT CCTTAAGAGA AAAACATTTA 1680
GAAAAAATAA TTTTTCCTAT CTCTGCCAC CCACACCTGT GATGTTGTGT GTGTTGGGG 1740
AGCTTCCACA GGAGCCACAC TGGGSAAGAG CTGTAGTATC TTCTTTGTTT AGCAAGTCAA 1800
ACTTCACAGC TGGGGAAGTT GAAAACCTTT GGAATAAGAG TCAGGAAAAG GCTGAGACCT 1860
65 CAATCGGTAA CAATTCCCA AAGCTGTTGT AAGACTTTGC ATTAAGAGCCT TTCTTTTTC 1920
TGATGTGCC TGGGTGGATG GATCTTTGCA GGAGCCTGGC CTGCTGCCTT TTAGTTACAA 1980
CAGCAATGTG GGATGTGTA TCTGTGCTT GTCTGGGAC CAATGGCACA GAGGTTTATA 2040
GCATGAACCTG AAGGGTCCAT GTCCACAGCT AGGTGCCAGC ACGAAACTTG TAGATGGGG 2100
GTGAATTTCA GATAGGCTAA TTCCCTGGTT GGTGAAACCC TTGGTTAGTA TTTGATTCCC 2160
70 AGCATCTGTG TGTCAAGCCA GAGTGGGGG TGCTGAAAGC AGAGCTTTTA TGGATGCCTG 2220
CCACAGAGCT GGTACATGGG CCCACTTAC GATAGAAGGA TGAAGGTAAA TCAGCCTCTA 2280
TTATGTAGCA TCCAGCTGGA CCTAGCTGAT TCTCAATGTA TGCCATCTCT TCATCCAGTC 2340
TCTTATCAA GCTCAGGTGG GATTCTGAAT TTTCCCTAAT ATGCTGCTCT GTAAAGGGAG 2400
GAGTCCAAGA AAGCCTGGCC CCAGCTGGCT TAGAGTAGGC TTGGCGATAG TGAAAATCCA 2460
75 GTATATATCT CCTCTGTGTG GACAAGGTTG CTTGCTCCT CTCAGAGATA CCACCTCTGC 2520
TGCAAGTCA AAGCATGGG TTTTGACATC AGAAGGGTTG GAATGGGTG GTCTCTACCC 2580
CAGAAATGGA ATTTGGAGTG CAGCTTCAAG TTCTGCCCTC TCCACAGATT CCAGGCAATC 2640
CTGAAGCAGA GATAATCAGT AGTACTAAAC TTTCAGAAGG GGAGTTCTGC CACCCCATTC 2700

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CTCCATCGAG AGGTCTTTGC AGTTGTGGTT GTGAGGCCAG AGCAACTTAA GAAGAATGAG 2760
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TTTAACTTTT CCCTTTGACT ATACTGCATG CCTGTGAGT GGCTGCTCTG AGCTTTGGCG 2880
GGGATGAGC AGGGTGAAGC TGAAGATGTT CTCTGATGTT GCTTTTCTT AGTGTCTCTT 2940
CTCTCCACG TTTCTAGTCC ATTGGAAGTT CTCCAGATCC TCTAGATTTC TGACCTCTTT 3000
TTACATTCTA AGAGGTGTCA TTTACCTGTG GGTGAGGGGC TTGAGGGGCC TGACTATTAA 3060
GCTTCCTATT ATGATTGGGG AAGGGGACTC AACATCTTCC CCTTGTCTGG TCCTGGGAAC 3120
TCAAGACTGC TGTCCATCCT TTATTAGTAA CCTAGTTTTC TTGAGAGAGA GGTGCAGCAT 3180
TTCCCTCAAG TACCTGCATG CTCATAGGTA TGCATGCCTA TAGGTATGCA TGCACACCAG 3240
CACCTTGACT TCCACCAGGA CAGTGAATCT GTAGTCCCCA TTAATGATAC TCTCAGAATG 3300
GTCTCCACCA ATGTGCACAA CTTCATGCAC ACAATTGIAT TCCTCTTTAG GAGAGACAGT 3360
GACCATGCCA GGCCTCTCAA ATACACACTC CTGTATTTTC ATTTCTGAAC TCCTGAAGC 3420
TTACCCACA TCTCCATGGC ACTGAATCAC TTTTCTGCCC AGGCTGGAGT TAGAAGAACC 3480
ATGGGTTGAA GGCCTTGGGA GAAGAGGTGG TAAGGAGCTA CCTGGTCTTT TGACTCCTC 3540
AGAAACTCC CGTGAAGACT ATATATATGA GCAATATATG AGCAATTAAG ATAGAACTAG 3600
CTCATTCAGG GACTCAGAAG GAACTGGCA AGGGCTAAG TAGCTGTGAG CTGCTCTTCC 3660
TGTTAACTGT CCTCAGGAGA GAAAAGTTGT CTTGATTAT TCCAGAGACT CCTCAGAATT 3720
TTGTACTGG AGCTATAGGA ACTAGGACTC CCTCCTCAGA CTCATCAGGA AATCTGGGAA 3780
AATCTCATCT CGTCTGTGCA GTCTCCCGC TTGGCACCAT CTAGGGCTCT GAAGATCTTT 3840
AAAGTGAGCG TTAATGAAG CAGGCCCTCT GGGGCATCGT GATGGAGCTC CTGAGGACTG 3900
GGAGGGCCGT TTTCTTCATA ATTCTACCC AGTTTAGGGA ATGAGAAAAG GCCCTGTGGC 3960
TCTTAAGTCT CCTGACTATA TCCACTAGTT TGGCCTTGAG TTTGAGACAC CTGGTAGATG 4020
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CCCAAGGTGA GCTTTTAAAT TGGAGAATTG AATAATCAGC ATATGTAAGC GCACCTAGAAC 4140
CCTGTGTTGA AAACCTGCCAG GTGTGGGTAT AAGAAAAGGC CGAGAGATCA CCACCTCCTC 4200
TTACCTTACC CCACACCCAT AAACCAGACA TGTCTCCAG GAAGCAGGTG TCCTGGACA 4260
CAGAGGATGA CAGGGCTCTA CAATCTGTGT AATTATTATT ATTATTATTA TTTTGTATT 4320
ATGGGGCCCA AGAAGGGGC CAGCAGAGGG TACACCCAG CTGGGGAGAG CAAAGCAGAT 4380
GGATCCAGTT TCTGTGTGT TCTTACCTCT GTACTTCCTC GTAGCTCTGC TGACAAAGCA 4440
AGCAGGGCTC CGGTGTCCAA GACCCCATTC CTCCCACCTG TGTACACCTA GGTGGGCAA 4500
TCTTGGAGCC TCTGGGCTCT GAAAAC TAGA CAATGATCAT TAAACCTGGC TTGAGTCTCT 4560
GTTCTGGC

Seq ID NO: 119 Protein Sequence

Protein Accession #: BAA36477.1

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1 11 21 31 41 51
HSLPSYALL DLSHNNLSRL RAEWTPTRLT QLHSLLSLHN HLNFISSBAF SPVFNRLRYLD 60
LSSNQLRLTD EFLPSDLQVL EVLLLYNNHI MAVDRCAFDD MAQLQLKLYLS QNQRISRFPLE 120
LVKBAKLPK LTLDLSSNK LKNLPLPDLO KLPWIKNGL YLHNNPLNCD CELYQLFSHW 180
QYRQLSSVMD FQEDLYCMNS KKLHNVFNLS FLNCGEYKER AWEAHLGDTL IIKCDTKQQG 240
MTKWVWTPSN ERVLDEVING TVSVSKDGS L LFQQQVEDG GVTCTYAMGE TFNETLSVEL 300
KVHNFTLHGH HDTLNTAYTT LVGCILSVVL VLIYLYLTPC RCWCRGVEKP SSHQGDLSLS 360
SMLSTTPNHD PMAGGDKDDG FDRRVAFLEP AGPGQQQNGK LKPGNTLPVP EATGKGQRRM 420
SDPEVSVSFV SDTPIVV

Seq ID NO: 120 DNA sequence

Nucleic Acid Accession #: NM_005071

Coding sequence: 9..1703

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70
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1 11 21 31 41 51
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GCCTGCGCCT GCAGACCATG ACCCTCGAGC ACGTGTGCG CTTCCTGCGC CGAAACGCTT 180
TCATTCTGCT GACGGTCAGC CCGGTGGTCA TTGGGGTCAG CCTGGCCTTT GCCCTGCGCC 240
CATATCAGCT CACCTACCGC CAGATCAAGT ACTTCTCTTT TCCTGGAGAG CTTCTGATGA 300
GGATGCTGCA GATGCTGGTG TTACCTCTCA TTGTCTCCAG CTGGTCCACA GGTATGGCAT 360
CCTCGGACAA CAAGGCCACG GGGCGGATGG GGATGCGGGC AGCTGTGTAC TCCGGAAGTGA 420
CCACCATCAT CGCGTCTTTC ATCGGCATCC TCATGCTCAC CATCATCCAT CACGGGAAGG 480
GCTCCAAGGA GGGGCTGCAC CGGGAGGGCC GGATCGAGAC CATCCCCACA GCTGATGCCT 540
TCATGGACCT GATCAGAAAT ATGTTCCAC CAAACCTTGT GGAGGCCTGC TTCAAACAGT 600
CTAAGACGCA GTACAGCACG AGGTTGGTAA CCAGGACCAT GGTGAGGACA GAGAACGGGT 660
CTGAGCCGGG TGCTTCCATG CCTCTCCAT TCTCAGTGA GAACGGAACC AGCTTCTCTG 720
AAAATGTAC TCGGGCTTGG GGTACCTGCA AGGAGATGCT GAGCTTTGAG GAGACTGTAC 780
CCGTGCTTGG CTCCGCCAAT GGCATCAACG CCCTGGGCTT CGTGGTCTTC TCTGTGGCTT 840
TTGGGCTGGT CATTGGTGGC ATGAAACACA AGGGCAGAGT CCTCAGGGAC TTCTTCGACA 900
GCCTCAATGA GGTCTATTAT AGGCTGGTGG GCATCATTAT CTGGTATGCA CCTGTGGGCA 960
TCCTGTTCTT GATTGCTGGG AAGATTCTGG AGATGGAAGA CATGCGCGTC CTGGGGGTC 1020
AGCTGGGAT GTACACCTG ACCGTGATG TGGGCTCTTT CCTCATGCC GGCATTGTTC 1080
TTCCCTCAT CTACTTCTCT GTCACTCAC GGAACCCCTT CCCCTTCATT GGGGGCATGC 1140
TACAAGCCT CATCACCGCT ATGGCAGCT CTTCCAGCTC GGCAACGCTG CCCATCACCT 1200
TCCGCTGCTT GAGGAGGGC CTGGTGTGG ACCGCCGAT CACCAAGTTC GTCTGTCCCG 1260
TGGGCGCCAC GGTCAACATG GATGGCACTG CCTCTACGA GGCCTGGCT GCCATCTTCA 1320
TTGCTCAAGT TAACAACATC GAGCTCAACC TGGGTGAGT CACAACCATC AGCATCACGG 1380
CCACAGCAGC CAGTGTGGG GCTGCTGGCA TCCCCACGC GSGTCTGGTC ACCATGGTCA 1440
TTGTGCTTAC GTCGGTGGC TTGCCACCG AAGACATCAC GCTCATCATC GCCGTGGACT 1500

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GGTTCCTTGA CCGGCTTCGC ACAATGACCA ACGTACTGGG GGACTCAATT GGAGCGGCCG 1560
TCATCGAGCA CTGTGCTCAG CGGGAGCTGG AGCTTCAGGA AGCTGAGCTT ACCCTCCCCA 1620
GCCTGGGGAA ACCCTACAAG TCCCTCATGG CACAGGAGAA GGGGGCATCC CGGGGACGGG 1680
GAGGCAACGA GAGTCTATG TGAGGGGCTT CCAGCTCTG

Seq ID NO: 121 Protein Sequence
Protein Accession #: NP_005062

1 11 21 31 41 51
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MSSHGNSLFL RESGQRLGRV GWLQRLQESL QQRALRTRLR LQTMLEHVL RFLRRNAPIL 60
LTVSAVVIGV SLAFALRPYQ LTYRQIKYFS FPGELLMRML QMLVLPLIVS SLVTGMASLD 120
NKATGRMGMR AAVYVMVTI IAVFIGILMV TIIHFGKSK EGLHREGRIE TIPTADAFMD 180
LIRNMFPPNL VEACFKQFKT QYSTRVVTRT MVRTENGSEP GASMPEPFSV ENGTSFLENV 240
15 TRALGTLQEM LSFEEVVPV GSANGINALG LVVFSVAPGL VIGGMKHKOR VLRDFDLSN 300
EAIMRLVGII IWAYPVGILF LIAGKILEME DMAVLGGQLG MYTLTVIVGL FLHAGIVLPL 360
IYFLVTHRNF PFFIOGMLQA LITAMGTSSS SATLPITFR C LEEGLGVDRR ITRFVLVPGA 420
TVNMDGTALY EALAAIFIAQ VMNYELNLGO ITTISITATA ASVGAAGIPQ AGLVTMVIVL 480
20 TSVGLPTEDI TLIIAVDWFL DRLRTMTNVL GDSIGAAVIE HLSQRELELQ EAEELTLP SLG 540
KPYKSLMAQE KGASRGRCN ESAM

Seq ID NO: 122 DNA sequence
Nucleic Acid Accession #: NM_031966.1
Coding sequence: 178..1479

1 11 21 31 41 51
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ACGAACAGGC CAATAAGGAG GGAGCAGTGC GGGGTTTAAA TCTGAGGCTA GGCTGGCTCT 60
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30 CGGGCCTCCG GTGTCTGCT TCTCCCCGCT GAGCTGCTGC CTGGTGAAGA GGAAGCCATG 180
GCGCTCCGAG TCACCAGGAA CTCGAAAATT AATGCTGAAA ATAAGGCGAA GATCAACATG 240
GCAGGCGCAA ACGCGCTTCC TACGGCCCTT GCTGCAACCT CCAAGCCCGG ACTGAGGCCA 300
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ATGAAGAAGG AAGCAAAACC TTCAGCTACT GGAAAAGTCA TTGATAAAAA ACTACCAAAA 420
35 CCTCTTGAAA AGCTACCTAT GCTGGTGCCA GTGCCAGTGT CTGAGCCAGT GCCAGAGCCA 480
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GCTGATCCAA ACCTTGTAG TGAATATGTG AAAGATATTT ATGCTTATCT GAGACAACTT 720
40 GAGGAGAGGC AAGCAGTCAG ACCAAAATAC CTACTGGGTC GGGGAAGTCAC TGGAAACATG 780
AGAGCCATCC TAATTGACTG GCTAGTACAG GTTCAAATGA AATTCAGGTT GTTGCAAGAG 840
ACCATGTACA TGACTGTCTC CATTATTGAT CGGTTTATGC AGAATAATTG TGTGCCCAAG 900
AAGATGCTGC AGCTGGTTGG TGTCACTGCC ATGTTTATTT CAAGCAAATA TGAAGAAATG 960
TACCCTCCAG AAATTGGTGA CTTTGCTTTT GTGACTGACA ACACCTATAC TAAGCACCAA 1020
45 ATCAGACAGA TGGAAATGAA GATTCTAAGA GCTTTAAACT TTGCTCTGGG TCGGCCTCTA 1080
CCTTTGCACT TCCTTCGGAG AGCACTAAG ATTGGAGAGG TTGATGTCGA GCACATACT 1140
TTGGCCAAAT ACCTGATGGA ACTAAGTATG TTGGACTATG ACATGGTGCA CTTTCTCTCT 1200
TCTCAAATG CAGCAGGAGC TTTTGTCTTA GCACTGAAAA TTCTGGATAA TGGTGAAATG 1260
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50 CACCTGGCTA AGAATGTAGT CATGGTAAAT CAAGGACTTA CAAGCAGACT GACTGTCAAG 1380
AACAGTATG ACACATCGAA GCATGCTAAG ATCAGCACTC TACCACAGCT GAATTCTGCA 1440
CTAGTTCAAG ATTTAGCCAA GGCTGTGGCA AAGGTGTAAC TTGTAACCTT GAGTTGAGT 1500
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AAAAAAAAA AAAAAAAAAA

Seq ID NO: 123 Protein Sequence
Protein Accession #: NP_114172.1

1 11 21 31 41 51
| | | | |
MALRVTRNSK INAENKAKIN MAGAKRVPTA PAATSKPGLR PRTALGDIGN KVSEQLQAKM 60
PMKKEAKPSA TGKVIDKKLP KPLEKVPMLV FVPVSEPVPE PEPEPEPEPV KEEKLSPEPI 120
LVDITASPSM ETSOCAPAE E DLQAFSDVI LAVNDVDAED GADPNLCSEY VKDIYAYLRQ 180
65 LEBEQAVRPK YLLGREVTGN MRAILIDWL VQVMKFRLLQ ETMYMTVSII DRFMQNNCVP 240
KKMLQLVGVT AMFIASKYEE MYPPEIGDFA FVTDNTYTKH QIRQMEMKIL RALNFGGLGRP 300
LPLHPLRRAS KIGEVDVEQH TLAKYLMELT MLDYDMVHFP PSQIAAGAF C LALKILDNGE 360
WTPTLQHYLS YTBESLLPVM QHLAKNVVMV NQGLTKHMTV KKKYATSKHA KISTLPQLNS 420
ALVQDLAKAV AKV

Seq ID NO: 124 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 13-1424

1 11 21 31 41 51
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TAGAAGTTTA CAATGAAGTT TCTTCTAATA CTGCTCCTGC AGGCCACTGC TTCTGGAGCT 60
CTTCCCCTGA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTGGT TGAAAGATAC 120

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GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTCGATGTGG AGTCCCGAT 300
GTCCATCAT TCAAGGAAAT GCCAGGGGGG CCGTATGGA GGAAACATTA TATCACCTAC 360
AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGAAAA 420
GCTTTCCCAAG TATGGAGTAA TGTTACCCCC TTGAAATTCA GCAAGATTAA CACAGGCATG 480
GCTGACATTT TGGTGGTTTT TGCCCGTGGG GCTCATGGAG ACTTCCATGC TTTTGATGGC 540
AAAGGTGGA TCCTAGCCCA TGCTTTTGGG CCTGGATCTG GCATTGGAGG GGATGCACAT 600
TTCGATGAGG ACGAATTCCT GACTACACAT TCAGGAGGCA CAAACTTGTT CCTCACTGCT 660
GTTCCAGAGA TTGGCCATTC CTTAGGTCTT GGCCATTCTA GTGATCCAAA GGCCGTAATG 720
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TCAGAACCGA CTCTCTGTGA CCCCATTG AGTTTTGATG CTGTCACTAC CGTGGGAAAT 900
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AATTTAAGAC CAGAGCCAAA TTATCCCAAG AGCATACATT CTTTGGTTTC TCCTAATCTT 1140
GTGAAAAAAA TTGATGCAGC TGTTTTTAAC CCACGTTTT ATAGGACCTA CTTCTTTGTA 1200
GATAACCACT ATTGGAGGTA TGATGAAAGG AGACAGATGA TGGACCCCTG TTATCCCAAA 1260
CTGATTACCA AGAATCTCCA AGGAATCGGG CTTAAATTTG ATGCAGTCTT CTAATCTAAA 1320
AACAAATACT ACTATTTCTT CCAAGGATCT AACCAATTTG AATATGACTT CCTACTCCAA 1380
CGTATACCA AACACTGAA AAGCAATAGC TGGTTTGGTT GTTGAAAAATG GTGTAATTAA 1440
TGGITTTTGT TAGTTCACCT CAGCTTAATA AGTATTTATT GCATATTTGC TATGTCCTCA 1500
GTGTACCACT ACTTAGAGAT ATGTATCATA AAAATAAAAT CTGTAAACCA TAGGTAATGA 1560
TTATATAAAA TACATAAAT TTTTCAATTT TGAAGACTCT AATTGTCCAT TCTTGTCTGA 1620
CTCTATATT AAGTTTGAAA ATAGTTACCT TCAAGCAAG ATAATTCTAT TTGAAGCATG 1680
CTCTGTAAAT TGCTTCCTAA CATCCTTGGG CTGAGAAAT ATACTTACTT CTGCGATAAC 1740
TAAATTAAG TATATATATT TTGGCTCAAA TAAATTTG

Seq ID NO: 125 Protein sequence:
Protein Accession #: Bos sequence

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1 11 21 31 41 51
MKFLILLQLL ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHFF REMPGGPFVR KHYITYRINN 120
YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAHGD FHFADGKGGI 180
LAHAFPGQSG IGGDAHFDEB EFWTHSGGT NLFLTAHVHEI GHSGLGLGHS DPKAVMPPTY 240
KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF 300
FKDRFFWLKV SERPKTSVNL ISSLWETLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360
EPNYPKSIHS FGPFPVKKI DAAVFNPRPY RTYFFVDNQY WRVDERRQMM DPGYPKLITK 420
NFGGIGPKID AVFYSKNKY YFPQGSNQFE YDFLLQRITK TLKSNWFGC

Seq ID NO: 126 DNA sequence
Nucleic Acid Accession #: NM_000077.2
Coding sequence: 272..742

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55
60
65
70

1 11 21 31 41 51
CCCAACCTGG GCGCACTTCA GGTGTGCCAC ATTCGCTAAG TGCTCGGAGT TAATAGCACC 60
TCCTCCGAGC ACTCGCTCAC GGCCTCCCCT TGCTCGGAAA GATACCGCGG TCCCTCCAGA 120
GGATTTGAGG GACAGGGTCG GAGGGGGCTC TTCGCGCAGC ACCGGAGGAA GAAAGAGGAG 180
GGGCTGGCTG GTACACAGAG GGTGGGGCGG ACCGCGTGGC CTCGGCGGCT GCGGAGAGGG 240
GGAGAGCAGG CAGCGGGCGG CGGGAGGCGG CATGAGCCCG GCGGGCGGGA GCAGCATGGA 300
GCCTTCGGCT GACTGGCTGG CCAAGGCCCG GCGCGGGGCT CGGGTAGAGG AGGTGCGGGC 360
GCTGCTGGAG GCGGGGGCGG TGCCCAACGC ACCGAATAGT TACGGTCGGA GGCCGATCCA 420
GGTCATGATG ATGGGACGCG CCGAGTGGC GGAGCTGCTG CTGCTCCACG GCGCGGAGCC 480
CAACTGCGCC GACCCCGCCA CTCACACCG ACCGCTGCAC GACGCTGCC GGGAGGGCTT 540
CCTGGACACG CTGGTGGTGC TGCACCGGGC GGGGGCGCGG CTGGACGTGC GCGATGCCTG 600
GGGCCGCTG CCGCTGGACC TGGCTGAGGA GCTGGGCCAT CGCGATGTGC CACGGTACCT 660
GCGCGCGGCT GCGGGGGGCA CCAGAGGCAG TAACCATGCC CGCATAGATG CCGCGGAAGG 720
TCCCTCAGAC ATCCCGGATT GAAAGAACCA GAGAGGCTCT GAGAAACCTC GGGAAACTTA 780
GATCATCAGT CACCGAAGGT CCTACAGGCG CACAACTGCC CCGGCCACAA CCCACCCGCG 840
TTTCGTAGTT TTCAATTAGA AAATAGAGCT TTTAAAAATG TCCIGCCTTT TAACGTAGAT 900
ATATGCCTTC CCCCACTACC GTAAATGTCC ATTTATATCA TTTTATATAT ATTCTTATAA 960
AATGTAAAA AAGAAAAACA CCGCTTCTGC CTTTCACTG TGTGGAGATT TTCTGGAGTG 1020
AGCACTCAGC CCCTAAGCGC ACATTCACTG GCGCATTTCT TGCGAGCCTC GCAGGCTCCG 1080
GAAGCTGTGC ACTTCATGAC AAGCATTTTG TGAAGTAGGG AAGCTCAGCG GGGTACTGG 1140
CTTCTCTTGA GTCACTATGC TAGCAATGG CAGAACCAAA GCTCAATAA AAATAAAATA 1200
ATTTCTATTC ATTCATCTC

Seq ID NO: 127 Protein Sequence
Protein Accession #: NP_000068.1

75

1 11 21 31 41 51
MEPAAGSSME PSADWLATAA ARGRVEEVRA LLEAGALPNA PNSYGRRIPIQ VMMGSGARVA 60
ELLLHGAEP NCADPATLTR PVHDAAREGF LDTLVVLHRA GARLDVRDAN GRLPVDLAE 120

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LGHDRVARYL RAAAGGTRGS NHARIDAAEG PSDIPD

Seq ID NO: 128 DNA sequence

Nucleic Acid Accession #: NM_058196.1

Coding sequence: 104..421

5

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1      11      21      31      41      51
|      |      |      |      |      |
10  TGTGTGGGGG TCTGCTTGGC GGTGAGGGGG CTCTACACAA GCTTCCTTTC CGTCATGCCG 60
    GCGCCACACC TGGCTCTGAC CATCTGTTC TCTCTGGCAG GTCATGATGA TGGGCAGCGC 120
    CCGAGTGGCG GAGCTGCTGC TGCTCCACGG CGCGGAGCCC AACTGCGCGC ACCCGGCCAC 180
    TCTCACCAGA CCGGTGCACG ACGCTGCCCG GGAGGGCTTC CTGGACACGC TGGTGGTGCT 240
    GCACCGGGCC GGGGCGCGGC TGGACGTGCG CGATGCCTGG GCGCGTCTGC CCGTGGACCT 300
    GGCTCAGGAG CTGGGCCATC GCGATGTGCG ACGGTACTCG CGCGCGGTG CGGGGGGCAC 360
    CAGAGGCAGT AACCATGCCC GCATAGATGC CGCGGAAGGT CCCTCAGACA TCCCGATTG 420
    AAAGAACACG AGAGGCTCTG AGAAACCTCG GGAAACTTAG ATCATCAGTC ACCGAAGGTC 480
    ATACAGGCCC ACAACTGCCC CCGCCACAAC CCACCCCGCT TTCGTAGTTT TCATTAGAA 540
    AATAGAGCTT TTAATAATGT CCTGCCTTTT AACGTAGATA TAAGCCTTCC CCCACTACCG 600
    TAAATGTCCA TTTATATCAT TTTTATATA TTCATTATAA AATGTAAAAA AGAAAAACAC 660
    CGCTTCTGCC TTTTCACTGT GTTGGAGTTT TCTGGAGTGA GCACCTACGC CCTAAGCGCA 720
    CATTGATGCG GGCATTTCCT GCGAGCCTCG CAGCCTCCGG AAGCTGTCCA CTTGATGACA 780
    AGCATTTTGT GAACTAGGGA AGCTCAGGGG GGTACTGGC TTCTCTTGTG TCACACTGCT 840
    AGCAAATGCG AGAACCAAG CTCAAATAAA AATAAAATAA TTTTCATTCA TTCACTC
```

25

Seq ID NO: 129 Protein Sequence

Protein Accession #: NP_478103.1

```
1      11      21      31      41      51
|      |      |      |      |      |
30  MMMGARVAE LLLHGAEPN CADPATLTRP VHDAAREGFL DTLVVLHRAG ARLDVRDAWG 60
    RLPVDLAEEL GHRDVARYLR AAGGTRGSN HARIDAEGB SDIPD
```

35

Seq ID NO: 130 DNA sequence

Nucleic Acid Accession #: NM_058197.1

Coding sequence: 272..646

```
1      11      21      31      41      51
|      |      |      |      |      |
40  CCCAACCTGG GCGGACTTCA GGTGTGCCAC ATTGCTAAG TGCTCGGAGT TAATAGCACC 60
    TCTCCGAGC ACTCGCTCAC GCGTCCCTT TGCCTGGAAA GATACCGCGG TCCCTCCAGA 120
    GGATTGTAGG GACAGGGTCG GAGGGGCTC TTCGCCAGC ACCGGAGGAA GAAAGAGGAG 180
    GGGCTGGCTG GTCAACAGAG GGTGGGGCGG ACCCGGTGCG CTCGGCGGCT GCGGAGAGGG 240
    GGAGAGCAGG CAGCGGGCGG CGGGAGCAG CATGGAGCCG GCGGCGGGGA GCAGCATGGA 300
    GCGGGCGGCG GGGAGCAGCA TGGAGCCTTC GCTGACTGG CTGGCCACGG CCGCGGCCCG 360
    GGGTGGGTA GAGGAGGTGC GGGCGTGTCT GGAGCGGGGG GCGCTGCCCA ACGCACCAG 420
    TAGTTACGGT CGGAGGCCGA TCCAGGTGGG TAGAAGGTCT GCACGCGGAG CAGGGGATGG 480
    CGGGCGACTC TGGAGGACGA AGTTTGAGG GGAATTGGAA TCAGGTAGCG CTTGATTCT 540
    CGGAAAGAG GGGAGGCTTC CTGGGGAGTT TTCAGAAGGG GTTTGTAATC ACAGACCTCC 600
    TCTGGCGGAC GCCTTGGGGG CTTGGGAAAC CAAGGAAGAG GAATGAGGAG CCAACGCGGT 660
    ACAGATCTCT CGAATCTGTA GAAGATCTGA ACGGGGGAAC ATATTGTAT TAGATGGAAG 720
    TCATGATGAT GGGCAGCGCC CGAGTGCGG AGCTGCTGCT GCTCCACGGC GCGGAGCCCA 780
    ACTGCGCGCA CCCCGCCACT CTCACCCGAC CCGTGCACGA CGCTGCCCGG GAGGGCTTCC 840
    TGGACACGCT GGTGGTGTCT CACCGGGCCG GGGCGCGGCT GGACGTGCGC GATGCTGGG 900
    GCGTCTGTCG CGTGGACCTG GCTGAGGAGC TGGGCCATCG CGATGTCGCA CGGTACTTGC 960
    GCGCGGCTGC GGGGGGCACC AGAGGCAGTA ACCATGCCCG CATAGATGCC GCGGAAGGTC 1020
    COTCAGACAT CCCCATTGTA AAGAACCAGA GAGGCTCTGA GAAACCTCGG GAACTTAGAT 1080
    CATCAGTCAC CGAAGTCTCT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCGCTTT 1140
    CGTAGTTTTC ATTAGAAAA TAGAGCTTTT AAAAATGTCC TGCTTTTAA CGTAGATATA 1200
    TGCCTTCCCC CACTACCGTA AATGTCCATT TATATCATT TTTATATATT CTTATAAAAA 1260
    TGTAAAAAAG AAAAACACCG CTTCTGCCTT TTCCTGTGT TGGAGTTTTC TGGAGTGAGC 1320
    ACTACGCCCC TAAGCGCACA TTCATGTGGG CATTCTTGC GAGCCTCGCA GCCTCCGGAA 1380
    GCTGTCGACT TCATGACAAG CATTTGTGA ACTAGGGAAG CTCAGGGGGG TTA CTGGCTT 1440
    CTCTTGAGTC AACTGCTAG CAAATGGCAG AACCAGGCT CAAATAAAAA TAAATAATT 1500
    TTCATTCACT CACTC
```

65

Seq ID NO: 131 Protein Sequence

Protein Accession #: NP_478104.1

```
1      11      21      31      41      51
|      |      |      |      |      |
70  MEPAAGSSME PAAGSSMEPS ADWLATAAAR GRVEEVALL EAGALPNAPN SYGRRPIQVG 60
    RRSAGAGGCG GRLWRKTFAG ELBSGSASIL RKGRLPGEF SEGVNHRPP PGDALGAWET 120
    KEEB
```

75

Seq ID NO: 132 DNA sequence

Nucleic Acid Accession #: NM_058195.1

Coding sequence: 163..684

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1      11      21      31      41      51
|      |      |      |      |      |
5  CCTCCCTACG GGCGCCCTCG GCAGCCCTTC CCGCGTGC GC AGGGCTCAGA GCGTTCCGA 60
   GATCTTGGAG GTCCGGGTGG GAGTGGGGGT GGGGTGGGGG TGGGGGTGAA GGTGGGGGGC 120
   GGGCGCGCTC AGGGAAGGCG GTGCGCGGCC TCGGGGGCGG AGATGGGCAG GGGCGGTGCG 180
   GTGGGTCCCA GTCTGCAGTT AAGGGGGCAG GAGTGGCGCT GCTCACCTCT GGTGCCAAAG 240
   GGC GGCGCAG CGGTGCCGA GCTCGGCCCT GGAGGGCGCG AGAACATGGT GCGCAGGTTC 300
   TTGGTGACCC TCGGATTTCG GCGCGCGTGC GCGCGCGCGC GAGTGAGGGT TTCTGTGGTT 360
10  CACATCCCGC GGTTCACGGG GGAGTGGGCA GCGCCAGGGG CCGCCGCCGC TGTGGCCCTC 420
   GTGCTGATGC TACTGAGGAG CCAGCGTCTA GGGCAGCAGC CGCTTCCTAG AAGACCAGGT 480
   CATGATGATG GGCAGGCGCC GAGTGGCGGA GCTGCTGCTG CTCCACGGCG CGGAGCCCAA 540
   CTGCGCGGAC CCGCCCACTC TCACCCGACC CGTGACAGAC GCTGCCCGGG AGGGCTTCCT 600
   GGACACGCTG GTGCTGCTGC ACCGGGCCGG GCGCGGGCTG GACGTGCGCG ATGCTGGGG 660
15  CGTCTGCCCC GTGACCTGG CTGAGGAGCT GGGCCATCGC GATGTCGCAC GGTACCTGCG 720
   CGCGGCTGCG GGGGGCACCA GAGGCAGTAA CCATGCCCGC ATAGATGCCG CGGAAGGTCC 780
   CTCAGACATC CCCGATTGAA AGAACAGAG AGGCTCTGAG AAACCTCGGG AAACCTAGAT 840
   CATCAGTCAC CGAAGTCTCT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCGCTTT 900
   CGTAGTTTTT ATTAGAAAA TAGAGCTTTT AAAATGTCC TGCCTTTTAA CGTAGATATA 960
20  TGCCTTCCCC CACTACCGTA AATGTCCATT TATATCATT TTTATATATT CTTATAAAAA 1020
   TGTAAAAAAG AAAAACACCG CTCTGCCTT TTCCTGTGT TGGAGTTTTT TGGAGTGAGC 1080
   ACTCAGCGCC TAAGCGCACA TTCATGTGGG CATTCTTTGC GAGCCTCGCA GCCTCCGGAA 1140
   GCTGTGCGAT TCATGACAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTAGTGGCTT 1200
   CTCTTGAGTC ACTCTGCTAG CAAATGGCAG AACCAAAGCT CAAATAAAAA TAAATAATT 1260
25  TTCAATCATT CACTC
```

Seq ID NO: 133 Protein Sequence
Protein Accession #: NP_478102.1

```
1      11      21      31      41      51
|      |      |      |      |      |
30  MGRGRCVGPS LQLRGQEWRC SPLVPKGGAA AELGPGGGE NMVRRFLVTL RIRACGPFR 60
   VRVFFVHIPR LTGEWAAPGA PAAVALVLM LRSQRLGQPP LPRRPGHDDG QPSGGAAAA 120
   PRRGALRRP RHSHPTRARR CPGLPGHAG GAAPGRGAAG RARCLGPSAR GPG
```

Seq ID NO: 134 DNA sequence
Nucleic Acid Accession #: NM_023915
Coding sequence: 1..1077

```
1      11      21      31      41      51
|      |      |      |      |      |
40  ATGGGGTTCA ACTTGACGCT TGCAAAATTA CCAAATAACG AGCTGCACGG CCAAGAGAGT 60
   CACAATTICAG GCAACAGGAG CGACGGGCCA GGAAAGAACA CCACCTTCA CAATGAATTT 120
   GACACAATTG TCTTGCCGCT GCTTTATCTC ATTATATTTG TGGCAAGCAT CTGTCTGAAT 180
   GGTTTAGCAG TGTGGATCTT CTTCACATT AGGAATAAAA CCAGCTTCAT ATTCIATCTC 240
45  AAAACATAG TGGTTGCAGA CCTCATAATG ACGCTGACAT TTCCATTTCG AATAGTCCAT 300
   GATGCAGGAT TTGACCTTG GTACTTCAAG TTTATTCTCT GCAGATACAC TTCAGTTTTG 360
   TTTTATGCAA ACATGTATAC TTCCATCGTG TTCCTTGGGC TGATAAGCAT TGATCGCTAT 420
   CTGAAGGTGG TCAAGCCATT TGGGGACTCT CGGATGTACA GCATAACCTT CACGAAGGTT 480
   TTATCTGTTT GTGTTTGGGT GATCATGGCT GTTTGTCTT TGCCAAACAT CATCCTAACA 540
50  AATGGTCAGC CAACAGAGGA CAATATCCAT GACTGCTCAA AACTTAAAG TCCTTTGGGG 600
   GTCAAATGCG ATACGCGAGT CACCTATGTG AACAGCTGCT TGTTTGTGGC CGTGTGGGTG 660
   ATTCTGATCG GATGTTACAT AGCCATATCC AGGTACATCC ACAAATCCAG CAGGCAATTC 720
   ATAAGTCAGT CAAGCCGAAA GCGAAAACAT AACCAGAGCA TCAGGGTTGT TGTGGCTGTG 780
55  TTTTITACCT GCTTCTACAC ATATCACTTG TGCAGAATTC CTTTACTTT TAGTCACTTA 840
   GACAGGCTTT TAGATGAATC TGCACAAAAA ATCCTATATT ACTGCAAGA AATTACACTT 900
   TTCTGTCTG CGTGAATGT TTGCTGGAT CCAATAATTT ACTTTTTCAT GTGTAGGTCA 960
   TTTTCAAGAA GGCTGTTCAA AAAATCAAAT ATCAGAACCA GGAGTGAAG CATCAGATCA 1020
   CTGCAAGATG TGAGAAGATC GGAAGTTCGC ATATATTATG ATTACACTGA TGTGTAA
```

Seq ID NO: 135 Protein Sequence
Protein Accession #: NP_076404

```
1      11      21      31      41      51
|      |      |      |      |      |
65  MGFNLTAKL PNNELHGQES HNSGNRSDGP GKNTILHNEF DTIVLPVLYL IIFVASILLN 60
   GLAVWIFPHI RNKTSFIFYL KNIVVADLIM TLTFPFRIHV DAGFGPWYFK FILCRYTSVL 120
   FYANMYTSIV FLGLISIDRY LKVVKPFQDS RMYSTPTKV LSVCVWVIMA VLSLENILTL 180
   NQOPTEDNIH DCSKLKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
70  ISQSSRKRRH NQSIKRVVAV FFTCFLPYHL CRIPFTFSL DRLLDESAQK ILYYCKEITL 300
   FLSACNVCLD PIIFYPMCRS FSRRLPKKSN ITRSEIRS LQSVRRSEVR IYYDYTDV
```

Seq ID NO: 136 DNA sequence
Nucleic Acid Accession #: NM_005329.1
Coding sequence: 1..1662

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1      11      21      31      41      51
|      |      |      |      |      |
75
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ATGCCGGTGC AGCTGACGAC AGCCCTGCGT GTGGTGGGCA CCAGCCTGTT TGCCCTGGCA 60
GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTTCATCCA CACGGAAAAG 120
CACTACCTGT CCTTCGGCCT GTACGGCCCC ATCTGGGGCC TGCACCTGCT CATTACAGAGC 180
CTTTTGTGCT TCCTGGAGCA CCGGGCGCATG CGACGTGCCG GCCAGGCCCT GAAGCTGCCC 240
TCCCCGCGGC GGGGCTCGGT GGCACGTGTG ATTGCCCGGT ACCAGGAGGA CCCTGACTAC 300
TTGGCGAAGT GCCTGCGCTC GGGCCAGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCATG 360
GTGGTGGATG GCAACCGCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420
GGCGGCACCG AGCAGGCGCG CTTCCTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480
GGTGAGACCG AGGCGAGCCT GCAGGAGGGC ATGGACCGTG TCGGGATGT GGTGCGGGCC 540
AGCACCTTCT CGTGCACTAT GCAGAAGTGG GGAGGCAAGC GCGAGGTGAT GTACACGGCC 600
TTCAAGGCCC TCGGCGATTG GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660
GATCCAGCCT GCACCATCGA GATGCTTCGA GTCTGGAGG AGGATCCCCA AGTAGGGGA 720
GTGCGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCTTT CCTGAGCAGC 780
GTGCGGTACT GGATGGCCTT CAACGTGGAG CGGGCCTGCC AGTCTTACTT TGGCTGTGTG 840
CAGTGATATTA GTGGGCCCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCCTGGAG 900
GACTGGTACC ATCAGAAGTT CCTAGCCAGC AAGTGCAGCT TCGGGATGA CCGGCACCTC 960
ACCAACCGAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCCTC 1020
ACAGAGACCC CCCTAAGATA CCTCCGGTGG CTCACACAGC AAACCCGCTG GAGCAAGTCT 1080
TACTTCGGGG AGTGGCTCTA CAACTCTCTG TGGTTCCTCA AGCACCACTT CTGATGACC 1140
TACGAGTCAS TGGTCACGGG TTTCTTCCCC TTCTTCCTCA TTGCCACGGT TATACAGCTT 1200
TTCTACCGGG GCCGCATCTG GAACATTCTC CTCTTCCTGC TGACGGTGCA GCTGGTGGGC 1260
ATTATCAAGG CCACCTACGC CTGCTTCCTT CGGGGCAATG CAGAGATGAT CTTTATGTCC 1320
CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCGGCCA AGATCTTTGC CATTGCTACC 1380
ATCAACAAAT CTGGCTGGGG CACCTCTGGC CGAAAAACCA TTGTGGTGAA CTTTATTGGC 1440
CTCATCTCTG TGTCCAICTG GGTGGCAGTT CTCTGGGAG GGCTGGCTGA CACAGCTTAT 1500
TGCCAGGACC TGTTCAGTGA GACAGAGCTA GCCTTCCTTG TCTCTGGGCG TATACTGTAT 1560
GGCTGCTACT GGGTGGCCCT CCTCATGCTA TATCTGGCCA TCATCGCCCC GCGATGTGGG 1620
AAGAACCCGG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA
  
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Seq ID NO: 137 Protein Sequence
Protein Accession #: NP_005320.1

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 40
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1      11      21      31      41      51
|      |      |      |      |      |
MPVQLTTLALR VVGTSLFALA VLGGILAAVY TGYQFIHTEK HYLSPGLYGA ILGLHLIIQS 60
LFAFLFLEHRRM RRAQQAALKLP SPRRGSVALC IAAYQEDPDY LRKCLRSAQR ISFPDLKVVM 120
VVDGNRQEDA YMLDIFHEVL GGTQAGFFV WRSNFHEAGE GETEASLQEG MDRVDRVVRA 180
STFSCIMQKW GSKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPVQVG 240
VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGFLGMY RNSLLQQFLE 300
DWYHQFELGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLWR LNQOTRWSKS 360
YFREWLYNLS WPHKHLWMT YESVVTGFFP FLIATVIQL FYRGRINIL LFLLTQVLVG 420
LIKATYACFL RGNAMIFMS LYSLLYMSL LPAKIFAIAI INKSGWTSRG RTIIVNFIG 480
LIPVSIWVAV LLGGLAYTAY QQDLFSETEL AFLVSGAILY GCYWVALLML YLAIIARRCG 540
KKPEQYSLAF AEV
  
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Seq ID NO: 138 DNA Sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89..631

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 55
 60
 65

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1      11      21      31      41      51
|      |      |      |      |      |
AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
CTGAGAGCCG GGCAGAGGCT CCGGAGCCAT GCAGGCCGAA GGCCGGGGCA CAGGGGGTTC 120
GACGGGCGAT GCTGATGGCC CAGGAGGCCC TGGCATTCCT GATGGCCGAG GGGGCAATGC 180
TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGCT CCCCAGGCGC CAGGGGCAGC 240
AAGGGCCTCG GGGCCGGGAG GAGGCGCCCC GCGGGTCCG CATGGCGGCG CGGCTTCAGG 300
GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGAG AGCCGCTGCG TTGAGTTCTA 360
CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCACTG TGTCCGGCAA 480
CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC 540
CTGTCTCCAG CAGCTTTCCC TGTGTATGTG GATCACGCAG TGCTTTCTCG CCGTGTTTTT 600
GGCTCAGCCT CCCTCAGGGC AGAGGCGCTA AGCCCAAGCT GGGCGCCCTT CCTAGGTGAT 660
GCCTCCTCCC CTAGGGAATG GTCCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
GTTTGTGCGT GGAGGAGGAC GCCTTACATG TTTGTTTCTG TAGAAAATAA AACTGAGCTA 780
  
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Seq ID NO: 139 Protein Sequence
Protein Accession #: NP_001318.1

70
 75

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1      11      21      31      41      51
|      |      |      |      |      |
MQAEGRGTTG STGDADCPGG FGIPDGPCCN AGGFGEAGAT GGRGPRGAGA ARASGPGGA 60
PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAEIARRSLA QDAPPLPVG 120
VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQLSLLM WITQCFLPVF LAQPPSGQRR 180
  
```

Seq ID NO: 140 DNA Sequence
Nucleic Acid Accession #: Eos sequence

WO 03/003906

PCT/US02/21338

Coding sequence: 53..459

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      CCTCGTGGGC CCTGACCTTC TCTCTGAGAG CCGGGGCAGAG GCTCCGGAGC CATGCAGGCC 60
      GAAGGCCAGG GCACAGGGGG TTCGACGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT 120
      CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAAG CGGGTCCAC GGGCGGCAGA 180
      GGTCCCGGGG GCGCAGGGGG AGCAAGGGCC TCGGGGCCGA GAGGAGGGCC CCGCGGGGGT 240
      CCGCATGGCC GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGGC CAGGAGGCCG 300
10     GACAGCCGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
      ATCAGCTCCT GTCTCCAGCA GCTTTCCTTG TTGATGTGGA TCACGCAGTG CTTTCTGCCC 420
      GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCCCTTC 480
      TAGTTCATGC CTCCTCCCCT AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTGTGGGG 540
      GCTGATTGT TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTCCTGTA GAAAAATAAG 600
15     CTGAGCTA

```

Seq ID NO: 141 Protein Sequence
Protein Accession #: Eos sequence

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20     1      11      21      31      41      51
      |      |      |      |      |      |
      MQAEGQQTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
      PRGPHGGAAS AODGRFCPGA RRPDSRLQF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
25     FLPVFLAQAP SGQRRR

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Seq ID NO: 142 DNA Sequence
Nucleic Acid Accession #: NM_130467.2
Coding sequence: 246..638

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30     1      11      21      31      41      51
      |      |      |      |      |      |
      AGGCAGAGCT CTGCAAGGAG AGGTTGTGTC TTCGTTCTTT CGCCATCTT CGTTCCTTCC 60
      AACATCTTCG TTCTTTCTCA CTGACCGAGA CTCAGCCGGT AGGTCTGCAG AGTGGTCTTC 120
35     CTGTAATTT AGTTGTGAGT GAATGTGTGG AGGAGCCAGC GGGCTTAGGA CAGGTCTCTG 180
      GGCACAGTCC GTGGCTTTGA GGGAAAAGGG CCTCGCGGTG GTCTCTCCGC TTCCCCCAGG 240
      TCGTGATGCA GGCGCCATGG GCCGTAATC GTGGCTGGGC TGAACGAGG GAGGAAGTGA 300
      GAGATATGAG TGAGCATGTA ACAAGATCCC AATCCTCAGA AAGAGGAAAT GACCAAGAGT 360
      CTCCAGGCC AGTTGGACCT GTGATTGTCC AGCAGCCAC TGAGGAAAAA CGTCAAGAAG 420
40     AGGAACCAAC AACTGATAAT CAGGGTATTG CACCTAGTGG GGAGATCAAA AATGAAGGAG 480
      CACCTGCTGT TCAAGGGACT GATGTGGAAG CTTTCAACA GGAACGTGGT CTGCTTAAGA 540
      TAGAGGATGC ACCTGGAGAT GGTCTGTATG TCAGGAGGG GACTCTGCCC ACTTTTGATC 600
      CCACTAAAGT GCTGGAAGCA GGTGAAGGGC AACTATAGGT TTAACCAAG ACAATGAAG 660
45     ACTGAAACCA AGAATATTGT TCTTATGCTG GAAATTGAC TGCTAACATT CTCTTAATAA 720
      AGTTTTACAG TTTTC

```

Seq ID NO: 143 Protein Sequence
Protein Accession #: NP_569734

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50     1      11      21      31      41      51
      |      |      |      |      |      |
      MSEHVTRSQS SERGNDQESS QPVGPIVIVQ PTEEKQREE PPTDNQGIAP SGEIKNEGAP 60
      AVQGTDVRAF QBELALLKIE DAPGDGPEVR EGTLPFDPT KVLAEAGQL

```

Seq ID NO: 144 DNA Sequence
Nucleic Acid Accession #: NM_001476.1
Coding sequence: 82..435

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60     1      11      21      31      41      51
      |      |      |      |      |      |
      GCCAGGGAGC TGTGAGGCAG TGCTGTGTGG TTCCTGCCGT CCGGACTCTT TTTCCTCTAC 60
      TGAGATTCAT CTGTGTGAAA TATGAGTTGG CGAGGAAGAT CGACCTATTA TTGGCCTAGA 120
      CCAAGGCGCT ATGTACAGCC TCCTGAAGTG ATTGGGCCTA TGCGGCCGA GCAGTTCAGT 180
      GATGAAGTGG AACCAGCAAC ACCTGAAGAA GGGGAACAG CAACTCAACG TCAGGATCCT 240
65     GCAGCTGCTC AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAAGGGCC GAAGCCTGAA 300
      GCTGATAGCC AGGAACAGGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA TGGTCTGAT 360
      GGGCAGGAGG TGGACCCGCC AAATCCAGAG GAGGTGAAAA CGCCTGAAGA AGGTGAAAAG 420
      CAATCACAGT GTTAAAAGAA GACACGTTGA AATGATGCAG GCTGCTCCTA TGTGGAAT 480
70     TTGTTCAATTA AAATCTCTCC AATAAAGCTT TACAGCCTTC TGCAAAA

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Seq ID NO: 145 Protein Sequence
Protein Accession #: NP_001467.1

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75     1      11      21      31      41      51
      |      |      |      |      |      |
      MSWRGRSTYY WPRPRRYVQP PEVIGPMRPE QFSDEVEPAT PEEGEPATQR QDPAAQEGE 60
      DEGASAGQGP KPEADSQEQG HPQTGCECED GPDGQEVDPD NPPEVKTPPE GEKQSQC

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WO 03/003906

PCT/US02/21338

Seq ID NO: 146 DNA Sequence
Nucleic Acid Accession #: NM_005562
Coding sequence: 90..3671

5

	1	11	21	31	41	51	
10	ACAGCGGAGC	GCAGAGTGAG	AACCACCAAC	CGAGGCGCGG	GGCAGCGACC	CCTGCAGCGG	60
	AGACAGAGAC	TGAGCGGCCC	GGCACCGCCA	TGCCTGCGCT	CTGGCTGGGC	TGCTGCCTCT	120
	GCTTCTCGCT	CCTCCTGCCC	GCAGCCCGGG	CCACCTCCAG	GAGGGAAGTC	TGTGATTGCA	180
	ATGGGAAGTC	CAGGCAGTGT	ATCTTTGATC	GGGAACCTCA	CAGACAAACT	GGTAATGGAT	240
	TCCGCTGCCT	CAACTGCAAT	GACAACACTG	ATGGCATTCA	CTGCGAGAAG	TGCAAGAATG	300
15	GCTTTTACCG	GCACAGAGAA	AGGGACCGCT	GTTTGCCCTG	CAATTGTAAC	TCCAAAGGTT	360
	CTCTTAGTGC	TCGATGTGAC	AACTCTGGAC	GGTGACAGTG	TAAACCAGGT	GTGACAGGAG	420
	CCAGATGCGA	CCGATGTCTG	CCAGGCTTCC	ACATGCTCAC	GGATGCGGGG	TGCACCCAAG	480
	ACCAGAGACT	GCTAGACTCC	AAGTGTGACT	GTGACCCAGC	TGGCATCGCA	GGGCCCTGTG	540
	ACGCGGGCCG	CTGTGTCTGC	AAGCCAGCTG	TTACTGGAGA	ACGCTGTGAT	AGGTGTGAT	600
20	CAGGTTACTA	TAACTGTGAT	GGGGGAAC	CTGAGGGCTG	TACCCAGTGT	TTCTGCTATG	660
	GGCATTACGA	CAGCTGCCCG	AGCTCTGCAG	AATACAGTGT	CCATAAGATC	ACCTCTACCT	720
	TTCATCAAGA	TGTTGATGGC	TGGAAGGCTG	TCCAACGAAA	TGGTCTCCTT	GCAAAGCTCC	780
	AATGGTCACA	CGGCCATCAA	GATGTGTTTA	GCTCAGCCCA	ACGACTAGAC	CCTGTCTATT	840
	TTGTGGCTCC	TGCCAAATTT	CTTGGGAATC	AACAGGTGAG	CTATGGGCAG	AGCCTGTCTT	900
25	TTGACTACCG	TGTGGACAGA	GGAGGCAGAC	ACCCATCTGC	CCATGATGTG	ATTCTGGGAG	960
	GTGCTGGTCT	ACGGATCACA	GCTCCCTTGA	TGCCACTTGG	CAAGACACTG	CCTTGTGGGC	1020
	TCACCAAGAC	TTACACATTC	AGGTTAAATG	AGCATCCAAG	CAATAATTGG	AGCCCCCAGC	1080
	TGAGTTACTT	TGAGTATCGA	AGGTTACTGC	GGAATCTCAC	AGCCCTCCGC	ATCCGAGCTA	1140
	CATATGGAGA	ATACACTACT	GGGTACATTG	ACAATGTGAC	CCTGATTTCA	GCCCGCCCTG	1200
30	TCTCTGGAGC	CCCAGCACCC	TGGGTTGAAC	AGTGTATATG	TCTGTGTTGG	TACAAGGGGC	1260
	AATTTCTGCCA	GGATTGTGCT	TCTGGCTACA	AGAGAGATTG	AGCGAGACTG	GGGCCCTTTG	1320
	GCACCTGTAT	TCCTTGTAACT	TGTCAGGGG	GAGGGGCTCT	TGATCCAGAC	ACAGGAGATT	1380
	GTTATTCAAG	GGATGAGAAT	CCTGACATTG	AGTGTGCTGA	CTGCCCAATT	GGTTTCTACA	1440
35	ACGATCCGCA	CGACCCCGCG	AGCTGCAAGC	CATGTCCCTG	TCATAACGGG	TTCACTGTCT	1500
	CAGTGATGCC	GGAGACGGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTACCCGGTG	1560
	CCCGCTGTGA	GCTCTGTGCT	GATGGCTACT	TTGGGGACCC	CTTTGGTGAA	CTGGCCCGAG	1620
	TGAGGCCCTTG	TCAGCCCTGT	CAATGCAACA	ACAATGTGGA	CCCCAGTGCC	TCTGGGAATT	1680
	GTGACCGGGT	GACAGGCAGG	TGTTTGAAGT	GTATCCACAA	CACAGCCGGC	ATCTACTGCG	1740
40	ACCAGTGCAA	AGCAGGCTAC	TTGCGGGACC	CATTGGCTCC	CAACCCAGCA	GACAAGTGTC	1800
	GAGCTTGCAA	CTGTAAACCC	ATGGGCTCAG	AGCCTGTAGG	ATGTCGAAGT	GATGGCACCT	1860
	GTGTTTGCAA	GCCAGGATTT	GGTGGCCCCA	ACTGTGAGCA	TGGAGCATTC	AGCTGTCCAG	1920
	CTTGCTATAA	TCAGGTGAAG	ATTCAGATGG	ATCAGTTTAT	GCAGCAGCTT	CAGAGAATGG	1980
	AGGCCCTGAT	TTCAAAGGCT	CAGGTTGGTG	ATGGAGTAGT	ACCTGATACA	GAGCTGGAAG	2040
45	GCAGGATGCA	GCAGGCTGAG	CAGGCCCTTC	AGGACATTCT	GAGAGATGCC	CAGATTTCTG	2100
	AAGGTGCTAG	CAGATCCCTT	GGTCTCCAGT	TGGCCAGGTT	GAGGAGCCAA	GAGAACAGCT	2160
	ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAAG	AGTTCCGGCT	CTGGGAAGTC	2220
	AGTACCAGAA	CCGAGTTCCG	GATACTCACA	GGCTCATCAC	TCAGATGCAG	CTGAGCTTGG	2280
	CAGAAAGTGA	AGCTTCCTTG	GGAAACACTA	ACATTCTCTG	CTCAGACCAC	TACGTGGGGC	2340
50	CAAAATGGCT	TAAAGTCTGT	GCTCAGGAGG	CCACAAGATT	AGCAGAAAGC	CACGTTGAGT	2400
	CAGCCAGTAA	CTAGGAGCAA	CTGACAAGGG	AAACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460
	CAGTGTGCGC	CAAGGCCCTG	CATGAAGGAG	TCGGAAGCGG	AAGCGGTAGC	CCGGACGGTG	2520
	CTGTGTGTCG	AGGGCTTTTG	GAAAAATTGG	AGAAAAACCA	GTCCCTGGCC	CAGCAGTTGA	2580
	CAAGGGAGGC	CACCTCAAGC	GAAATTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCC	2640
55	TCCTGGATTG	AGTGTCTCGG	CTTCAGGGAG	TCAGTGATCA	GTCCCTTCAG	GTGGGAAGAG	2700
	CAAAAGAGAT	CAAAACAAAA	GCGGATTTCAC	TCTCAACGCT	GGTAACCCAG	CATATGGATG	2760
	AGTTCAAGCG	TACACAAAG	AATCTGGGAA	ACTGGAAGAA	AGAAAGCAGC	CAGCTCTTAC	2820
	AGAAATGAAA	AGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCGTCGCC	AATCTTGCTA	2880
60	AAAGCAGAGC	ACAAGAAGCA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTTGAGAGCA	2940
	TCCTTAAAAA	CCTCAGAGAG	TTTGACCTGC	AGGTGGACAA	CAGAAAAGCA	GAAGCTGAAG	3000
	AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAGACCC	3060
	AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAATGGGG	3120
	CCGGGGAGGC	CCTGGAAATC	TCCAGTGAGA	TTGAACAGGA	GATTGGGAGT	CTGAACTTGG	3180
65	AAGCCAAATG	GACAGCAGAT	GGAGCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAGA	3240
	GTGAGATCAG	GGAAATGGAA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300
	TGGATGCAGT	ACAGATGGTG	ATTACAGAAG	CCAGAAGGTT	TGATACCAGA	GCCAAGAACG	3360
	CTGGGGTTAC	AATCCAAGAC	ACACTCAACA	CATTAGACCG	CCTCCTGCAT	CTGATGGACC	3420
	AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAAGCTT	TCCGAGGCCA	3480
70	AGACCCAGAT	CAACAGCCAA	CTGCGGCCCA	TGATGTGAGA	GCTGGAAGAG	AGGGCACGTC	3540
	AGCAGAGGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGGATCTGT	GCTGATGTGA	3600
	AGAACTTCGA	GAACMTTAGG	GACAACTGTC	CCCCAGGCTG	CTACAATACC	CAGGCTCTTTG	3660
	AGCAACAGTG	AAGCTGCCAT	AAATATTTCT	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
	GGCTCGGGAG	CCATGTCTATG	TGAGTGGGTG	GGATGGGGAC	ATTTGAAACAT	GTTTAAATGGG	3780
75	TATGCTCAGG	TCAACTGACC	TGACCCCAT	CCTGATCCCA	TGGCCAGGTG	GTGTCTTTAT	3840
	TGCACCATAC	TCCTTGCTTC	CTGATGCTGG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
	ATGATCAAGG	ATCTGGACCC	CAAAGAATAG	ACTGGATGGA	AAGACAAACT	GCACAGGCAG	3960
	ATGTTTGCCT	CATAATAGTC	GTAAGTGGAG	TCTTGGAATT	TGGACAAGTG	CTGTTGGGAT	4020
	ATAGTCAACT	TATCTTTTGA	GTAATGTGAC	TAAAGGAAAA	AACCTTGACT	TTGCCACAGG	4080
	ATGAAATTCCT	TCCTAATGTC	AGAACAGAGT	GCAACCCAGT	CACACTGTGG	CCAGTAAAAA	4140
	ACTATTGCCT	CATATTGTCC	TCTGCAAGCT	TCTTGTCTGAT	CAGAGTTCCT	CCTACTTACA	4200

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PCT/US02/21338

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ACCCAGGGTG TGAACATGTT CTCCATTTTC AAGCTGGAAG AAGTGAGCAG TGTGAGAGTG 4260
AGGAGCTGTA AGGCAGGCCC ATTCAGAGCT ATGGTGCTTG CTGGTGCCCTG CCACCTTCAA 4320
GTTCTGGACC TGGGCATGAC ATCCTTTCTT TTAATGATGC CATGGCAACT TAGAGATTGC 4380
ATTTTTATTA AAGCATTTCC TACCAGCAA GCAATGTTG GGAAGTATT TACTTTTTCG 4440
GTTTCAAAGT GATAGAAAAG TGTGGCTTGG GCATTGAAAG AGGTAAATTT CTCTAGATT 4500
ATTAGTCCTA ATTCAATCCT ACTTTTCGAA CACCAAAAT GATGCGCATC AATGTATTTT 4560
ATCTTATTTT CTCATCTCC TCCTCTTTT CTCCACCCAT AATAAGAGAA TGTCTCTACT 4620
CACACTTCAG CTGGGTCACA TCCATCCCTC CATTCACTCT TCCATCCATC TTTCATCCA 4680
TTACCTCCAT CCATCCTTCC AACATATATT TATTGAGTAC CTACTGTGTG CCAGGGGCTG 4740
GTGGGACAGT GGTGACATAG TCTCTGCCCT CATAGAGTTG ATTGTCTAGT GAGGAAGACA 4800
AGCATTTTTA AAAAATAAAT TTAAACTTAC AAACTTTGTT TGTACAAAGT GGTGTTTATT 4860
GCAATAACCG CTGTTTGTG AACCTCTTTG CTCAACAGAA CATATGTTGC AAGACCTTCC 4920
CATGGGGGCA CTTGAGTTTT GGCAAGGCTG ACAGAGCTCT GGGTTGTGCA CATTTCCTTG 4980
CATCCCATGT GTCACTCTGT GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA 5040
TAACACCACT GGGAAATTGCT GGAGGAACCA GAGGCACTTC CACCTTGGCT GGAAGACTA 5100
TGGTGCTGCC TTGCTTCTGT ATTTCTTGTG ATTTCTCTGA AAGTGTITTT AATAAAGAA 5160
CAATTGTTAG ATGCC

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20 Seq ID NO: 147 Protein Sequence
Protein Accession #: NP_005553

25
30
35
40

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1 11 21 31 41 51
| | | | |
MPALWLGCCL CFSLLLPAA RATSREVCDC NGKSRQCI FD RELHRQTGNG FRCLNCNDNT 60
DGIHCEKCKN GFYRHRERDR CLPCNCNSKG SLSARCDNSG RCSCCKPGVTG ARCDRCCLPGF 120
HMLTDAGCTQ DQRLDLSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYYNLDGGN 180
PBGCTQCFPY GHASACRSEA EYSVHKITST FHQDVGWKA VQRNGSPAKL QWSQRHQDVF 240
SSAQLRLDPVY FVAPAKFLGN QQVSYGQSL FDIRVDRGGR HPSAHDVILE GAGLRITAPL 300
MPLGKTLPCG LTKTYTFRNL EHPNWNWSPQ LSYFEYRRL RNLTLALRIRA TYGEYSTGYI 360
DNVTILISARP VSGAPAPWVE QCICPVGYKG QFCQDCASGY KRDSARLGPF GTCIPCNCQG 420
GGACDPDPTG CYSGDENPDI ECADCPIGFY NDPHDPRSCK PCPCNHGPFSC SVMPETEEVV 480
CNMCPPGVTG ARCELADGAY PGDPFGHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCLK 540
CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCPMGS EPVGCRRSDGT CVCKPFGGPG 600
NCEHGAPFSCP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAEOAL 660
QDILRDAGIS EGASRLGLQ LAKVRSQENS YQSRLLDLKM TVERVRALGS YQNRVRDTH 720
RLITQMQLSL AESEALGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR 780
ETEDYSKQAL SLVRKALHEG VSGSGSPDG AVVQGLVEKL EKTSLAQOL TREATQAEIE 840
ADRSYQHSRL LLDVSRLQG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EFKRTQKNLG 900
NWKEBAQQLL NGKSGREKS DQLLSRANLA KSRAQEALSM GNATFYEVES ILKNLREFDL 960
QVDNRKAABE EAMKRLSYIS QKVSADSKT QOAEALGSA ADAQRAKNG AGEALEISSE 1020
IQEITGSLNL EAMVTADGAL AMEKGASLAK SEMREVEGEL ERKLEFDTN MDAVQMVITE 1080
AQKVDTRAKN AGVTIQDTLN TLDGLLHMD QFLSVDEEGL VLLBQKLSRA KTQINSQLRP 1140
MMSELEERAR QQRGHLHLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQQ

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45 Seq ID NO: 148 DNA Sequence
Nucleic Acid Accession #: NM_021048.2
Coding sequence: 327..1436

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60
65
70
75

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1 11 21 31 41 51
| | | | |
GGCACGAGGG AGAAGCGAGG TTCTCGTTCT GAGGGACAGG CTTGAGATCG GCTGAAGAGA 60
GCGGGCCCGAG GCTCTGTGAG GAGGCAAGGG AGGTGAGAAC CTGTCTCTCA GAGGGTGACT 120
CAAGTCAACA CAGGGAACCC CTCTTTTCTA CAGACACAGT GGGTCGCAGG ATCTGACAAG 180
AGTCCAGGTT CTCAGGGGAC AGGGAGAGCA AGAGGTCAAG AGCTGTGGGA CACCACAGAG 240
CAGCACTGAA CGAGAAAGCC TGCTGTGGG TCCCCATCGC CCAAGTCCTG CCCACACTCC 300
CACCTGCTAC CCTGATCAGA GTCATCATGC CTCGAGCTCC AAAGCGTCAG CGCTGCATGC 360
CTGAAGAAGA TCTTCAATCC CAAAGTGAGA CACAGGGCCT CGAGGGTGCA CAGGCTCCCC 420
TGGCTGTGGA GGAGGATGCT TCATCATCCA CTTCCACAGG CTCCTCTTTT CCATCCTCTT 480
TTCCCTCCTC TCCTCTTCC TCCTCCTCCT CCTGCTATCC TCTAATACCA AGCACCCGAG 540
AGGAGGTTTC TGCTGATGAT GAGACACCAA ATCCTCCCCA GAGTGCTCAG ATAGCTGCT 600
CCTCCCCCTC GGTGCTGTCT TCCCTTCCAT TAGATCAATC TGATGAGGGC TCCAGCAGCC 660
AAAAGGAGGA GAGTCCAAGC ACCCTACAGG TCCTGCCAGA CAGTGAGTCT TTACCCAGAA 720
GTGAGATAGA TGAAGAGGTG ACTGATTGG TGCAGTTTCT GCTCTTCAAG TATCAAATGA 780
AGGAGCCGAT CACAAGGCA GAAATACTGG AGAGTGTCTA AAAAAATTAT GAAGACCACT 840
TCCCTTTGTT GTTTAGTGAA GCCTCCGAGT GCATGCTGCT GGTCTTGGC ATTGATGTAA 900
AGGAAGTGGA TCCCACTGGC CACTCCTTTG TCCTTGTGTC CTCCTGGGGC CTCACCTATG 960
ATGGGATGCT GAGTGATGTC CAGAGCATGC CCAAGACTGG CATCTCATA CTTATCCTAA 1020
GCATATCTT CATAGAGGGC TACTGCACCC CTGAGGAGGT CATCTGGGAA GCATGAATA 1080
TGATGGGGCT GTATGATGGG ATGGAGCACC TCATTTATGG GGAGCCGAGG AAGCTGCTCA 1140
CCCAAGATTG GGTGCAGGAA AACTACCTGG AGTACCGGCA GGTGCCTGGC AGTGATCCTG 1200
CAGGATATGA GTTCTGTGG GGTCCAAGGG CTCATGCTGA AATTAGGAAG ATGAGTCTCC 1260
TGAATTTTTT GGCCAAGGTA AATGGGAGTG ATCCAAGATC CTTCCCACTG TGGTATGAGG 1320
AGGCTTTGAA AGATGAGGAA GAGAGAGCCC AGGACAGAAT TGCCACCACA GATGATACTA 1380
CTGCCATGGC CAGTGCAAGT TCTAGCGCTA CAGGTAGCTT CTCCTACCCT GAATAAAGTA 1440
AGACAGATTCT TCACTGTGT TTTAAAGGC AAGTCAAATA CCACATGATT TTACTCATAT 1500
GTGGATCTTA AAAAAAAAAA AAAAAAAAAA

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PCT/US02/21338

Seq ID NO: 149 Protein Sequence
Protein Accession #: NP_066386.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MPRAPKRQRC MPEEDLQSQS ETQGLEGAQA PLAVEEDASS STSTSSSFPS SFFSSSSSSS 60
SSCYPLIPST PEEVSADDET FNPPQSAQIA CSSPSVVASL PLDQSDGESS SQKEESPSTL 120
QVLDPDESILP RSEIDKQVTD LVQFLLFKYQ MKEPITKAEI LESVIKNYED HFPLLFSEAS 180
ECMLLVFGID VKEVDPTGHS FVLVTSGLT YDGM LSDVQS MPKTGILILI LSIIFIEGYC 240
10    TPEEVIWEAL NMMGLYDGME HLIYGEPRKL LTQDWVQENY LEYRQVPGSD PARYEFLWGP 300
RAHAIEIRKMS LLKPLAKVNG SDPRSFLWY EEALKDEEER AQDRIATDD TTAMASASSS 360
ATGSFSYPE

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Seq ID NO: 150 DNA Sequence
Nucleic Acid Accession #: NM_003695
Coding sequence: 12..398

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20      1      11      21      31      41      51
      |      |      |      |      |      |
CGACATCAGA GATGAGGACA GCATTGCTGC TCCTTGCGAGC CTGGCTGTG GCTACAGGGC 60
CAGCCCTTAC CCTGCGCTGC CACGTGTGCA CCAGCTCCAG CAACTGCAAG CATTCTGTGG 120
TCTGCCCGGC CAGCTCTCGC TTCTGCAAGA CCACGAACAC AGTGGAGCCT CTGAGGGGGA 180
ATCTGGTGAA GAAGGACTGT GCGGAGTCGT GCACACCCAG CTACACCCCTG CAAGGCCAGG 240
25    TCAGCAGCGG CACCAGCTCC ACCCAGTGCT GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC 300
ACAAAGCTGC ACCCACCCTG ACCGCCCTCG CCCACAGTGC CCTCAGCCTG GGGCTGGCCC 360
TGAGCTCTCT GGCCGTCTATC TTAGCCCCCA GCCTGTGACC TTCCCCCAG GGAAGGCCCC 420
TCATGCCTTT CCTTCCCTTT CTCTGGGGAT TCCACACCTC TCTTCCCAG CCGGCAACGG 480
GGGTGCCAGG AGCCCCAGG TGAGGCTTC CCGAAAGTC TGGGACCAGG TCCAGGTGGG 540
30    CATGGAATGC TGATGACTTG GAGCAGGCCC CACAGACCCC ACAGAGGATG AAGCCACCCC 600
ACAGAGGATG CAGCCCCCAG CTGCATGGAA GGTGGAGGAC AGAAGCCCTG TGGATCCCCG 660
GATTTACAC TCCTTCTGTT TTGTTGCCGT TTAITTTGTA CTCAAATCTC TACATGGAGA 720
TAAATGATTT AAACC

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Seq ID NO: 151 Protein Sequence
Protein Accession #: NP_003686

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35      1      11      21      31      41      51
      |      |      |      |      |      |
MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCPA SSRFCKTNT VEPLRGNLVK 60
40    KDCAESCTPS YTLQGQVSSG TSSTQCCQED LCNEKLHNAA PTRTALAHS LSLGLALSL 120
AVILAPSL

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Seq ID NO: 152 DNA Sequence
Nucleic Acid Accession #: NM_006398.1
Coding sequence: 19..516

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45      1      11      21      31      41      51
      |      |      |      |      |      |
GGCCCCCTGT CTGCAGAGAT GGCTCCCAAT GCTTCTGCCC TCTGTGTGCA TGTCCGTTCC 60
50    GAGGAATGGG ATTTAATGAC CTTTGATGCC AACCCATATG ACAGCGTGAA AAAAATCAAA 120
GAACATGTCC GGTCTAAGAC CAAGGTTCTT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC 180
AAGATCTTAA AGCCACGAGG AAGCCTCTCA TCTTATGGCA TTGACAAAAG GAAGACCATC 240
CACCTTACCC TGAAAGTGGT GAAGCCCACT GATGAGGAGC TGCCCTTGTT TCTTGTGGAG 300
55    TCAGGTGATG AGCCAAAGAG GCACCTCCTC CAGGTGCGAA GGTCCAGCTC AGTGGCACAA 360
GTGAAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG ACACCCAGAT TGTCACTTGC 420
AATGGAAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGGCATCAG AAAGGGCAAC 480
TTACTCTTCC TGGCATCTTA TTGTATTGGA GGGTGACCAC CCTGGGGATG GGGTGTGGC 540
AGGGGTCAAA AAGCTTATTT CTTTAACTCT CTTACTCAAC GAACACATCT TCTGATGATT 600
60    TCCCAAAATT AATGAGAATG AGATGAGTAG AGTAAGATTT GGGTGGGATG GGTAGGATGA 660
AGTATATTGC CCAACTCTAT GTTCTTTTGA TTCTAACACA ATTAATTAAG TGACATGATT 720
TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTAA GGCAAAATAG AGCATTC

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Seq ID NO: 153 Protein Sequence
Protein Accession #: NP_006389.1

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65      1      11      21      31      41      51
      |      |      |      |      |      |
MAPNASCLCV HVRSEEWDLN TFDANFYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR 60
70    RSLSSYGIDK EKTIHLLTKV VKPSDEELPL FLVESGDEAK RHLLQVRRSS SVAQVKAMIE 120
TKTGIIIPETQ IVTNCKRLE DKKMMADYGI RKNLLFLAS YCIGG

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Seq ID NO: 154 DNA Sequence
Nucleic Acid Accession #: BC017490.1
Coding sequence: 74..2788

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75      1      11      21      31      41      51
      |      |      |      |      |      |
GTGGGTCACG TGAACCACTT TTCGCGCGAA ACCTGGTTGT TGCTGTAGTG GCGGAGAGGA 60

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5 TCGTGGTACT GCTATGGCGG AATCATCGGA ATCCTTCACC ATGGCATCCA GCCCGGCCCA 120
 GCGTCGGCGA GGCAATGATC CTCTCACCTC CAGCCCTGGC CGAAGCTCCC GGCCTACTGA 180
 TGCCCTCACC TCCAGCCCTG GCGGTGACCT TCCACCATT T GAGGATGAGT CCGAGGGGCT 240
 CCTAGGCACA GAGGGGCCCC TGGAGGAAGA AGAGGATGGA GAGGAGCTCA TTGGAGATGG 300
 CATGGAAAGG GACTACCGCG CCATCCCAGA GCTGGACGCC TATGAGGCCG AGGGACTGGC 360
 TCTGGATGAT GAGGACGTAG AGGAGCTGAC GGCCAGTCAG AGGGAGGCAG CAGAGCGGGC 420
 CATGCGGCAG CCGTACCGGG AGGCTGGCCG GGGCTCGGCC CGCATGCCCC GTGGGCTCCT 480
 GTATGACAGC GATGAGGAGG ACGAGGAGCG CCCTGCCCGC AAGCGCCGCC AGGTGGAGCG 540
 GGCCACGGAG GACGGCGAGG AGGACGAGGA GATGATCGAG AGCATCGAGA ACCTGGAGGA 600
 10 TCTCAAAGGC CACTCTGTGC GCGAGTGGGT GAGCATGGGC GGCCCCCGGC TGGAGATCCA 660
 CCACCGCTTC AAGAACTTCC TGGCAGCTCA CGTGCAGAG CACGGCCACA ACGTCTTCAA 720
 GGAGCGCATC AGCGACATGT GCAAAAGAGAA CCGTGAGAGC CTGGTGGTGA ACTATGAGGA 780
 CTTGGCAGCC AGGGAGCAGC TGCTGGCCTA CTTCCTGCCT GAGGCACCGG CGGAGCTGCT 840
 GCAGATCTTT GATGAGGCTG CCCTGGAGGT GGTACTGGCC ATGTACCCCA AGTACGACCG 900
 15 CATCACCAAC CACATCCATG TCCGCACTCT CCACCTGCCT CTGGTGGAGG AGCTGCGCTC 960
 GCTGAGGCAG CCGCAGCTGA ACCAGCTGAT CCGCACCAGT GGGGTGGTGA CCGAGCTGCAC 1020
 TGGCGTCTGT CCCCAGCTCA GCATGGTCAA GTACAACATG AACAAGTGCA ATTTCTGTCT 1080
 GGTCTCTTTC TGCCATCTCC AGAACAGGA GGTGAAACCA GGCTCTGTCT CTGAGTGCCA 1140
 20 GTGCGCCGCG CCCTTTGAGG TCAACATGGA GGAGACCATC TATCAGAACT ACCAGCGTAT 1200
 CCGAATCCAG GAGAGTCCAG GCAAAAGTGGC GGCTGGCCGG CTGCCCCGCT CCAAGGACGC 1260
 CATTTCTCTC TCGGAGGCG TGGACAGCTG CAAGCCAGGA GACGAGATAG AGCTGACTGG 1320
 CATCTATCAC AACAATATG ATGGCTCCCT CAACACTGCC AATGGCTTCC CTGTCTTTGC 1380
 CACTGTCATC CTAGCCAACC AGTGGCCAA GAAGGACAAC AAGGTTGCTG TAGGGAACT 1440
 25 GACCGATGAA GATGTGAAGA TGATCACTAG CCTCTCCAAG GATCAGCAGA TCGGAGAGAA 1500
 GATCTTTGCC AGCATGTGCT CTTCATCTA TGGTCATGAA GACATCAAGA GAGGCTTGGC 1560
 TCTGGCCCTG TTCCGAGGGG AGCCCAAAAA CCGAGTGGC AAGCACAAGG TACGTGGTGA 1620
 TATCAACGTG CTCTTGTGCG GAGACCTTGG CACAGCGAAG TCGAGTTTC TCAAGTATAT 1680
 TGAGAAAGTG TCCAGCCGAG CCATCTTCAC CACTGGCCAG GGGGCGTCCG CTGTGGGCTC 1740
 30 CACGGCGTAT GTCCACGCGC ACCCTGTGAG CAGGGAGTGG ACCTTGGAGG CTGGGGCCCT 1800
 GGTTCGTGCT GACCGAGGAG TGTGTCTCAT TGATGAATTT GACAGATGA ATGACCAGGA 1860
 CAGAACACAG ATCCATGAGG CCGATGGAGCA ACAGAGCATC TCCATCTCGA AGGCTGGCAT 1920
 CGTCACCTCC CTGCAAGCTC GCTGCACGGT CATTCCTGCC GCCAACCCCA TAGGAGGGCG 1980
 CTACGACCCC TCGCTGACTT TCTCTGAGAA CGTGGACCTC ACAGAGCCCA TCATCTCAG 2040
 35 CTTTGACATC CTGTGTGTGG TGAGGGACAC CGTGGACCCA GTCCAGGACG AGATGCTGGC 2100
 CCGCTTCGTG GTGGGCGAGC ACCTCAGACA CCAACCCAGC AACAGGAGG AGGAGGGGCT 2160
 GGCCAAATGG AGCGCTGCTG AGCCCGCCAT GCCCAACAGG TATGGCGTGG AGCCCTTGCC 2220
 CCAGGAGGTC CTGAAGAAGT ACATCATCTA CGCCAAAGGAG AGGGTCCACC CGAAGCTCAA 2280
 CCAGATGACG CAGGACAAGG TGGCCAAGAT GTACAGTGAC CTGAGGAAAG AATCTATGGC 2340
 40 GACAGGACG ATCCCCATTA CGGTGCGGCA CATCGAGTCC ATGATCCGCA TGGCGGAGGC 2400
 CCACGCGCGC ATCCATCTGC GGGACTATGT GATCGAAGAC GACGTCAACA TGGCCATCCG 2460
 CGTGATGCTG GAGAGCTTCA TAGACACACA GAAGTTCAGC GTCATGCCCA GCATGCGCAA 2520
 GACTTTTGCC CGCTACCTTT CATTCGCGCG TGACAACAAT GAGCTGTGTC TCTTCATACT 2580
 GAAGCAGTGA GTGGCAGAGC AGGTGACATA TACAGCGAAC CGCTTTGGGG CCCAGCAGGA 2640
 45 CACTATTGAG TCCCTGAGA AGGACTTGGT GGATAAGGCT CGTCAGATCA ACATCCACAA 2700
 CCTCTCTGCA TTTTATGACA GTGAGCTCTT CAGGATGAAC AAGTTCAGCC ACACCTGAA 2760
 AAGGAAAATG ATCTCTGAGC AGTTCTGAGG CCCTATGCCA TCCATAAGGA TTCCTTGGGA 2820
 TTTCTGTTTG GGGTGTGTAG TGCCCTCTGT GCTTTATGGA CACAAAACCA GAGCACTTGA 2880
 TGAACCTGGG GTACTAGGCT CAGGGCTTAT AGCAGGATGT CTGGCTGCAC CTGGCATGAC 2940
 50 TGTTTGTTTC TCCAAGCTCT CTTTGTGCTT CTCACCTTTG GGTGGGATGC CTTGCCAGTG 3000
 TGTCTTACTT GGTGTCTGAA CATCTTGCCA CCTCCGAGTG CTTTGTCTCC ACTCAGTACC 3060
 TTGGATCAGA GCTGCTGAGT TCAGGATGCC TGGCTGTGGT TTAGTGTTTA GCCTTCTTAC 3120
 ATGGATGTCA GGAGAGCTGC TGCCCTCTTG GCGTGAGTTG CGTATTGAGG CTGCTTTTGC 3180
 TGCCTTTGGC CAGAGAGCTG GTTGAAAGATG TTTGTAATCG TTTTCAGTCT CTGCGAGGTT 3240
 55 TCTGTGCCCC TGTGCTGAA GAGGGCACCA CAGTCCCACT GCAGCGTTCT GGGCTCCTCA 3300
 GTCGAGGGG TGGAATGTGA GTCATGCGGA TTATCCACG GCCACAGTTA TCAGCTGCCA 3360
 TTGCTCCCTG TCTGTTTCCC CACTCTCTTA TTTGTGATT CGGTTTGGTT TCTGTAGTTT 3420
 TAATTTTAA TAAAGTTGAA TAAATATAA AAAAAA AAAAAA

Seq ID NO: 155 Protein Sequence
 Protein Accession #: AAH17490.1

60 1 11 21 31 41 51
 | | | | | |
 65 MAESSSEPTM ASSPAQRRRG NDPLTSSPGR SSRRIDALTS SPGRDLPPFE DESEGLLGTE 60
 GPLEEEEDGE ELIGDGMERD YRAIPELDAY EAEGALDDE DVEELTASQR EAAERAMRQR 120
 DREAGRGLGR MRRGLLYDSO EDEERFARK RQVERATED GEEDDEMIES IENLEDLKGH 180
 SVREWWSMAG PRLEIHHRPK NPLRTHVDSH GHNVEKERIS DMCKENRESL VVNYEDLAAR 240
 EHVLAFLPE APAELQLIFD EAALEVVLMAM YPKYDRITNH IHVRISHLPL VEELRSLRQL 300
 70 HLNQLIRTSQ VVTSCTGVLP QLSMVKYNCN KCNFVLGPPC QSQNQEVKPG SCPEQCSAGP 360
 FEVNMETIY QNVQRIRIQE SPGKVAAGRL PRSKDAILLA DLVDSCKPGD EIELTGIYHN 420
 NYDGSINTAN GFVFVATVIL ANHVAKKDNK VAVGELTDED VKMITSLSKD QQIGEKIFAS 480
 IAPSIYGHED IKRGLALALF GGEPKNPGGK HKVRGDIVNL LCGDPGTAKS QFLKYIEKVS 540
 SRAIFTTGGQ ASAVGLTAYV QRHPVSRREW LEAGALVLAD RGVCLIDEFD KMNDQDRTSI 600
 HEAMEQQSIS ISKAGIVTSL QARCTVIAAA NPIGGRYDPS LTFSENVDLT EPIISRFDIL 660
 75 CVVRDTPDEV QDEMLARFVV GSHVRHHPSN KEEBGLANGS AEPAMPNTY GVEPLPQEV 720
 KKYIYAKER VHPKLNQMDQ DKVAKMYSYL RKESMATGSI PITVRHIESM IRMAEAHARI 780
 HLRDYVIDED VNMAIRVMLE SFIDTQKFSV MRSMRKTFAR YLSFRDNNE LLLFILKQLV 840
 AEQVYYQRNR FGAQQPTIEV PEKDLVDKAR QTNIHNLASF YDSELFPMNK FSHDLKRRMI 900

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PCT/US02/21338

LQQF

Seq ID NO: 156 DNA Sequence
Nucleic Acid Accession #: NM_002497.1
Coding sequence: 135..1472

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25
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1	11	21	31	41	51	
GGCAGGAGTA	GGGGTGGCGG	GTCAGTGTCTG	CTCGGGGGCT	TCTCCATCCA	GGTCCCTGGA	60
GTTCTCTGGTC	CCTGGAGCTC	CGCACTTGGC	GCGCAACCTG	CGTGAGGCAG	CGCGACTCTG	120
GCGACTGGCC	GGCCATGCCCT	TCCCGGGCTG	AGGACTATGA	AGTGTGTAC	ACCATTGGCA	180
CAGGCTCCTA	CGGCCGCTGC	CAGAAGATCC	GGAGGAAGAG	TGATGGCAAG	ATATTAGTTT	240
GGAAAGAACT	TGACTATGGC	TCCATGACAG	AAGCTGAGAA	ACAGATGCTT	GTTTCTGAAG	300
TGAATTTGCT	TCGTGAACCTG	AAACATCCAA	ACATCGTTCG	TTACTATGAT	CGGATTATTG	360
ACCGGAGCAA	TACAACACTG	TACATTGTAA	TGGAATATTG	TGAAGGAGGG	GATCTGGCTA	420
GTGTAAATAC	AAAGGGAACC	AAGGAAAGGC	AATACCTAGA	TGAAGAGTTT	GTTCTTCGAG	480
TGATGACTCA	GTTGACTCTG	GCCCTGAAGG	AATGCCACAG	ACGAAGTGAT	GGTGGTCATA	540
CCGTATTGCA	TCGGGATCTT	AAACGAGCCA	ATGTTTTCCT	GGATGGCAAG	CAAAACGTCA	600
AGCTTGGAGA	CTTTGGGCTA	GCTAGAATAT	TAAACCATGA	CACGAGTTTT	GCAAAAACAT	660
TTGTTGGGAC	ACCTTAATTAC	ATGTCTCCTG	AACAAATGAA	TGCGATGTCC	TACATGAGA	720
AATCAGATAT	CTGGTCATTG	GGCTGCTTGC	TGTATGAGTT	ATGTGCATTA	ATGCCTCCAT	780
TTACAGCTTT	TAGCCAGAAA	GAACTCGCTG	GGAAAAATCAG	AGAAGGCCAA	TTGAGGCCAA	840
TTCCATACCG	TTACTCTGAT	GAATTGAATG	AAATTATTAC	GAGGATGTTA	AACTTAAAGG	900
ATTACCACG	ACCTTCTGTT	GAAGAAATTC	TTGAGAACCC	TTTAATAGCA	GATTTGGTTG	960
CAGACGAGCA	AAGAAGAAAT	CTTGAGAGAA	GAGGGCGACA	ATTAGGAGAG	CCAGAAAAAT	1020
CGCAGGATTC	CAGCCCTGTA	TTGACTGAGC	TGAAACTGAA	GGAAATTCAG	TTACAGGAGC	1080
GAGAGCGAGC	TCTCAAAGCA	AGAGAAGAAA	GATTGGAGCA	GAAAGAACAG	GAGCTTTGTG	1140
TTCGTGAGAG	ACTAGCAGAG	GACAACTGG	CTAGAGCAGA	AAATCTGTTG	AAGAACTACA	1200
GCTTGTCTAAA	GGAAOOGAAG	TTCTGTCTC	TGGCAAGTAA	TCCAGAACTT	CTTAATCTTC	1260
CATCTCTCAGT	AATTAAGAAG	AAAGTTTCA	TCAGTGGGGA	AAGTAAAGAG	AACATCATGA	1320
GGAGTGAGAA	TTCTGAGAGT	CAGCTCACAT	CTAAGTCCAA	GTGCAAGGAC	CTGAGAGAAA	1380
GGCTTCACGC	TGCCCAGCTG	CGGGCTCAAG	CCCTGTCTAGA	TATTGAGAAA	AATTACCNAAC	1440
TGAAAAGCAG	ACAGATCCTG	GGCATGCGCT	AGCCAGGTAG	AGAGACACAG	AGCTGTGTAC	1500
AGGATGTAA	ATTACCAACC	TTTAAAGACT	GATATTCAAA	TGCTGTAGTG	TTGAATACTT	1560
GGCCCCATGA	GCCATGCCTT	TCTGTATAGT	ACACATGATA	TTTCGGAATT	GGTTTTACTG	1620
TTCTTCAGCA	ACTATTGTAC	AAAATGTTCA	CATTTAATTT	TTCTTTCTTC	TTTTAAGAAC	1680
ATATTATAAA	AAGAATACTT	TCTTGTTTGG	GCTTTTAATC	CTGCTGTGTA	TTACTAGTAG	1740
GAACATGAGA	TGTGACATTC	TAAATCTTGG	GAGAAAAAAT	AATATTAGGA	AAAAAATATT	1800
TATGACAGAA	GGTAGCAGCT	CACCTGAATAG	TTTTAAATGA	CTGAGTGGTA	TGCTTACAAT	1860
TGTCATGTCT	AGATTTAAAT	TTTAAAGTCTG	AGATTTTAAA	TGTTTTTGAG	CTTAGAAAAAC	1920
CCAGITAGAT	GCAATTTGGT	CATTAATACC	ATGACATCTT	GCTTATAAAT	ATTCCATTGC	1980
TCTGTAGTTC	AAATCTGTTA	GCTTTGTGAA	AATTCATCAC	TGTGATGTTT	GTATTTCTTTT	2040
TTTTTTTCTG	TTTAAACAGAA	TATGAGCTGT	CTGTCAATTA	CCTACTTCTT	TCCCACTAAA	2100
TAAAGAAT	CTTCAGTTA					

Seq ID NO: 157 Protein Sequence
Protein Accession #: NP_002488.1

50
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1	11	21	31	41	51	
MPSRADYEV	LYTIGTGSYG	RCQKIRKSD	GKILVWKELD	YGSMTAEKQ	MLVSEVNLLR	60
ELKHENIVRY	YDRIIDRTNT	TLYIVMEYCE	GGDLASVITK	GTKERQYLDE	EFVLRVMTQL	120
TLALKECHRR	SDGGHTVLHR	DLKPANVFLD	GKQNVKLGDF	GLARILNHDT	SFAKTFVGTG	180
YYMSPEQMNR	MSYNEKSDIW	SLGCLLYELC	ALMPPTAFPS	QKELAGKIRE	GKFRIPYRY	240
SDBLNEIITR	MLNLKDYHRP	SVBEILENPL	IADLVADEQR	RNLERRGRQL	GEPEKSQDSS	300
PVLSSELKKE	IQLQERERAP	KAREERLEQK	EQELCVRERL	AEDKLARAEN	LLKNYSLLKE	360
RKFLSLASNP	ELLNLPSSVI	KKKVHFSGES	KENIMRSSENS	ESQLTSKSKC	KDLKKRLHAA	420
QLRAQALSDI	EKNYQLKSRQ	ILGMR				

Seq ID NO: 158 DNA Sequence
Protein Accession #: Eos sequence

65
70
75

1	11	21	31	41	51	
TGAGTTTGCC	CCCTTACCCC	CATCCCAGTG	AATATTTGCA	ATTCCTAAAG	ACGTGTTTTG	60
ATTGTACACAT	CTGGGTGGGG	AACATGCTAC	TGGCATCTAA	TGCATAGAGG	GCAGTAATGC	120
TGCTAAATAC	CTTTCAACGC	ACAGGACAGA	GCCCCACAAA	AGAGAATTAT	CTAGCCCCAA	180
ATGTCCATAA	CAGTGTCTGT	GAGAAAACCT	ACCGCAGGAT	CTTACTGGGC	TTCATAGGTA	240
AGCTTGCCTT	TGTTCTGGCT	TCTGTAGATA	TATAAAATAA	AGACACTGCC	CAGTCCCTCC	300
CTCAACGTC	CGAGCCAGGG	CTCAAGGCAA	TTCCAATAAC	AGTAGAATGA	ACACTAAATA	360
TTGATTTCAA	AACTCTAGCA	ACTAGAAGAA	TGACCAACCA	TCCTGGTTGG	CCTGGGACTG	420
TCCTAGTTTT	AGCATTGAAA	GTTCAGGTT	CCAGGAAAGC	CCTCAGGCCT	GGGCTGCTGG	480
TCACCCTAGC	AGCTGAGGGA	CTCTTCAATA	CAGAATTAGT	CTTTGTGCAC	TGGAGATGAA	540
TATACTTTAA	TTTGTAAACAT	GTGAAAACAT	CTATAAACAT	CTACTGAAGC	CTGTCTGTCT	600
TGCACCGACA	TTTTTATTGA	GTACGGATTC	TTCTTACCAG	ATACAGCTGC	TCTACAACTT	660
TCGAGGGCTG	GTATAAACT	AGCTTTTACC	TATTTTAA	AATTACATGA	ATAGTAAAAA	720
CTTGGATTAA	CCCAGTATTC	GGGTATTTTC	AATTTCCCTG	GGAGCTTACA	GGACGGACAA	780
ATAAAAAGAT	TATTTCACAA	TCAAAATATAY	GCTATTGTTT	ACATATGAAG	ATAACACAT	840

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ATATGTATAA ATTCAACGTT ACTTTTATAG AATACTATAA AATCCAACAG AAAAAATAG 900
CATTACTAT

5 Seq ID NO: 159 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 264..782

	1	11	21	31	41	51	
10	CCCTGCTCCA	GTCACACCCG	GAAGCTGACT	GGTCCACGCA	CAGCTGAAGC	ATGAGGAAAC	60
	TCATCGCGGG	ACTAATTTTC	CTTAAATTTT	AGACTTGCAC	AGTAAGGACT	TCAACTGACC	120
	TTCTCTCAGC	TGAGAACTGT	TTCCAGTATA	TACATCAAGT	CACCTGAGATC	TCCAGCACCC	180
	TGCCGGTGGC	ACTACTGAGA	GACGAGGTGC	CAGGGTGGTT	CCTGAAAGTG	CCTGAGCCCC	240
15	AACCTATCAG	CAAGGAGCTC	ATCATGCTGA	CAGAAGTCAT	GGAGGTCTGG	CATGGCTTAG	300
	TGATCGCGGT	GGTGTCCCTC	TTCTGTCAGG	CCTGCTTCCT	CACCGCCATC	AACTACCTGC	360
	TCAGCAGGCA	CATGGCCAC	AAGAGTGAAC	AGATACTGAA	AGCGGCCAGT	CTCCAGGTTT	420
	CCAGGCCAC	CCCTGGCCAC	CATCATCCAC	CTGCTGTCAA	AGAGATGAAG	GAGACTCAGA	480
	CAGAGAGAGA	CATCCCAATG	TCTGATTCCC	TTTACAGGCA	TGACAGCGAC	ACACCCTCAG	540
20	ATAGCTTGA	TAGCTCCTGC	AGTTCGCCTC	CTGCCTGCCA	GGCCACAGAG	GATGTGGATT	600
	ACACACAAGT	CGTCTTTTCT	GACCTGGAG	AACTAAAAAA	TGACTCCCCG	CTGGACTATG	660
	AGAACATAAA	GGAAATCACA	GATTATGTCA	ATGTCAATCC	AGAAAGACAC	AAGCCAGTTT	720
	TCTGGTATTT	TGTCAACCTT	GCTCTGTCTG	AGCCAGCGGA	ATATGATCAA	GTGGCCATGT	780
	GAATTCCAA	TATTTTAAAT	GGGTCOCAGT	TCTCTATGGA	TTCTTACATT	TAATTTGTAG	840
25	GGAAATGCCA	TTTTTCCCC	TTAAACAAGG	CATGGGGCTC	ACAACTCTAT	GGACACAGGC	900
	CAAAAGAAT	GTGAGAGA	AAACTGATAA	ATACACAGAG	GTCTCAAGA	CCCTGGACT	960
	CCTGGTCTGT	ACCCAAAAAA	GCTGTTCTGT	CCTCAAAAAA	AAAAACAAGG	CTTGGCTGGG	1020
	AAAACAGGCC	AATGCCCCCG	CAAGAAAGGT	TGAGATCAGA	TGTTAGGAAG	AACTTTCAGG	1080
	TAAAGTATGA	GAACTATGGA	GTCCATCAGC	AGAGATAGTA	GTGAAGTCTC	TCCCCAGGGA	1140
30	AAATTTTAAA	AAGGTTGAAT	CAGCTGTGTG	AGAGTTCTAT	TTGGCAATCT	CATGGTTAAA	1200
	TGACTTCCCT	TTGAGCTCTT	TAATTATTGG	CAATAAACAA	CTTCTTTAAA	AGTTTATAAT	1260
	AAAATAGCAA	CCACACCA					

35 Seq ID NO: 160 Protein Sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
40	MLTEVMEVWH	GLVIAVVSFL	LQACFLTAIN	YLLSRHMAHK	SEQILKAASL	QVPRPSPGHH	60
	HPPAVKEMKE	TQTERDIPMS	DSLVRHSDI	PSDSLSDSCS	SPPACQATED	VDYTVVFS	120
	PGEKNDSP	DYENIKEITD	YVNVNPERHK	PSFWYFVNPA	LSEPAEYDQV	AM	

45 Seq ID NO: 161 DNA Sequence
Nucleic Acid Accession #: NM_012152
Coding sequence: 43..1104

	1	11	21	31	41	51	
50	CTTCTTTAAA	TTTCTTTCTA	GGATGTTTAC	TTCTTCTCCA	CAATGAATGA	GTGTCACTAT	60
	GACAAGCACA	TGCACTTTT	TTATAATAGG	AGCAACACTG	ATAGTCTCGA	TGACTGGACA	120
	GGAAACAAAG	TTGTGATTGT	TTTGTGTGTT	GGGACGTTTT	TCTGCCTGTT	TATTTTTTTT	180
	TCTAATTCTC	TGGTCATCGC	GGCAGTGATC	AAAAACAGAA	AATTTTCATT	CCCTTCTTAC	240
	TACCTGTGG	CTAATTTAGC	TGCTGCCGAT	TTCTTCGCTG	GAATTGCCTA	TGTATTCTCTG	300
55	ATGTTTAA	CAGGCCCACT	TTCAAAAAC	TTGACTGTCA	ACCGCTGGTT	TCTCCGTCAG	360
	GGGCTTCTGG	ACAGTAGCTT	GACTGCTTCC	CTCACCACCT	TGCTGGTTAT	CGCCGTGGAG	420
	AGGCACATGT	CAATCATGAG	GATGCGGGTC	CATAGCAACC	TGACCAAAAA	GAGGGTGACA	480
	CTGCTCATTT	TGCTTGTCTG	GGCCATCGCC	ATTTTATG	GGGCGGTCCC	CACACTGGGC	540
	TGGAATTGCC	TCTGCAACAT	CTCTGCCTGC	TCTTCCCTGG	CCCCATTTA	CAGCAGGAGT	600
60	TACCTGTGTT	TCTGGACAGT	GTCCAACTC	ATGGCCTTCC	TCATCATGGT	TGTGGTGTAC	660
	CTGCGGATCT	ACGTGTACGT	CAAGAGGAAA	ACCAACGCTC	TGTCTCCGCA	TACAAGTGGG	720
	TCCATCAGCC	GCCGGAGGAC	ACCCATGAAG	CTAATGAAGA	CGGTGATGAC	TGTCTTAGGG	780
	GCGTTTGTGG	TATGCTGGAC	CCCGGGCCTG	GTGGTTCTGC	TCCTCGACGG	CCTGAACTGC	840
	AGGCAGTGTG	GCCTGCAGCA	TCTGAAAAGG	TGGTTCCTGC	TGCTGGCGCT	GCTCAACTCC	900
	GTCGTGAACC	CCATCATCTA	CTCTACAAG	GACGAGGACA	TGTATGGCAC	CATGAAGAAG	960
65	ATGATCTGCT	GCTTCTCTCA	GGAGAACCCA	GAGAGGCGTC	CCTCTCGCAT	CCCCCTCACA	1020
	GTCTCAGCA	GGAGTGACAC	AGGCAGCCAG	TACATAGAGG	ATAGTATTAG	CCAAGGTGCA	1080
	CTCTGCAATA	AAAGCACTTC	CTAAACTCTG	GATGCCTCTC	GGCCACCCA	GGTGATGACT	1140
	GTCTTAGG						

70 Seq ID NO: 162 Protein Sequence
Protein Accession #: NP_036284

	1	11	21	31	41	51	
75	MNECHYDKHM	DEFFYNRSNTD	TVDDWTGTLK	VIVLCVGTFF	CLFIFFSNSL	VIAAVIKNRK	60
	PHFPPFYLLA	NLAAADPFAG	IAYVELMENT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
	LVIIVERHMS	IMMRVHSNL	TKKRVTLILL	LWVAIAIPMG	AVPTLGWNCL	CNISACSSLA	180
	PIYSRSYLVE	WTVSNLMAFL	IMVVVYLRIY	VYVKKRTNVL	SPHTSGSISR	RRTPMKLMKT	240

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VMTVLGAFVV CWTPLGLVLL LDGLNCRQCG VQHKVRWFL LALLNSVVPN IIYSYKDEDM 300
YGTMKRMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

5 Seq ID NO: 163 DNA Sequence
Nucleic Acid Accession #: NM_020242
Coding sequence: 72..4240

10	1	11	21	31	41	51	
	CAGTCGCGCG	CGGTGCAGTC	GGGAGGTGGA	GGCACCGGCT	GCATTGTTTT	CGGGATCGAG	60
	GGGTGAGGGC	GCTATGGCAC	CGGGCTGCAA	AACCTGAGTTA	CGCAGCGTGA	CAAATGGTCA	120
	GTCTAACCAA	CCAAGTAATG	AAGGTGATGC	CATCAAAGTT	TTTGTGCGAA	TTGCTCTCTC	180
	TGCAGAAAGA	TCTGGGTGAG	CTGATGGAGA	GCAGAACTTA	TGCTTATCTG	TGCTGTCTCT	240
15	CACGAGTCTC	CGGTGCACTG	CCAACTCTGA	GCCCCAAGACC	TTCACTGTTG	ATCATGTTGC	300
	AGATGTGGAT	ACCATCAGG	AATCTGTATT	TGCAACTGTG	GCTAAAAGCA	TTGTGGAGTC	360
	TTGCATGAGC	GGTTATAATG	GTACCATCTT	TGCATATGGA	CAGACTGGCT	CAGGGAAGAC	420
	ATTTACTATG	ATGGGACCAT	CTGAATCTGA	TAATTTTCTT	CATAACTCTG	GAGGAGTAAT	480
	CCCCAGAGT	TTTGAATATT	TGTTTTCCTT	AATTGATCGT	AAAAAAGAAA	AGGCTGGAGC	540
20	TGGAAAGAGT	TTTCTTTGTA	AGTGTTCCTT	TATTGAAATC	TACAACGAGC	AGATATATGA	600
	TCTACTGGAC	TCTGCATCGG	CTGGACTGTA	CTTAAGGGAG	CATATCAAGA	AGGGAGTCTT	660
	TGTTGTTGTT	GCGGTGGAGC	AGGTGGTAAC	CTCAGCTGCT	GAAGCCTATC	AGGTGCTGTC	720
	TGAGAGGATG	AGGAATAAGC	GTGTGGCATC	AACATCAATG	AACAGAGAAT	CGTCTAGGTC	780
	TCCATGCGTC	TTTACAAATA	CAATAGAGTC	AATGGAGAAA	AGTAATGAGA	TTGTGAATAT	840
25	ACGGACCTCC	CTACTCAACC	TGGTGGATTT	AGCAGGATCT	GAAAGGCCAA	AAGATACCCA	900
	TGCAGAGGG	ATGAGATTGA	AGGAAGCAGG	TAACATAAAT	CGATCATTTG	GCTGCTGGG	960
	CCAAGTGATT	ACAGCACTTG	TCGACGTGGG	TAATGGAAAA	CAGAGACATG	TTTGCTACAG	1020
	AGACTCCAAA	CTTACCTTCT	TACTACGGGA	TTCCCTTGGA	GGTAATGCCA	AAACAGCCAT	1080
	AATTGCAAAAT	GTTCATCTCT	GATCCAGGTG	TTTTGGGGAA	ACCCTATCAA	CACCTTAACTT	1140
30	TGCTCAAAAG	GCCCAAGCTG	TTAAAAACAA	GGCAGTAGTA	AATGAAGACA	CCCAAGGAAA	1200
	TGTGAGCCAG	TCCCAAGCTG	AAGTGAAGAG	GCTCAAGAAA	CRACTGGCGG	AGCTTGCTTC	1260
	AGGACAGACA	CCACCAGAAA	GCTTCTTGAC	CAGAGACAAA	AAGAAGACTA	ACTATATGGA	1320
	GTATTTCCAG	GAAGCAATGT	TATTTCTTAA	GAAATCTGAA	CAGGAAAAAG	AGTCTCTGAT	1380
	AGAAAAAGTT	ACCCAATTAG	AAGACCTCAC	CCTCAAAAAG	GAAAAATTTA	TTCAATCTAA	1440
35	TAAAAATGAT	GTGAAATTCC	GAGAGGATCA	AATAATACGC	TTGAAAAAGC	TCCACAAGGA	1500
	ATCCCCGGGA	GGTTTTCTGC	CTGAGGAGCA	GGATCGTTTG	CTCTCAGAAT	TAAGGAATGA	1560
	GATTCAAACT	CTCGAGGAAC	AAATAGAGCA	CCACCCGAGA	GTGCAAAAGT	ATGCTATGGA	1620
	AAATCATTC	CTCAGGGAGG	AGAATAGAAG	ACTGAGATTA	TAGAGCCTTG	TGAAAAAGAGC	1680
	TCAGAAATG	GATCCCGAGA	CCATGCAAAA	ACTAGAAAAA	GCTTTCTCTG	AAATAAGTGG	1740
40	CATGGAGAAA	AGTGACAAAA	ATCAGCAAGG	ATTTTCACCT	AAAGCTCAGA	AAGAGCCATG	1800
	TTTGTITTGA	AACACTGAGA	AGTTAAAAAG	ACAACTCCTG	CAAATTCAGA	CAGAGCTGAA	1860
	TAATTCAAA	CAGAAATATG	AAGAATTCAA	AGAACTTACT	AGGAAAAGGC	AGCTAGAAAT	1920
	GGAAATCAG	CTTCAGTCTT	TGCAAAAAGC	GAACCTTAAT	CTTGAAAAAC	TTTTGGAAGC	1980
	AACAAAAGCC	TGCAAGCGGC	AAGAAGTTTC	TCAGCTGAAT	AAAAATTCATG	CTGAAACACT	2040
45	TAAGATTATA	ACTACACCAA	CCAAGGCCTA	CCAACCTTAT	TCCCGACCAG	TACCAAAATT	2100
	AAGCCCTGAA	ATGGGAAGCT	TTGGCTCTCT	ATACACTCAG	AATTCATGCA	TATTAGATAA	2160
	TGATATATTA	AATGAGCCAG	TTCTCTCTGA	GATGAATGAA	CAAGCTTTTG	AGGCCAATTC	2220
	TGAAGAGCTT	AGAACAGTGC	AGGAACAAAT	GAGTGCTCTT	CRAAGCAAA	TGGATGAAGA	2280
	AGAGCTATAA	AACCTAAAG	TTGAGCAGCA	TGTTGACAAA	CTGGAACATC	ATTCTACCCA	2340
50	AATGCAAGG	CTTTTCTCAT	CAGAAAGAAT	TGATTGGACC	AAACAGCAGG	AAGAGCTTCT	2400
	CTCACAGTTG	AATGTCTCTG	AAAAGCAGCT	TCAAGAGACT	CAAACTAAAA	ATGACTTTTT	2460
	GAAAACTGAG	GTACATCTTG	TGCGAGTAGT	CCTTCTATCT	GCTGACAAGG	AGCTTTCTTC	2520
	AGTGAATTTG	GAATATAGTT	CATTCAAATC	GAATCAGGAG	AAAGAATTCA	ACAAACTTTC	2580
	TGAAAAGAC	ATGCATGTAC	AGCTTCAATT	AGATAATCTC	AGTTTAGAAA	ACGAAAAGCT	2640
55	GCTTGAGAGC	AAAGCCTGCC	TACAGGATTC	CTATGACAA	TTACAAGAAA	TAATGAAATT	2700
	TGAGATTGAC	CAACTTTCAA	GAAACCTCCA	AAACTTCAAA	AAAGAAAATG	AAACTCTGAA	2760
	ATCTGATCTG	AATAATTGTA	TGGAGCTTCT	TGAGGCGAG	AAAGAACGCA	ATACAAATTT	2820
	ATCATTACAG	TTTGAAGAAG	ATAAGAAAA	CAGTTCTAAA	GAAATCTTAA	AAGTTCTTGA	2880
	GGCTGTACGT	CAGGAGAAAC	AGAAAGAGAG	GGCCAAAGTG	AGCAGCAGCA	TGGCAAAAGT	2940
60	ACAGAAACTA	GAAGAGAGCT	TGCTTGCTAC	TGAAAAAGTG	ATCAGTTCCC	TGAAAAAGTC	3000
	TAGAGATTCT	GATAAGAAAG	TTGTAGCTGA	CCTCATGAAC	CAGATCCAGG	AGCTAAGAAC	3060
	ATCGGTCTGT	GAGAAAACAG	AAACTATAGA	CACCTGAAA	CAAGAACTGA	AGGACATAAA	3120
	TTGCAATAC	AACCTCTGCT	TGTTTGACAG	AGAAGAGAGC	AGAGTGTGTA	TCAAGAAGCA	3180
	GGAAGTGGAT	ATTCTGGATC	TGAAAGAAAC	CCTTAGGCTG	AGAACTACTT	CTGAGGACAT	3240
65	AGAGAGGGAT	ATGCTCTGTG	AGGACCTGGC	TCATGCCACT	GAGCAGCTGA	ACATGCTCAC	3300
	AGAGGCCTCA	AAAAACACT	CGGGCTGCT	GCAGTCTGCC	CAGGAAGAAC	TGACCAAGAA	3360
	GGAAGCCCTG	ATTCAGGAAC	TTCAGCACAA	GCTAAACCAA	AAGAAAGAGG	AAGTAGAACA	3420
	GAAGAAGAT	GAATATAACT	TCAAAATGAG	GCAACTAGAA	CATGTGATGG	ATTCTGCTGC	3480
70	TGAGGATCCC	CAGAGTCTTA	AGACACCACC	TCACTTTCAA	ACACATTGCG	CAAACTCTCT	3540
	GGAACACAAA	GAAACAAGAG	TAGAAGATGG	AAGAGCCTCT	AAGACTTCTT	TGGAACACCT	3600
	TGTAACCAA	CTAATGAAG	ACAGAGAAGT	CAAAATGCT	GAAATCTTCA	GAATGAAGGA	3660
	GCAGTTGCGT	GAAATGGAAA	ACCTACGCCT	GGAAGTCAG	CAGTTAATAG	AGAAAACTG	3720
	GCTCCTGCAA	GGTCAGCTGG	ATGATATTAA	AAGACAAAAG	GAAACAGTGT	ATCAGAAATCA	3780
	TCCAGATAAT	CAACAGCTGA	AGAATGAACA	AGAAGAAAGT	ATCAAGAAAA	GACTTGCAAA	3840
75	AAGTAAAAAT	GTTGAAGAAA	TGCTGAAAAT	GAAAGCAGAC	CTAGAAAGAG	TCCAAAGTGC	3900
	CCTTTACAAC	AAAGAGATGG	AATGCCTTAG	AATGACTCAT	GAAGTCGAAC	GAACCCAAAC	3960
	TTTGGAGTCT	AAAGCATTC	AGGAAAAGAA	ACAACTGAGA	TCAAAGCTGG	AAGAAATGTA	4020
	TGAGAAAGA	GAGTGAACAT	CCCAGGAGAT	GGAAATGTTA	AGGAAGCAGG	TGGAGTGTCT	4080

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TGCTGAGGAA AATGGAAAGT TGGTAGGTCA CCAAATTG CATCAGAAGA TTCAGTACGT 4140
AGTCCGACTA AAGAAGGAAA ATGTCAGGCT TGCTGAGGAG ACAGAAAAGT TGCCTGCCGA 4200
AAATGTATTT TTTAAAGAAA AGAAAAGAAG TGAATCTTGA GGATTCGGGT CAGCTACCTA 4260
GGCATCACCT TGTTTGAAGA TGTTCCTTCT CTTTACAAAG TAAGACCTAC TCCTGGCCAC 4320
TTAGGAGAGC TGAATTTATG GACCTTAATT ATTAATGTGT TATAAGGTGG TGGTAAACCA 4380
CTCAAGTTTC TGATGAACAT TCTGCATCCA TATACACCCT GTGACAGTCA GCAGTCTGCT 4440
ATTAAGTGGC CTACTTCAAG GCTTTGAATC AACTTAAGGG AAAACCTTTT GTCTTTGTAA 4500
AAATAAAAGC CTGTAGCTAA GGTTTACAGT GGACATTAGC CAGATCATTT TCTTCTTAGA 4560
TTATGCCATA ATCTCCTTTG ATTCTTAGTG AAGTTCTAAC AATATATGTT GGTTCACAAC 4620
CCTGCAGTGA GTTTAATGAC TGACTTAGTA GCAGGTACAA GAAGCAAACT TGTTAATATA 4680
GATTATTTTT GTATTCTTAC TTTAGGTATT TTACTTGAGC ATTTTCCATG ACTGTAAATA 4740
AAGCCATTTT TTAAGATAAA AAAAAAAAAA AAAAA

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Seq ID NO: 164 Protein Sequence
Protein Accession #: NP_064627

20
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1 11 21 31 41 51
MAPGCKTELK SVTNGQSNQP SNEGDAIKVF VRIRPPAERS GSADGEQNLC LSVLSSTSLR 60
LHSNPPEKTF TFDHADVDT TQESVFATVA KSIVESCMSG YNGTIFAYGQ TGSCKTFTMM 120
GPESDNPFSH NLRGVI PRSF EYLFSLIDRE KEKAGAGKSF LCKCSFIEIY NEQIYDLLDS 180
ASAGLYLREH IKKGVFVVG AVEQVVTSAE AYQVLSGGWR NRRVASTSMN RESSRSHAVF 240
TTTIESMEKS NEIVNIRTS LNLVDLAGSE RQKDTAEAGM RLKEAGNINR SLSCLGQVIT 300
ALVDVVGNGK RHVCYRDSKL TFLLRDSLGG NAKTAIIANV HPGSRCFGET LSTLNFACRA 360
KLIRNKAVVN EDTQGNVSQL QAEVKRLKEQ LAELASGQTP PESFLTRDKK KTNMYEYFQE 420
AMLFKKSEH EKKSLEIKVT QLEDLTLKKE KFTQSNKMIV KFPREDQIIRL EKLHKESSRG 480
FLPEEQDRLL SELRNEIQT REQIEHHPRV AKYAMENHSL REENRRLRL EPVKRAQEMD 540
AQTTIAKLEK FSEISGMEKS DKMQQGFSPK AQKEPCLFAN TEKLKQQLLQ IQTELNNKSKQ 600
EYEEFKELTR KRQLESESEL QSLQKANLNL ENLLEATKAC KRQEVSQLNK IHABTLKIIT 660
TPTKAYQLHS RVPVKLSPEM GSFGLSYTQN SSILDNDILN EPVPPPMNEQ AFEAISEELR 720
TVQEQMSALG AKLDEEHEKN LKLQQHEVDKL EHHSTQMQL FSSERIDWTQ QQEBLLSQLN 780
VLEKQLQETQ TKNDPLKSEV HDLRVVLHSA DKELSSVKLE YSSFKTNQEK EFNKLSERHM 840
HVQLQLDNL LENEKLLSEK ACLQDSYDNL QEIMKFEIDQ LSRNLQNFKK ENETLKSDELN 900
NLMELLEAEK ERNNKLSLQF EEDKENSSEK ILKVLBAVRQ EKQKETAKCE QQMAKVQKLE 960
ESLATEKVI SSLEKSRSDS KKVVDLMNQ IQELRTSVCE KTETIDTLKQ ELKDINCKYN 1020
SALVDREESR VLIKKEQVDI LDLEKTLRLR ILSEDIERDM LCEDLAHAHE QLNMLTEASK 1080
KHSGLLQSAQ EELTKKEALI QELQKLNQK KEEVEQKKNE YNFKMRQLEH VMDSAEDPQ 1140
SPKTPPHFQT HLAKLLETQE QEIEDGRASK TSLEHLVTKL NEDREVKNAE ILRMKEQLRE 1200
MENLRLESQV LIEKNWLLQG QLDDIKRQKE NSDQNHDPNQ QLKNEQEESI KERLAKSKIV 1260
EEMLMKMDLR EBVSQALYNK EMECLRMTE VERTQTLSEK AFQEKELRS KLEEMYBEER 1320
RTSQEMEMLR KQVECLAEBN GKLVGHQNLH QKIQYVVRLE KENVRLAEET EKLRAENVFL 1380
KEKKRSES

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Seq ID NO: 165 DNA Sequence
Nucleic Acid Accession #: CAT cluster

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55
60
65

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1 11 21 31 41 51
TTTTTTTTTT TTTTTCACAT TGCTGATGTT GCTGCCGATG ATTTCAACGC CTGGCTTTGA 60
GATTCCTGTA GTAGTCTTGA ATAATTAAAT ATTCGAAAT CAAATCTAC TTATTTCTC 120
TTAATGCTAT TGTATTTCTT AATTCTCAGC TTTAACATGT AAGAAAGTAC TTTCCTAGG 180
GGTCTTAATT GAATGGTGGG GTCGAGATGA ATCGGTCAGA ATTAATCTC TGGAGACCT 240
CTGAGCTCCT TTTAAATACA TCAACAAGCG AAAATCCTTA TCAATAGCGA TGTGGGAATG 300
CATTAGGTAC AGTATTTTAA ACATACAAAA CCTAGGCATA TTAAGAAAGCA CTCTCTGGT 360
AATTTAATAA GGAATAATGA TGTCCTTAAG TTTATTTTAA TCAGCAAGTA TGACTCAAT 420
TGAAAATATG AGAACAAATA GATTAAATA GGAACACCCA GTAAACTATG GTATGCAAT 480
AAACTCAGAG GTAAACTTGT GAATACATAA ATCTAAATAA GTCAGTTACC ATCAAAATAT 540
TACGTGATCA TATATTTTTC TGTCACCGTC TTAAGAGTAT TTTTACCTT GGGGCTTTAT 600
TTTCTTTCCC TCTTCCCAAG ATTATCCAAG GCAGTTCCAA TACGCGTTT CAATAATGTT 660
AATTAACCTT TTGGAGGGTA ATCGCCAGCT GTTTCAGAA AAATACTTTT AATAGGTGCT 720
AGTCTCCTCT GTAACCTGGT TTTCCCGGGA ATCCGGGGGG GGCATGTTGT TTTTATTGTC 780
GCCATTTTGT TTTCTCTTTT TTTGTTTGT TGGTGGTCAG GTTTTCTTTT CATAGCGGG 840
GAGAAGATTT TGGTCGGACT AGCGCCATCC AGCGGGTTTA GAGAAGGAGC ACACCTTTTC 900
CCGAATAGTG GCTTTTGAT GAACAATGAA

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Seq ID NO: 166 DNA Sequence
Nucleic Acid Accession #: NM_006953.1
Coding sequence: 33..896

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75

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1 11 21 31 41 51
CGGTTCGCGC CTCTGGCGGC TCCICCCGGG CGATGCCTCC GCTCTGGGCC CTGCTGGCCC 60
TCGGCTGCCCT GCGGTTTCGGC TCGGCTGTGA ACCTGCAGCC CCAACTGGCC AGTGTGACTT 120
TCGCCACCAA CAACCCACCA CTTACCACCT TGGCCTTGGA AAAGCCTCTC TGCATGTTTG 180
ACAGCAAGA GGCCTTCACT GGCACCCACG AGTCTACCT GTATGCTCTG GTCGACTCAG 240
CCATTTCAGG GAATGCCTCA GTGCAAGACA GCACCAACAC CCCACTGGGC TCAACGTTCT 300
TACAAACAGA GGGTGGGAGG ACAGGTCCCT ACAAGCTGT GGCCTTTGAC CTGATCCCCT 360
GCAGTGACCT GCCCAGCCTG GATGCCATGG GGCATGTGTC CAAGGCCTCA CAGATCCTGA 420

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ATGCCTACCT GGTGAGGGTG GGTGCCAAGC GGACCTGCCT GTGGGATCCC AACTTCCAGG 480
GCCTCTGTAA CGCACCCCTG TCGGCAGCCA CGGAGTACAG GTTCAAGTAT GTCCGTGGTCA 540
ATATGTCCAC GGGCTTGGTA GAGGACCAGA CCTGTGGTTC GGACCCCATC CGCACCAACC 600
AGCTCACCCC ATACTCGACG ATCGACACGT GCGCAGGCCG GCGGAGCGGA GGCATGATCG 660
TCATCACTTC CATCTGGGC TCCTTGCCT TCTTCTACT TGTGGGTTTT GCTGGCGCCA 720
TTGCCCTCAG CCTCGTGGAC ATGGGGAGTT CTGATGGGA AACGACTCAC GACTCCCAA 780
TCACTCAGGA GGCTGTTCCT AAGTCGCTGG GGGCTCGGA GTCTTCTAC ACGTCCGTGA 840
ACCGGGGGCC GCGACTGGAC AGGGCTGAGG TGTATTCCAG CAAGCTCCAA GACTGAGCCC 900
AGCACCAACC CTGGGCAGCA GCATCTTCTT CTCTGGCCTT GCGCCAGGCC CTGAGCGGT 960
GCTTGTCA CAACCTGACTTC AGGAAGGTG AAACAGGGCT TGTCCCTCCA ACTGAGGAA 1020
AACCCTTAAT AAAATCTTCT GATGAGTTCT AAAAAAAAA
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Seq ID NO: 167 Protein Sequence
Protein Accession #: NP_008884.1

1 11 21 31 41 51
| | | | |
MPPLWALLAL GCLRFGSAVN LQPQLASVTF ATNNPTLTTV ALEKPLCMFD SKEALTGTHE 60
VYLYVLVDSA ISRNASVQDS TNTPLGSTFL QTEGGRTGPY KAVAFDLIPC SDLPSLDAIG 120
DVSKASQILN AYLVVRVGANG TCLWDPNPFQ LCNAPLSAAT EYRFKYVLVN MSTGLVEDQT 180
LWSDPIRINQ LTPYSTIDTW PGRRSGGMIV ITSILGSLPF FLLVGFAGAI ALSLVDMGSS 240
DGETTHDSQI TQEAVPKSLG ASESYSYSVN RGPPLDRAEV YSKSLQD

Seq ID NO: 168 DNA Sequence
Nucleic Acid Accession #: NM_005672.1
Coding sequence: 18..389

1 11 21 31 41 51
| | | | |
AGGGAGAGGC AGTGACCATG AAGGCTGTGC TGTGTGCCCT GTTGATGGCA GGCTTGGCCC 60
TGCAGCCAGG CACTGCCCTG CTGTGCTACT CCTGCAAAGC CCAGGTGAGC AACGAGGACT 120
GCCTTGAGGT GAGGAATGTC ACCCAGCTGG GGGAGCAGTG CTGGACCCGC CGCATCCCGG 180
CAGTTGGCCT CCGTACCGTC ATCAGCAAAG GCTGCAGCTT GAACCTGCTG GATGACTCAC 240
AGGACTACTA CGTGGGCAAG AAGAATCA CGTCTGTGA CACCGACTTG TGCAACGCCA 300
CGGGGGCCCA TGCCTTGAG CCGGCTGCCG CCATCCTTGC GCTGCTCCTT GCACTGGCC 360
TGCTGCTCTG GGGACCCGGC CAGCTATAGG CTCTGGGGGG CCCCCTGCA GCCCACTG 420
GGTGTGGTGC CCCAGGCCTT TGTGCCATC CTCACAGAAC CTGGCCAGT GGGAGCCTGT 480
CCTGGTTTCT GAGGCACATC CTAACGCAAG TTGACCATG TATGTTTGCA CCCCTTTTCC 540
CCNAACCTTG ACCTTCCCAT GGGCCTTTTC CAGGATTCN ACCNGGCAGA TCAGTTTATG 600
TGANACANAT CCGCNTGCAG ATGGCCCTTC CAACNTTIN TGTGNTGTT TCCATGGCCC 660
AGCATTTTCC ACCCTTAACC CTGTGTTTCA GCACTTNTTC CCCCAGGAG CCTTCCCTGC 720
CCACCCCATT TATGAATTGA GCCAGTTTG GTCCGTGGTG TCCCCCGCAC CCAGCAGGGG 780
ACAGGCAATC AGGAGGGGCC AGTAAAGGCT GAGATGAAGT GGACTGAGTA GAACTGGAGG 840
ACAAGAGTTG ACGTGAATTG CTGGGAGTTT CCAGAGATCG GCCTGAGG CCTGAGGGA 900
GGGGCCAGG CTCACATTTG TGGGNTCCC GAATGGCAGC CTGAGCACAG CGTAGGCCCT 960
TAATAAACAC CTGTTGGATA AGCCAAAAA

Seq ID NO: 169 Protein Sequence
Protein Accession #: NP_005663.1

1 11 21 31 41 51
| | | | |
MKAVLLALLM AGLALQPGTA LLCYSCKAQV SNEDCLQVEN CTQLGEQCWT ARIRAVGLLT 60
VISKGCSLNC VDDSQDYVVG KKNITCCDTD LCNASGAHAL QPAAAILALL PALGLLLWGP 120
GQL

Seq ID NO: 170 DNA Sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

1 11 21 31 41 51
| | | | |
AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCGTTGC TTCCAGGGCC TGCTGATTTT 60
TGGAAATGTG ATTATTGGTT GTTGCGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAAAGATG ACATCTATGG 180
GGCTGCCCTG ATCGGCATAT TTGTGGGCAT CTGCCCTTTC TGCTGTCTG TTCTAGGCAT 240
TGTAGGCATC ATGAAGTCCA GCAGGAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT 300
AGTATATGCC TTGGAAGTGG CATCTTGTAT CACAGCAGCA ACACACAGAG ACTTTTTCAC 360
ACCCAACTTC TTCTTGAAGC AGATGCTAGA GAGGTACCAA AACAAACAGC CTCCAAACAA 420
TGATGACCAG TGGAAACAACA ATGGAGTCAC CAAACCTGG GACAGGCTCA TGCTCCAGCA 480
CAATTGCTGT GGGCTAAATG GTCCATCAGA CTGGCAAAA TACACATCTG CCTTCCGGAC 540
TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
AGAACCTCTC AACCTGAGG CTTGTAAACT AGGCGTGCTT GGTTTTATC ACAATCAGGG 660
CTGCTATGAA CTGCTCTCTG GTCCATGAA CCGACACGCC TGGGGGGTTG CCGGTTTGG 720
ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCTGGGT ACCATGTTCT ACTGGAGCAG 780
AATTGAATAT TAAGAA

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Seq ID NO: 171 Protein Sequence
Protein Accession #: NP_008883.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLEEAT DNDDIYGAAW 60
      IGIFVVGICLF CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL 120
      FLKQMLERYQ NNSPPNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN 180
      DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPNNRHA WGVAFGFAL 240
10     LCWTFWVLLG TMFYWSRIEY
```

Seq ID NO: 172 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..672

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15      1      11      21      31      41      51
      |      |      |      |      |      |
      ATGAGGCTCC AAAGACCCCG ACAGGCCCGG GCGGGTGGGA GGCGCGCGCC CCGGGGCGGG 60
      CGGGGCTCCC CCTACCGGCC AGACCCGGG AGAGGCGCGC GGAGGCTCGC AAGGTTCAG 120
20     AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCTGGG CACCGCTGGG GACGATGGCG 180
      CTGCTCGCCT TGCTGCTGGT CGTGGCCCTA CCGCGGTGT GGACAGACGC CAACCTGACT 240
      GCGAGACAAC GAGATCCAGA GGAATCCAG CGAACGACG AGGGTGACAA TAGAGTGTGG 300
      TGTCACTTTT GTGAGAGAGA AACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAATGG 360
      ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTT CACGTTTTTT CATGTTGCG 420
25     AAGCAGTGCT CCGCTGGTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
      CTCCTGGAAG AGCCCATGCC CTCTTTTAC CTCAAGTGT GTAAAATTCG CTACTGCAAT 540
      TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAGAAT ATGCTGGGAG CATGGGTGAG 600
      AGCTGTGGTG GGCTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGGCCTC 660
30     AGCCTGTCTT GA
```

Seq ID NO: 173 Protein Sequence
Protein Accession #: Eos sequence

```
35      1      11      21      31      41      51
      |      |      |      |      |      |
      MRLQRPRQAP AGGRRAPRG RGSPYRPDPG RGARRLRRFQ KGGEGAPRAD PPWAPLGTMA 60
      LLALLLVVAL PRVWTDANLI ARQRDPEDSQ RTDEGDNRVW CHVCERENIF ECQNPRRCKW 120
      TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKPEEKRF LLEEMPFFFY LKCKKIRYCN 180
40     LEGPPINSSV FKEYAGSMGE SCGGLWLAIL LLLASTAAGL SLS
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Seq ID NO: 174 DNA Sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

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45      1      11      21      31      41      51
      |      |      |      |      |      |
      GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60
      CGCGCGGGAG CCAGACGCTG ACCACGTTC TCTCTCGGT CTCCTCGGC TCAGACTCCG 120
50     CGCTGCCCGG CAGCCGGGAG CCATGCCACC CCAGGCCCCC GCGCCTCCC CGCAGCGGCT 180
      CCGCGGCCTC CTGCTGTGTC TGCTGCTGCA GCTGCCCCGC CGTCTGAGCG CCTCTGAGAT 240
      CCCCAGGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
      AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGTCTGAGAC GGGAGCCCTG GGGCCAATGG 360
      CATTCCGGGT ACACCTGGGA TCCCAGGTGC GGATGGATTC AAAGGAGAAA AGGGGAATG 420
55     TCTGAGGGAA AGCTTTGAGG AGTCTGGAC ACCCACTAC AAGCAGTGTT CATGGAGTTC 480
      ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540
      AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACTTCGG CTAAAATGCA GAAATGCATG 600
      CTGTCAGCGT TGGTATTTC CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTGA 660
      AGCTATAATT TATTTGGACC AAGGAAGCCC TGAATGAAT TCAACAATTA ATATTCATCG 720
60     CACTTCTTCT GTGGAAGGAC TTTGTGAAG AATTGGTGCT GCATTAGTGG ATGTTGCTAT 780
      CTGGGTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
      TTCTCGCATC ATTATTGAAG AACTACCAA ATAAATGCTT TAATTTTCAT TTGTACCTC 900
      TTTTTTTAT ATGCTTGAAG ATGTTCACT TAAATGACAT TTTAAATAAG TTTATGIATA 960
      CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
65     TTTAAATCTA GCATTATCTA TTTTGCTTCA ATCAAAAGTG GTTTCAATAT TTTTTTTAGT 1080
      TGGTIAGAAT ACTTCTCTCA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTTGT 1140
      GGTCTTTTGT TTTTCTCTCT AGTATAGCAT TTTTAAAAA ATATAAAGC TACCAATCTT 1200
      TGTACAATTT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260
70     CAACCTTAAA AAAAAAAAAA AAAA
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Seq ID NO: 175 Protein Sequence
Protein Accession #: XP_057014

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75      1      11      21      31      41      51
      |      |      |      |      |      |
      MRPQGPAAAP QRLRGLLLLL LLQLPAPSSA SEIPKCKQKA QLRRQREVVDL YNGMCLQGPA 60
      GVPGRDGGSP ANGIPGTPGI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
      GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWFT FNGAECSEGL PIEAITLDDQ 180
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GSPEMNSTIN IHRSSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIIEE 240
LPK |

5 Seq ID NO: 176 DNA Sequence
Nucleic Acid Accession #: XM_084007
Coding sequence: 1..2268

	1	11	21	31	41	51	
10	ATGGCGAGGA	AGTTATCTGT	AATCTTGATC	CTGACCTTTG	CCCTCTCTGT	CACAAATCCC	60
	CTTCATGAAC	TAAAGCAGC	TGCTTTCCCC	CAGACCACTG	AGAAAATTAG	TCCGAATTGG	120
	GAATCTGGCA	TAAATGTTGA	CTTGGCAATT	TCCACACGGC	AATATCATCT	ACAAACAGCTT	180
	TTCTACCGCT	ATGGAGAAAA	TAATTCTTTG	TCAGTTGAAG	GGTTCAGAAA	ATTACTTCAA	240
	AATATAGGCA	TAGATAAGAT	TAAAAGAATC	CATATACACC	ATGACCACGA	CCATCACTCA	300
15	GACCAAGAGC	ATCACTCAGA	CCATGAGCGT	CACCTCAGAC	ATGAGCATCA	CTCAGACCC	360
	GAGCATCACT	CTGACCATGA	TCATCACTCC	CACCATAATC	ATGCTGCTTC	TGGTAAAAAT	420
	AAGCGAAAAG	CTCTTTGCCC	AGACCATGAC	TCAGATAGTT	CAGGTAAAGA	TCCTAGAAAC	480
	AGCCAGGGGA	AAGGAGCTCA	CCGACCAGAA	CATGCCAGTG	GTAGAAGGAA	TGTCAAGGAC	540
	AGTGTAGTGT	CTAGTGAAGT	GACCTCAACT	GTGTACAACA	CTGTCTCTGA	AGGAACTCAC	600
20	TTTCTAGAGA	CAATAGAGAC	TCCAAGACCT	GGAAAACCTC	TCCCAAGAA	TGTAAGCAGC	660
	TCCACTCCAC	CCAGTGTGAC	ATCAAAGAGC	CGGCTGAGCC	GGCTGGCTGG	TAGGAAAAACA	720
	AATGAATCTG	TGAGTGAGCC	CCGAAAAGCC	TTTATGTATT	CCAGAAACAC	AAATGAAAAAT	780
	CCTCAGGAGT	GTTTCAATGC	ATCAAAGCTA	CTGACATCTC	ATGGCATGGG	CATCCAGGTT	840
	CCGCTGAATG	CAACAGAGTT	CAACTATCTC	TGTCCAGCCA	TCATCAACCA	AATTGATGCT	900
25	AGATCTTGTC	TGATTCAATC	AACTGAAAAG	AAGCCTGAAA	TCCCTCCAAA	GACCTATTCT	960
	TTACAAATAG	CCTGGGTGG	TGGTTTTATA	GCCATTTC	TCATCAGTTT	CCTGTCTCTG	1020
	CTGGGGGTTA	TCTTAGTGCC	TCTCATGAAT	CGGGTGTITT	TCAAAATTTCT	CCTGAGTTTC	1080
	CTTGTGGCAC	TGGCCGTGG	GACTTTGAGT	GGTGATGCTT	TTTTACACCT	TCTTCCACAT	1140
	TCTCATGCAA	GTCACCCACA	TAGTCATAGC	CATGAAGAAC	CAGCAATGGA	AATGAAAAGA	1200
30	GGACCACTTT	TCAGTCACTC	GTCTTCTCAA	AACATAGAAG	AAAGTGCCTA	TTTTGATTCC	1260
	ACGTGAAGG	GTCTAACAGC	TCTAGGAGGC	CTGTATTTC	TGTTTCTGTT	TGAACATGTC	1320
	CTCACATTGA	TCAAACAATT	TAAAGATAAG	AAGAAAAAGA	ATCAGAAGAA	ACCTGAAAAT	1380
	GATGATGATG	TGGAGATTAA	GAAGCAGTTG	TCCAAGTATG	AATCTCAACT	TTCAACAAAT	1440
	GAGGAGAAAG	TAGATACAGA	TGATCGAACT	GAAGGCTATT	TACGAGCAGA	CTCACAAAG	1500
35	CCCTCCCACT	TTGATTCTCA	GCAGCCTGCA	GTCTTGGAAG	AAGAAGAGGT	CATGATAGCT	1560
	CATGCTCATC	CACAGGAAGT	CTACAATGAA	TATGTACCCA	GAGGGTGCAA	GAATAAATGC	1620
	CATTACATT	TCCACGATAC	ACTCGGCCAG	TCAGACGATC	TCAATCACCA	CCATCATGAC	1680
	TACCATCATA	TTCTCCATCA	TCACCAACCAC	CAAAACCACC	ATCCTCACAG	TCACAGCCAG	1740
	CGCTACTCTC	GGGAGGAGCT	GAAAGATGCC	GGCGTCGCCA	CTTTGGCCCTG	GATGGTGATA	1800
40	ATGGGTCATG	GCCTGCACAA	TTTCAGCGAT	GGCCTAGCAA	TTGGTGCTGC	TTTTACTGAA	1860
	GGCTTATCAA	GTGGTTTAAG	TACTTCTGTT	GCTGTGTTCT	GTCAATGAGT	GCCTCATGAA	1920
	TTAGGTGACT	TGCTGTTCT	ACTAAAGGCT	GGCATGACCG	TTAAGCAGGC	TGCTCTTTAT	1980
	AATGCATTGT	CAGCCATGCT	GGCGTATCTT	GGAATGGCAA	CAGGAATTTT	CATTGGTTCAT	2040
	TATGCTGAAA	ATGTTTCTAT	GTGGATATTT	GCACCTTACTG	CTGGCTTATT	CATGATGTTT	2100
45	GCTCTGGTTG	ATATGGTACC	TGAAATGCTG	CACAATGATG	CTAGTGACCA	TGGATGTAGC	2160
	CGCTGGGGGT	ATTCTCTTTT	ACAGAAATGCT	GGGATGCTTT	TGGGTTTTGG	AATTATGTTA	2220
	CTTATTTC	TATTGTAACA	TAAATCTG	TTTCGTATAA	ATTTCTAG		

50 Seq ID NO: 177 Protein Sequence
Protein Accession #: XP_084007

	1	11	21	31	41	51	
55	MARKLSVILI	LTFALSVNTP	LHELKAAAFP	QTTEKISPNN	ESGINVDLAI	STRQYHLQQL	60
	FYRYGENNSL	SVGEFRKLLQ	NIGIDKIKRI	HIHHDHDHHS	DHEHSDHER	HSDHEHSDH	120
	EHHSDHDHHS	HHNHAASGKN	KRKALCPDHD	SDSSGKDPNN	SQKGGAHRPE	HASGRNVKD	180
	SVSASEVTST	VYNTVSEGTG	FLETIETPRP	GKLFPPKDVSS	STPPSVTSKS	RVSRLAGRKT	240
	NESVSEPRKG	FMYSRNTNEN	PQECFNASKL	LISHGMGIQV	PLNATEFNFL	CPAIINQIDA	300
60	RSCLHTSEK	KAEIPPKTYS	LQIAWVGFI	AISIISFLSL	LGVILVPLMN	RVFFKFLLSF	360
	LVALAVGTL	GDAPHLHLLP	SHASHHSHS	HEEPAMEMKR	GPLFSLSSQ	NIESAYFDS	420
	TWKGTLALGG	LYFMFLVEHV	LTLIKQFKDK	KKKNQKKPEN	DDDVEIKQL	SKYESQLSTN	480
	EEKVDITDRT	EGYLRAADSQ	PSHFDSQQA	VLEEEVMIA	HAHPQEVYNE	YVPRGCKNKC	540
	HSFHDITLGG	SDDLIIHHHD	YHHILHHHHH	QNHHPHSHSQ	RSREELKDA	GVATLAWMVI	600
	MGDGLHNFSD	GLAIGAAFFE	GLSSGLSTSV	AVFCHPLPHE	LGDFAVLLKA	GMTVKQAVLY	660
65	NALSAMLAYL	GMATGIFIGH	YAENVSMWIF	ALTAGLFMYV	ALVDMVPEML	HNDASDHGCS	720
	RWGYFPLQNA	GMLLGFGLML	LISIFEHKIV	FRINF			

70 Seq ID NO: 178 DNA Sequence
Nucleic Acid Accession #: BC010423
Coding sequence: 248..1780

	1	11	21	31	41	51	
75	CACAGCGTGG	GAAGCAGCTC	TGGGGGAGCT	CGGAGCTCCC	GATCACGGCT	TCITGGGGGT	60
	AGCTACGGCT	GGGTGTGTAG	AACGGGGCCG	GGGCTGGGGC	TGGGTCCCT	AGTGGAGACC	120
	CAAGTGGCAG	AGGCAAGAAC	TCTGCAGCTT	CCTGCCTTCT	GGGTCACTTC	CTTATTCAAG	180
	TCTGCAGCCG	GCTCCAGGG	AGATCTCGGT	GGAACCTCAG	AAACGCTGGG	CAGTCTGCCT	240
	TTCAACCATG	CCCCGTGCCC	TGGGAGCCGA	GATGTGGGG	CCTGAGGCT	GGCTGTGCT	300

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5 GCTGCTACTG CTGGCATCAT TTACAGGCCG GTGCCCCGGG GGTGAGCTGG AGACCTCAGA 360
 CGTGGTAACT GTGGTGCTGG GCCAGGAGCG AAAACTGCCC TGCTTCTACC GAGGGGACTC 420
 CGGCGAGCAA GTGGGGCAAG TGGCATGGGC TCGGGTGGAC GCGGGCGAAG GCGCCCAAGG 480
 ACTAGCGCTA CTGCACTCCA AATACGGGCT TCATGTGAGC CCGGCTTACG AGGGCCCGGT 540
 GGAGCAGCCG CCGCCCCAC GCAACCCCTT GGACGGCTCA GTGCTCCTGC GCAACGCAGT 600
 GCAGGCGGAT GAGGGCGAGT ACGAGTGCCG GGTGAGCACC TTCCCCSCCG GCAGCTTCCA 660
 GGGCGGGCTG CCGCTCCGAG TGCTGGTGCC TCCCCTGCCC TCACTGAATC CTGGTCCAGC 720
 ACTAGAAAGAG GGCACAGGCC TGACCTTGGC AGCCTCCTGC ACAGCTGAGG GCAGCCACAG 780
 CCCCAGCGTG ACCTGGGACA CGAGGTCAA AGGCACAACG TCCAGCCGTT CCTTCAAGCA 840
 10 CTCCCGCTCT GCTGCGCTCA CCTCAGAGTT CCAGTGTGGT CCTAGCCGCA GCATGAATGG 900
 GCAGGCCACTG ACTTGTGTGG TGTCCTATCC TGGCCTGCTC CAGGACCAAA GGATCACCCA 960
 CATCCTCCAC GTGCTCTTCC TTGCTGAGGC CTCTGTGAGG GGCCTTGAAG ACCAAAATCT 1020
 GTGGCACATT GGCAGAGAAG GAGCTATGCT CAAGTGCCGT AGTGAAGGGC AGCCCCCTCC 1080
 CTATACAAC TGGACACGGC TGGATGGGCC TCTGCCAGT GGGTACGAG TGGATGGGGA 1140
 15 CACTTTGGGC TTCCCCCAC TGACCACTGA GCACAGCGGC ATCTACGTCT GCCATGTGAG 1200
 CAATGAGTTT ATCTCAAGGG ATTCTCAGGT CACTGTGGAT GTTCTTGACC CCCAGGAAGA 1260
 CTCTGGGAAG CAGGTGGAGC TAGTGTGAGC CTGGTGGTG GTGGTGGTG TGATCGCCGC 1320
 ACTCTGTGTC TGCTTCTGCG TGGTGGTGGT GGTGCTCATG TCCCGATACC ATCGCGCGAA 1380
 GGCCAGCAG ATGACCCAGA AATATGAGGA GGAGCTGACC CTGACCAGGG AGAACTCCAT 1440
 20 CCGGAGGCTG CATTCCTATC ACACGGACCC CAGGAGCCAG CCGGAGGAGA GTGTAGGGCT 1500
 GAGAGCCGAG GGCACCCCTG ATAGTCTCAA GAGCAACAGT AGCTGCTCTG TGATGAGTGA 1560
 AGAGCCCGAG GGGCGCAGTT ACTCCACGCT GACCACGGTG AGGGAGATAG AAACACAGAC 1620
 TGAACGTGCT TCTCCAGGCT CTGGGCGGGC CGAGGAGGAG GAAGATCAGG ATGAAGGCAT 1680
 25 CAAACAGGCG ATGAACCAT TTGTTGAGGA GAATGGGACC CTACGGGCCA AGCCACCGGG 1740
 CAATGGCATC TACATCAATG GCGGGGGACA CCTGTCTGTA CCCAGGCGCTG CTTCCCTTCC 1800
 CTAGGCGTGG CTCCTTCTGT TGACATGGGA GATTTTAGCT CATCTTGGGG GCCTCCTTAA 1860
 ACACCCCATC TTCTTGCGGA AGATGCTCCC CATCCCACTG ACTGCTTGAC CTTTACCTCC 1920
 AACCCCTCTG TTATCGGGA GGGCTCCACC AATTGAGTCT CTCCACCAT GCATGCAGGT 1980
 30 CACTGTGTGT GTGCATGTGT GCCTGTGTGA GTGTTGACTG ACTGTGTGTG TGTGGAGGGG 2040
 TGACTGTCCG TGGAGGGGTG ACTGTGTCCG TGGTGTGTAT TATGCTGTCA TATCAGAGTC 2100
 AAGTGAAC TGCTGTATGT GCCACGGGAT TTGAGTGGTT GCGTGGGCAA CACTGTGAGG 2160
 GTTTGGCGTG TGTGTCTATG GGCTGTGTGT GACCTCTGCC TGAAGAGCA GGTATTTTCT 2220
 CAGACCCAG AGCAGTATTA ATGATGCAGA GGTGGAGGA GAGAGGTGGA GACTGTGGCT 2280
 35 CAGACCCAGG TGTGCGGGCA TAGCTGGAGC TGGAACTCTG CTCCGGTGTG AGGGAACCTG 2340
 TCTCCTACCA CTTGCGAGCC ATGGGGGCAA GTGTGAAGCA GCCAGTCCCT GGGTCAGCCA 2400
 GAGGCTTGAA CTGTTACAGA AGCCCTCTGC CCTCTGTTGG CCTCTGGGCC TGCTGCATGT 2460
 ACATATTTTC TGTAAATATA CATGCGCCGG GAGCTTCTTG CAGGAATACT GCTCCGAATC 2520
 ACTTTTAAAT TTTTCTTTT TTTTCTTTG CCTTTCCAT TAGTTGTAAT TTTTATTAT 2580
 40 TTTTATTTT ATTTTITTT AGAGTTTGAG TCCAGCCTGG ACGATATAGC CAGACCCCTGT 2640
 CTGTAAAAA ACCAAAAACC AAAAAAATA AAAAAAATA

Seq ID NO: 179 Protein Sequence
 Protein Accession #: AAH10423

45 1 11 21 31 41 51
 | | | | |
 MPLSLGAEMW GPEAWLLLL LLASFTGRCP AGELETSDEV TVVLGQDAKL PCFYRGDSGE 60
 QVQVAVARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA 120
 DEGEYECRVF TFPAGFEQAR LRLRLVLPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAFS 180
 50 VTWDIEVKCT TSSRSFKHRS SAAVTSEFHL VPSRSMNGQP LTCVVSHPLG LQDQRITHIL 240
 HVSFLAEASV RGLBDQNLWH IREGAMLKLC LSEGGPPPSY NWTRLDGFLP SGVRVDGDTL 300
 GFPLPLTTEHS GIYVCHVSNF PSSRDSQVTV DVLDPQEDSG KQVLDVLSASV VVVGVIAALL 360
 FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHTDPRS QPEESVGLRA 420
 55 EGHFDSLKDN SSCSVSEEP EGRSYSTLTT VREIETQTEL LSPFGSRAEE EEDQDEGIKQ 480
 AMNHFVQENG TLRKPTGNG IYINGRHLV

Seq ID NO: 180 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 482..3007

60 1 11 21 31 41 51
 | | | | |
 AACTGAGCTA ACAAGAAATA CTAGAAAAGG AGGAAGGAGA ACATTGCTGC AGCTTGATC 60
 TACAACCTAA GAAAGCAAGA GTGATCAATC TCAGCTCTGT TAAACATCTT GTTTACTTAC 120
 65 TGCAATTCAG AGCTTGCAAA TGGTTAACTA TATGCAAAAA AGTCAGCATA GCTGTGAAGT 180
 ATGCGGTGAA TTTTAATTGA GGGAAAAAGG GACAATTGCT TCAGGATGCT CTAGTATGCA 240
 CTCTGCTTGA AATATTTTCA ATGAAATGCT CAGTATTCTA TCTTTGACCA GAGGTTTAA 300
 CTTTATGAAG CTATGGGACT TGACAAAAAG TGATATTTGA GAAGAAAGTA CGCAGTGGTT 360
 70 GGTGTTTTCT TTTTITTAAT AAAGGAATTG AATTACTTTG AACACCTCTT CCAGCTGTGC 420
 ATTACAGATA ACGTCAAGAA GAGTCTCTGC TTTACAGAA CCGATTTCAT CACATGACAA 480
 CATGAAGCTG TGAATTCATC TCTTTTATTC ATCTCTCCTT GCCTGTATAT CTTTACACTC 540
 CCAAACTCCA GTGCTCTCAT CCAGAGGCTC TTGTGATTCT CTTTGCAATT GTGAGGAAAA 600
 AGATGGCACA ATGCTAATAA ATTGTGAAGC AAAAGGTATC AAGATGGTAT CTGAAATAAG 660
 75 TGTGCCACCA TCACGACCTT TCCAATAAG CTTATTAAAT AACGGCTTGA CGATGCTTCA 720
 CACAAATGAC TTTTCTGGGC TTACCAATGC TATTTCAATA CACCTTGGAT TTAAACAATAT 780
 TGCAGATATT GAGATAGGTC CATTTAATGG CCTTGGCCTC CTGAAACAAC TTCAATCAA 840
 TCACAAATCT TTAGAAATTC TTAAGAGGA TACTTTCCAT GGACTCGAAA ACCTGGAATT 900
 CCTGCAAGCA GATAACAATT TTATCACAGT GATTGAACCA AGTGCTTTTA GCAAGCTCAA 960

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	CAGACTCAAA	GTGTTAATTT	TAAATGACAA	TGCTATTGAG	AGTCTTCCTC	CAAAACATCTT	1020
	CCGATTGTGT	CCTTTAACC	ATCTAGATCT	TCGTGGAAAT	CAATTACAAA	CATTGCCTTA	1080
	TGTTGGTTTT	CTCGAACACA	TTGGCCGAAT	ATTGGATCTT	CAGTTGGAGG	ACAACAAATG	1140
5	GGCCTGCAAT	TGTGACTTAT	TGCAGTTAAA	AACTTGGTTG	GAGAACATGC	CTCCACAGTC	1200
	TATAATTGGT	GATGTTGTCT	GCAACAGCCC	TCCATTTTTT	AAAGGAAGTA	TACTCAGTAG	1260
	ACTAAAGAAG	GAATCTATTT	GCCCTACTCC	ACCAGTGTAT	GAAGAACATG	AGGATCCTTC	1320
	AGGATCATT	CATCTGGCAG	CAACATCTTC	AATAAATGAT	AGTCGCATGT	CAACTAAGAC	1380
	CAGTCCATT	CTAAAACTAC	CCACCAAAGC	ACCAGGTTTG	ATACCTTATA	TTACAAAGCC	1440
	ATCCACTCAA	CTTCCAGGAC	CTTACTGCCC	TATTCCTTGT	AACTGCAAAG	TCCTATCCCC	1500
10	ATCAGGACTT	CTAATACATT	GTGAGGAGCG	CAACATTGAA	AGCTTATCAG	ATCTGAGACC	1560
	TCCTCGCAA	AATCCTAGAA	AGCTCATTCT	AGCGGGAAT	AITATTACACA	GTTTAAATGAA	1620
	GTCGTGCTA	GTGGAATATT	TCACTTTGGA	AATGCTTAC	TTGGGAAACA	ATCGTATTGA	1680
	AGTTCTTGAA	GAAGGATCGT	TTATGAACCT	AACGAGATTA	CAAAAACCTCT	ATCTAAATGG	1740
	TAACCCCTG	ACCAAATTA	GTAAAGGCAT	GTTCCTTGGT	CTCCATAATC	TTGAATACTT	1800
15	ATATCTTGAA	TACAATGCCA	TTAAGGAAAT	ACTGCCAGGA	ACCTTTAATC	CAATGCCTAA	1860
	ACTTAAAGTC	CTGTATTTTA	ATAACAACCT	CCTCCAAGTT	TTACCACCAC	ATATTTTTTC	1920
	AGGGGTCTCT	CTAACTAAGG	TAAATCTTAA	AACAAACCAG	TTTACCCATC	TACCTGTAAG	1980
	TAATATTTTG	GATGATCTTG	ATTTACTAAC	CCAGATTGAC	CTTGAGGATA	ACCCCTGGGA	2040
20	CTGCTCCICT	GACCTGGTTG	GACTGCAGCA	ATGGATACAA	AACTTAAGCA	AGAACACAGT	2100
	GACAGATGAC	ATCTCTGCGA	CTTCCCCCGG	GCATCTCGAC	AAAAAGGAAT	TGAAAGCCCT	2160
	AAATAGTGAA	ATTCTCTGTC	CAGGTTTAGT	AAATAACCCA	TCCATGCCAA	CACAGACTAG	2220
	TTACCTTATG	GTCACCACTC	CTGCAACAAC	AACAAATACG	GCTGATACTA	TTTACGATC	2280
	TCTTAGCGAC	GCTGTGCCAC	TGTCTGTTCT	AATATTGGGA	CTTCTGATTA	TGTTTCATCAC	2340
25	TATTGTTTTC	TGTGCTGCGA	GGATAGTGGT	TCTTGTCTTT	CACCGCAGGA	GAAGATACAA	2400
	AAAGAAACAA	GTAGATGAGC	AAATGAGAGA	CAACAGTCTT	GTGCATCTTC	AGTACAGCAT	2460
	GTATGGCCAT	AAAACCACTC	ATCACACTAC	TGAAAGACCC	TCTGCCTCAC	TCTATGAACA	2520
	GCACATGGTG	AGCCCCATGG	TTCATGTCTA	TAGAAGTCCA	TCCTTTGGTC	CAAAGCATCT	2580
	GGAAGAGGAA	GAAGAGAGGA	ATGAGAAAGA	AGGAAGTGAT	GCAAAACATC	TCCAAGAAG	2640
30	TCFTTTGGAA	CAGGAAAATC	ATTCAACACT	CACAGGGTCA	AATATGAAAT	ACAAAACCAC	2700
	GAACCAATCA	ACAGAAATTT	TATCCTTCCA	AGATGCCAGC	TCATTGTACA	GAAACATTTT	2760
	AGAAAGAGAA	AGGGAACCTC	AGCAACTGGG	AATCACAGAA	TACCTAAGGA	AAAACATTGC	2820
	TCAGCTCCAG	CCTGATATGG	AGGCACATTA	TCCTGGAGCC	CACGAAGAGC	TGAAGTTAAT	2880
	GGAAACATTA	ATGTACTCAC	GTCCAAGGAA	GGTATTAGTG	GAACAGACAA	AAATGAGTA	2940
35	TTTTGAACCT	AAAGCTAAAT	TACATGCTGA	ACCTGACTAT	TTAGAAGTCC	TGGAGCAGCA	3000
	AACATAGATG	GAGAGTTTGA	GGGCTTTCGC	AGAAATGCTG	TGATTCTGTT	TTAAGTCCAT	3060
	ACCTTTGAAA	TAAGTGCCCT	ACGTGAGTGT	GTCAATCAATC	AGAACCTAAG	CACAGCAGTA	3120
	AACTATGGGG	AAAAAAAAG	AAGAAGAAAA	GAAACTCAGG	GATCACTGGG	AGAAGCCATG	3180
	GCATTATCTT	CAGGCAATTT	AGTCTGTCCC	AAATAAAATC	AATCCTTGCA	TGTAAATC	3238

40 Seq ID NO: 181 Protein Sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
45	MKLWIHLFYS	SLACISLHS	QTPVLSSRGS	CDSLNCNEEK	DGTMLINECA	KGIKVMSEIS	60
	VPPSRFPQLS	LLNNGLTMLH	TNDFSGLTNA	ISIHGFMNI	ADIEIGAFNG	LGLLKQLHIN	120
	HNSLEILKED	TFHGLENLLEF	LQADNMFITV	IEPSAFSKLN	RLKVLILNDN	AIESLPPNIF	180
	RFVPLTHLDL	RGNQLQTLPY	VGFLEHIGRI	LDLQLEDNKW	ACNCDLLQLK	TWLENMPPQS	240
	IIGDVVCSNP	PFFKGSILSR	LKKESICPTP	PVYEBHEDEP	GSLHLAATSS	INDSRMSTKT	300
50	TSILKLPFKA	PGLIPYITKP	STQLPGPYCP	IPCNCVLSP	SGLLIHCQER	NIESLSDLRP	360
	PPQNPRLKIL	AGNIHSLMK	SDLVEYFTLE	MLHLGNNRIE	VLEEGSFMNL	TRLQKLYLNG	420
	NHLTKLSKMK	FLGLHNLEVL	VLEYNAIKEI	LPQTFNPMFK	LKVLYLNNNL	LQVLPPHIFS	480
	GVPLTKVNKL	TNQFTHLPVS	NILDDLDDLT	QIDLEDNPDW	CSCDLVGLQQ	WIQKLSKNTV	540
	TDDLCTSPG	HLDKKELKAL	NSEILCPGLV	NNPSMPTQTS	YLMVTTPATT	TNTADTILRS	600
55	LTDAPVLSVL	ILGLLIMFIT	IVFCAAGIVV	LVLHRRRRYK	KKQVDEQMRD	NSPVHLQYSM	660
	YGHKTTHHTT	ERPASLYBQ	HMVSPMVHVY	RSPSPGPKHL	EBEEBERNKE	GSDAKHLQRS	720
	LLQENHSPL	TGSNMKYKTT	NGSTEFLSFQ	DASSLYRNIL	EKERELQQLG	ITEYLRKNIA	780
	QLQPDMEAHY	PGAHEELKLM	ETLMYSRPRK	VLVEQTKNEY	FELKANLHAE	PDYLEVLEQQ	840
60	T						

65 Seq ID NO: 182 DNA Sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 1..1524

	1	11	21	31	41	51	
70	ATGCCGGGTG	CGGGCCCGAA	GCGGCGCGCG	CTAGCGGCGC	CGGCGGCCGA	GGAGAAGGAA	60
	GAGGCGCGGG	AGAAAGATGCT	GGCGGCCAAG	AGCGCGGACG	GCTCGGCGCC	GGCAGGCGAG	120
	GGCGAGGGCG	TGACCTTGCA	GCGGAACATC	ACGCTGCTCA	ACGGCTGGCG	CATCATCGTG	180
	GGGACCATTA	TCGGCTCGGG	CATCTTCGTG	ACGCCACCGG	GCGTGTCTCA	GGAGGCGAGC	240
	TCGCGGGGCG	TGGGCTGGT	GGTGTGGGCC	CGGTGGGCGG	TCTTCTCCAT	CGTGGGCGCG	300
	CTCTGCTACG	CGGAGCTCGG	CACCACCATC	TCCAAATCGG	GCGGCGACTA	CGCCTACATG	360
	CTGAGGTCT	ACGCTCGCT	GCCCGCCTTC	CTCAAGCTCT	GGATCGAGCT	GCTCATCATC	420
75	CGGCTTTCAT	CGCAGTACAT	CGTGGCCCTG	GTCTTCGCCA	CCTACCTGCT	CAAGCCGCTC	480
	TTCCCCACCT	GCCCGGTGCC	CGAGGAGGCA	GCCAAGCTCG	TGCGCTGCCT	CTGCTGTCTT	540
	CTGCTCACGG	CCGTGAACCTG	CTACAGCGTG	AAGGCCGCCA	CCGCGGTCCA	GGAATGCTTTG	600
	GCCGCGCCA	AGCTCTCTGC	CCTGGCCCTG	ATCATCTCTG	TGGGCTTCGT	CCAGATCGGA	660

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5 AAGGGTGATG TGTCCAATCT AGATCCCAAC TTCTCATTTG AAGGCACCAA ACTGGATGTG 720
 GGGAAACATTG TGCTGGCATT ATACAGCGGC CTCTTTGCGT ATGGAGGATG GAATTACTTG 780
 AATTTCGTGA CAGAGGAAAT GATCAACCCC TACAGAAACC TGCCCTTGGC CATCATCATC 840
 TCCCTGCCCA TCGTGACGCT GGTGTACGTG CTGACCAACC TGGCCTACTT CACCACCCTG 900
 TCCACCGAGC AGATGCTGTC GTCCGAGGCC GTGGCCGTGG ACTTCGGGAA CTATCACCTG 960
 GGCCTCATGT CCTGGATCAT CCCCCTCTTC GTGGGCCCTGT CCTGCTTCGG CTCCGTCAAT 1020
 GGGTCCCTGT TCACATCCTC CAGGCTCTTC TTCGTGGGTG CCGGGGAAGG CCACCTGCCC 1080
 TCCATCCTCT CCATGATCCA CCCACAGCTC CTCACCCCGG TGCCGTCCCT CGTCTTCAG 1140
 TGTGTGATGA CGCTGCTCTA CGCCTTCTCC AAGGACATCT TCTCCGTGAT CAATCTCTTC 1200
 10 AGCTTCTTCA ACTGGCTCTG CGTGGCCCTG GCCATCATCG GCATGATCTG GCTGGGCCAC 1260
 AGAAAGCCTG AGCTTGAGCG GCCCATCAAG GTGAACCTGG CCCTGCCTGT GTTCTTCATC 1320
 CTGGCCTGCC TCTTCCTGAT CGCCGTCTCC TTCTGGAAGA CACCCGTGGA GTGTGGCATC 1380
 GGCTTACCA TCATCCTCAG CGGCGTGCCC GTCTACTTCT TCGGGGTCTG GTGAAAAAC 1440
 15 AAGCCCAAGT GGCTCCTCCA GGCATCTTC TCCACGACCG TCCTGTGTCA GAAGCTCATG 1500
 CAGGTGGTCC CCCAGGAGAC ATAG

Seq ID NO: 183 Protein Sequence
Protein Accession #: XP_035292.2

20 1 11 21 31 41 51
 | | | | | |
 MAGAGPKRRA LAAPAAEKEE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAILV 60
 GTIIGSGIFV TPTGVLKEAG SPGLALVWVA ACGVFSIVGA LCYAEELGTTI SKSGDYAYM 120
 25 LEVYGSPLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FWTCPVPBEA AKLVACLCLV 180
 LLTAVNCYSV KAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSPFEGTKLDV 240
 QNIVLALYSG LFAYGGMNYL NFVTEEMINP YRNLPLAIII SLPITVTLVYV LTNLAYFTTL 300
 STEQMLSSSEA VAVDFGNVHL GVMSWIIIPVF VGLSCFPGSVN GSLFTSSRLF FVGSREBHLF 360
 SILSMIHPQL LTPVPSLVFT CVMILLYAFS KDIFSVINFF SFFNWLCLVAL AIIGMIWLRH 420
 30 RKPELERPIK VNLALPVFFI LACFLIAVS FWKTPVECGI GFTIILSLGLP VYFFGVWVKN 480
 KPKNLQGIIF STTVLCQKLM QVVPQET

Seq ID NO: 184 DNA Sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 1..822

35 1 11 21 31 41 51
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 ATGAAGTGA GTATCTTTGA GGGACTCCTG AGTGGGGTCA ACAAGTACTC CACAGCCTTT 60
 GGGGCGATCT GGCTGTCTCT GGTCTTCATC TTCCGCGTGC TGGTGTACCT GGTGACGGCC 120
 40 GAGGCGTGTG GGAGTGATGA CCACAAGGAC TTCGACTGCA ATACTCGCCA GCCCGGCTGC 180
 TCCAACTCT GCTTTGATGA GTTCTTCCCT GTGTCCCATG TGGCCTCTG GCCCCTGCAG 240
 CTTATCTCG TGACATGCCC CTCACCTGCTC GTGGTCATGC ACCTGGCCTA CCGGGAGGTT 300
 CAGGAGAAGA GGCACCGAGA AGCCCATGGG GAGAACAGTG GCGCCTCTA CCTGAACCCC 360
 GGCAAGAAGC GGGGTGGGCT CTGGTGGACA TATGTCTGCA GCCTAGTGTT CAAGGCGAGC 420
 45 GTGGACATCG CTTTCTCTA TGTGTCCAC TCATTCTACC CCAATATAT CTCTCCTCCT 480
 GTGGTCAAGT GCCACGCAGA TCCATGTCCC AATATAGTGG ACTGCTTCAT CTCCAAGCCC 540
 TCAGAGAAGA ACATTTTCAC CCTCTTCATG GTGGCCACAG CTGCCATCTG CATCCTGCTC 600
 AACCTCGTGG AGCTCATCTA CTTGGTGAGC AAGAGATGCC ACGAGTGCTT GGCAGCAAGG 660
 50 AAAGCTCAAG CCATGTGCAC AGGTCTATCACC CCCACGGTA CCACCTCTTC CTGCAACAA 720
 GACGACCTCC TTTCCGGTGA CCTCATCTTT CTGGGCTCAG ACAGTCATCC TCCTCTCTTA 780
 CCAGACCGCC CCCGAGACCA TGTGAAGAAA ACCATCTTGT GA

Seq ID NO: 185 Protein Sequence
Protein Accession #: NP_005259.1

55 1 11 21 31 41 51
 | | | | | |
 MNWSIFBGLL SGVNKYSTAF GRIWLSLVFI FRVLVLVLTA ERVWSDDHKD FDCNTRQPGC 60
 60 SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP 120
 GKRRGGLWWT YVCSLVFKAS VDIAFLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
 SEKNIFTLFM VATAAICILL NLVELIYLV S KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ 240
 DDLSSGDLIF LQSDSHPLLL PDRPRDHVKK TIL

Seq ID NO: 186 DNA Sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 25..457

70 1 11 21 31 41 51
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 CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCTCTCTCC TACCCCTCCT 60
 CGCCCTGCTG GCGCTCACCT CCGCGGTGCG CAAAAAGAAA GATAAGGTGA AGAAGGCGCG 120
 CCCGGGAGC GAGTGGCTG AGTGGGCTG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
 CGGCGTGGGT TTCCCGGAGG GCACCTGGCG GGGCCAGACC CAGCGCATCC GGTGCAAGGT 240
 75 GCCCTGCAAC TGAAGAAGG AGTTTGGAGC CGACTGCAAG TACAAGTTTG AGAACTGGGG 300
 TGGTGTGAT GGGGGCAGC GCACCAAGT CCGCCAAGGC ACCCTGAAGA AGCGCGCTA 360
 CAATGCTCAG TGCCAGGAGA CCATCGCGT CACCAAGCCC TGCAACCCCA AGACCAAGC 420
 AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480
 GCCCTGGTG TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540

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CACCAGTGGC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600
 ACTCCCCAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
 TGAGCCTCCC CCAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTC 720
 ATTACTAAGA AACACATCAA ATAAACTGAC TTTTTCCTCC CAATAAAAGC TCTTCTTTT 780
 TAATAT

Seq ID NO: 187 Protein Sequence
 Protein Accession #: NP_002382.1

1 11 21 31 41 51
 | | | | |
 MQHRGFLILT LLALLALTSA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DCGVGFREBT 60
 CGAQTGRIRC RVPENWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLLKA RYNAQQQETI 120
 RVTKPCTPKT KAKAKAKGK GKD

Seq ID NO: 188 DNA Sequence
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902

1 11 21 31 41 51
 | | | | |
 CCGCAGAGGA GCCTCGGCCA GGCTAGCCAG GCGGCCCCCA GCCCTCTCCC AGGCCGCGAG 60
 CGCCCCTGCC CCGGTGCGCT GCCTCCCCCTC CCAGACTGCA GGGACAGCAC CCGTAACTG 120
 CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
 GGGTCCGGCC GGCGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCAGAG 240
 ATGCCCTCTGC CTTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
 GGGAAACGCG CCAGTGCAGG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC 360
 TGTCACTATG GAACATAAAT GGCTTCTGTC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
 TGTGAAGCTA CATCGGAACC TCGATGTAAG TTGTTGAGT GCTGGGACC AAACRAATGC 480
 AGATGCTTTC CAGGATACAC CGGAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
 AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACAG GAAGCTACAA GTGCTTTTGC 600
 CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
 ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
 TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT 780
 GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTTGGAAG CTACTACTGC 840
 AAATGTCACT TGTGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
 AATGAATGTA CTATGATGAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
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 ATCCCTGAAA ATTCTGTGAA GGAAGTCTCT AGAGCACCTG GTACCATCAA AGACAGAATC 1080
 AAGAAGTTGC TTGCTCACAA AAAACAGCATG AAAAAGAGGG CAAAAATTAA AAATGTTACC 1140
 CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACTTGC AGCCCTTCAA CTATGAAGAG 1200
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 CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220
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Seq ID NO: 189 Protein Sequence
 Protein Accession #: NP_056322.2

1 11 21 31 41 51
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 MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRSKGV 60
 CEATCEPQCK FGECVGNPKC RCFPGYTGKT CSQDVNECGM KPRPCQHRV NTHGSYKFCF 120
 LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEGPQCLCPG SGLRLAPNGR DCLDIDECAS 180
 GKVICPYNRR CVNTFGSYC KCHIGFELQV ISGRYDCIDI NECTMDSHTC SHHANCFTNQ 240
 GSFKCKCKQK YKGNGLRCSA IPENSUKEVL RAPGTIKDRI KLLLAHKNSM KKKAKIKNVT 300
 PEPTRTPPK VNLQFPNYEB IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER 360
 SLRGDVFPPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD 420
 WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLFYDRL AGDKVKGRLV 480
 FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERKGKGTG EIAVDGVLLV 540
 SGLCPDSELLS VDD

WO 03/003906

PCT/US02/21338

Seq ID NO: 190 DNA Sequence
Nucleic Acid Accession #: NM_006475
Coding sequence: 12..2522

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	ACCCATATAA	CGCCAAACAAT	CATTATGACA	AGATCTTGGC	TCATAGTCGT	ATCAGGGGTC	120
	GGGACCAAGG	CCCAAAATGTC	TGTGCCCTTC	AACAGATTIT	GGGCACCAAA	AAGAAATACT	180
10	TCAGCACTTG	TAAGAACTGG	TATAAAAAGT	CCATCTGTGG	ACAGAAAACG	ACTGTTTTAT	240
	ATGAATGTTG	CCCTGGTTAT	ATGAGAATGG	AAGGAATGAA	AGGCTGCCCA	GCAGTTTTGC	300
	CCATTGACCA	TGTTTATGGC	ACTCTGGGCA	TCGTGGGAGC	CACCACAACG	CAGCGCTATT	360
	CTGACGCCCT	AAAACGTAGG	GAGGAGATCG	AGGAAAAGGG	ATCCTTCACT	TACTTTGCAC	420
	CGAGTAATGA	GGCTTGGGAC	AACCTGGATT	CTGATATCCG	TAGAGGTTTG	GAGAGCAACG	480
15	TGAATGTTGA	ATTACTGAAT	GCITTTACATA	GTCAATGAT	TAATAAGAGA	ATGTTGACCA	540
	AGGACTTAAA	AAATGGCATG	ATTATTCCCT	CAATGTATAA	CAATTTGGGG	CTTTTCATTA	600
	ACCATTATCC	TAATGGGGTT	GTCACTGTTA	ATTGTGCTCG	AATCATCCAT	GGGAACCCAGA	660
	TGCAACAAA	TGGTGTGTTC	CATGTCATTG	ACCGTGTGCT	TACACAAAIT	GGTACCTCAA	720
	TTCAAGACTT	CATTGAAGCA	GAAGATGACC	TTTCATCTTT	TAGAGCAGCT	GCCATCACAT	780
20	CGGACATATT	GGAGGCCCTT	GGAAAGAGAC	GTCACTTCAC	ACTCTTTGCT	CCCACCAATG	840
	AGGCTTTTGA	GAAACTTCCA	CGAGGTGTCC	TAGAAAAGGT	CATGGGAGAC	AAAGTGGCCT	900
	CGAAGCTCT	TATGAAGTAC	CACATCTTAA	ATACTCTCCA	GTGTTCTGAG	TCTATTATGG	960
	GAGGAGCAGT	CTTTGAGACG	CTGGAAGGAA	ATACAATTGA	GATAGGATGT	GACGGTGACA	1020
	GTATAACAGT	AAATGGGAAT	AAAAATGGTG	ACAAAAAGGA	TATTGTGACA	AATAATGGTG	1080
25	TGATCCATT	GATGATCAG	GTCCCTAAAT	CTGATTCTGC	CABAACAGTT	ATTGAGCTGG	1140
	CTGGAATAA	CAAAACCAAC	TTACCGGATC	TTGTGGCCCA	ATTAGGCTTG	GCATCTGCTC	1200
	TGAGGCCAGA	TGGAGAATAC	ACTTTGCTGG	CACCTGTGAA	TAATGCATT	TCTGATGATA	1260
	CTCTCAGCAT	GGTTCAGCGC	CTCCCTAAAT	TAATTCGTCA	GAATCACATA	TTGAAAGTAA	1320
	AAGTTGGCCT	TAATGAGCTT	TACAACGGGC	AAATCTGGA	AACCATCGGA	GCCAAACAGC	1380
30	TCAGAGTCTT	CGTATTCGT	ACAGCTGTCT	GCATTGAAA	TTGATGCATG	GAGAAAGGGA	1440
	GTAAGCAAGG	GAGAAACGGT	GCGATTACCA	TATTCGCGCA	GATCATCAAG	CCAGCAGAGA	1500
	AATCCCTCCA	TGAAAAGTTA	AAACAAGATA	AGCGCTTTAG	CACCTTCCTC	AGCCTACTTG	1560
	AAGCTGCAGA	CTTGAAAGAG	CTCCGTGACAC	AACCTGGAGA	CTGGACATTA	TTGTGCCCAA	1620
	CCAATGATCG	TTTAAAGGGA	ATGACTAGTG	AAGAAAAAGA	AATTCTGATA	CGGGACAAAA	1680
35	ATGCTCTTCA	AAACATCAT	CTTTATCACC	TGACACCAGG	AGTTTTCATT	GGAAAAGGAT	1740
	TTGAACCTCG	TGTTACTAAC	ATTTTAAAGA	CCACACAAGG	AAGCAAAATC	TTTCTGAAAG	1800
	AAGTAAATGA	TACACTTCTG	GTGAATGAAT	TGAAATCAAA	AGAATCTGAC	ATCATGACAA	1860
	CAAAATGCTG	AATTCATGTT	GTAGATAAAC	TCCTCTATCC	AGCAGACACA	CCTGTTGGAA	1920
	ATGATCAACT	GCTGGAAATA	CTTAATAAAT	TAATCAAATA	CATCCAAATT	AAGTTTGTTT	1980
40	GTGCTAGCAC	CTTCAAGGAA	ATCCCGGTGA	CTGCTATATC	AACTAAATTT	ATAACCAAAG	2040
	TTGTGGAACC	AAAAATTAAG	GTGATTGAAG	GCAGTCTTCA	GCCTATTATC	AAAACGGAAG	2100
	GACCCACATG	CAAAAGAGTC	AAAAATGAAG	GTGAACCTGA	ATTCAGACTG	ATTAAGGAAG	2160
	GTGAAACAA	AACGGAAGTG	ATCCATGGAG	AGCCAATTAT	TAAAAAATAC	ACCAAAATCA	2220
	TTGATGAGT	GCTGTGGGAA	ATAACTGAAA	AAGAGACACG	AGAAGAACGA	ATCATTACAG	2280
45	GTCCTGAAAT	AAAATACACT	AGGATTICTA	CTGGAGGTGG	AGAAACAGAA	GAAACTCTGA	2340
	AGAAAATGTT	ACAAGAAGAG	GTCAACCAAGG	TCACCAAAAT	CATTGAAGST	GGTGATGGTC	2400
	ATTTATTGGA	AGATGAAGAA	ATTAAGAGAC	TGCTTCAGGG	AGACACACCC	GTGAGGAAGT	2460
	TGCAAGCCAA	CAAAAAGATT	CAAGGTCTTA	GAAGACGATT	AAGGGAAGST	CGTTCTCAGT	2520
	GAATAATCCA	AAACAGAGAA	AAAAATGTTT	TACACACCTA	AGTCAATTAAC	CTGACCTTGA	2580
50	AAAAATGTTG	GAGCCAAGTT	GACTTCAGGA	ACTGAAACAT	CAGCACAAAG	AAGCAATCAT	2640
	CAAAATATTC	TGAACACAAA	TTTAATATTT	TTTTTTCTGA	ATGAGAAACA	TGAGGGAAAT	2700
	TGTGGAATTA	GCCTCCTGTG	GTAAAGGAAT	TGAAGAAAT	ATAACACCTT	ACACCTTTT	2760
	TCATCTTGAC	ATTAAAGATT	CTGGCTAACT	TTGGAATCCA	TTAGAGAAAA	ATCCTTGCTA	2820
	CCAGATTTCAT	TACAATTCAA	ATCGAAGAGT	TGTGAACCTG	TATCCCATTG	AAAAGACCGA	2880
55	GCCTTGTATG	TACGTATTGG	ATACATAAAA	TGCACGCAAG	CCATTATCTC	TCCATGGGAA	2940
	GCTAAGTTAT	AAAAATAGST	GCITGGTGTA	CAAAACTTTT	TATATCAAAA	GGCTTTGCAC	3000
	ATTTCTATAT	GAGTGGGTTT	ACTGGTAAAT	TATGTTATTT	TTTACAACTA	ATTTGTGACT	3060
	CTCAGAAATG	TGTGATATG	CTTCTTGCAA	TGCATATTTT	TTAATCTCAA	ACGTTTCAAT	3120
60	AAAACCAATT	TTGAGATATA	AAGAGAATTA	CTTCAAAATT	AGTAATTCAG	AAAAACTCAA	3180
	GATTTAAGTT	AAAAAGTGGT	TTGGACTTGG	GAA			

Seq ID NO: 191 Protein Sequence
Protein Accession #: BAA02836.1

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	KRWYKKSICG	QKTTVLYECC	PGYMRMEGMK	GCPAVLPIDH	VYGTGLGIVGA	TTTQRYSDAS	120
70	KIRBEIEGKG	SFTYFAPSNE	AWNDLDSDIR	RGLESHNVVE	LLNALHSHMI	NKRMLTKDLK	180
	NGMIIPSMYN	NIGLFINHYP	NGVVTVNCAR	I IHGNQIATN	GVVHVIVDRVL	TQIGTSIQDF	240
	IEAEDDLSSP	RAAAITSDIL	EALGRDGHFT	LFAPTNEAPE	KLPRGVLERF	MGDKVASEAL	300
	MKYHILNTLQ	CSESIIMGAV	FETLEGNTE	IGCDGDSITV	NGIKMVNKKD	IVTNGVIHL	360
	IDQVLIIPDSA	KQVIELAGKQ	QTTFTDLVAQ	LGLASALRPD	GEYTLAPVN	NAFSDDTLSM	420
75	IQRLKLILQ	NHILKVKVGL	NELYNQILE	TIGGKQLRVF	VYRTAVCIEN	SCMEKGSKQG	480
	RNGAIHFIRE	IIKPAEKSLH	EKLKQDKRFS	TFLSLLEAAD	LKELLTQPGD	WTLFVPTNDA	540
	PKGMTSBEKE	ILIRDKNALQ	NILYHLTPG	VFIGKGFEPG	VINILKTQG	SKIFLKEVND	600
	TLNVNELKSK	ESDINTTNGV	IHVVDKLLYP	ADTFVGNQDL	LEILNKLIKLY	IQIKFVRGST	660

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FKEIPVTVYT TKIITKVVEP KIKVIEGSLQ PIKTEGPTL TKVKIEGEPE FRLIKEGETI 720
TEVIHGEPII KKYTKIIDGV PVEITEKETR EERIITGPEI KYTRISTGGG ETEBTLKKLL 780
QBEVTKVTEF IEGGDGHLFE DEEIKRLLQG DTFVRKLQAN KKVQGSRRRL REGRSQ

5 Seq ID NO: 192 DNA Sequence
Nucleic Acid Accession #: NM_006670
Coding sequence: 85..1347

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GACGGGCGTC TGCGGCTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCTCGTCT 180
TCTCCACCT CCTCGGCATC CTCCTTCTCC TCCTCGGCGC CGTTCCTGGC TTCCGCCGTG 240
15 TCGCCGCAGC CCCCGCTGCC GGACCACTGC CCGCGCTGT GCGAGTGTCT CGAGGCAGCG 300
CGCACACTCA AGTCCGTTAA CCGCAATCTG ACGAGGTGCG CCAAGGACCT GCCCGCTAC 360
GTGCGCAACC TCTTCCTTAC CGGCAACCAG CTGGCCGTGC TCCTGCGCGG CGCCTTCGCC 420
CGCGGCGCGC CGCTGGCGGA GCTGGCGCGC CTCAACTCA GCGGCAGCGG CTTGACGAG 480
20 GTGCGCGCGG GCGCCTTCGA GCATCTGCC AGCCTGCCGC AGCTCGACCT CAGCCACAAC 540
CCACTGCGCG ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCGT CTGGGCCCCC 600
AGTCCCTTG TGGAACTGAT CCTGAACCAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC 660
CGGAGCTTGG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCGGTGCACT GCAGGGGCTC 720
CGCGGCTTGG AGCTGGCACC CAACCACTTC CTTTACCTGC CCGGGCATGT GCTGGCCCAA 780
25 CTGCCCAGCC TCAGGCACCT GGAATTAAGT AATAATTGCG TGGTGAGCCT GACCTACGTG 840
TCCTTCGCA ACCTGACACA TCTAGAAAGC CTCCACTTGG AGGACAATGC CCTCAAGGTC 900
CTTCACAATG GCACCCCTGGC TGAGTTGCAA GGTCTACCCC ACATTAGGCT TTTCTCGGAC 960
AACAACTCCT GGGTCTCGCA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020
GAGGTAGTGC AGGGCAAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
30 GTCCTCTTGG AACTCAAACG TGCTGACCTG GACTGTGACC CGATTCTTCC CCATCCCTG 1140
CAAACCTCTT ATGCTCTCCT GGGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCCTG 1200
GTTTGTGATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCCTG 1260
AGGGATCACA TGGAAAGGTA TCATTACAGA TATGAAATCA ATGCCGACCC CAGATTAAAC 1320
AACCTCAGTT CTAACCTCGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACCTG 1380
CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCACCTTTCA TCCTCCACTA 1440
35 TAGATACAAC GGACTTTGAC TAAAAGCAST GAAGGGGATT TGCTTCTCTG TTAGTAAAG 1500
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TGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
40 ACAGATAGCA TTCAACAAAA GCTGCTCAA CTTTTCGAG AAAAACTTT TATTATAAA 1740
TATCAGTTT ATTCTCATGT ACCTAAGTTG TGGAGAAAT AATTGCATCC TATAAACTGC 1800
CTGCAGACGT TAGCAGGCTC TTCAAAATAA CTCATGTGTC CACAGGACCA CTTGCATCCA 1860
AGAGCATGCT TACATTTTAC TGTCTGCAT ATTACAAAAA ATAACCTTGA ACTTCATAAC 1920
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45 TTTTATAAAA CTGCATCGAG ATCCAAACGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040
ATTCTTAAAA GAA

Seq ID NO: 193 Protein Sequence
Protein Accession #: CAA82324.1

50 1 11 21 31 41 51
| | | | | |
MPGGCSRGPA AGDGRRLRLR LALVLLGWVS SSSPTSSASS FSSSAFFLAS AVSAQPPLPD 60
QCPALCEBSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLAVLPAGA FARRPPLAEL 120
AALNLSRSLR QNRFAFAEH LPSLRQLDLS HNPLADLSPF AFSGSNAVS APSPLVELIL 180
55 NHIVPPEDER DVSFEGMVV AALLAGRALG GLRRLLELAS HFLYLPDVL AQLPSLRHLD 240
LSNNSLSLT YVSFRNLTHL ESLHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWVDC 300
HMADMVIMLK ETEVVQKDR LTCAYPEKMR NRVLLELNSA DLDGDPILPP SLQTSYVFLG 360
IVLALIGAF LVLVLYLNKRG IKKWMHINRD ACRDHMEGYH YRVEINADPR LTNLSSNSDV

60 Seq ID NO: 194 DNA Sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86..1126

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GACGCCAAGG GAGCAGGACG GAGCCATGGA CCCCGCCAGG AAAGCAGGTC CCCAGGCCAT 120
70 GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA 180
GTGCTACAGC TGCGTGCAGA AAGCAGATGA CCGATGCTCC CGAACAAGA TGAAGACAGT 240
GAAGTGCAGC CCGGCGCTGG ACCTCTGCAC CGAGGCGGTG GGGGCGGTGC AGACCATCCA 300
CGGACAATTC TCGCTGGCAG TCGSGGGTTC CGGTCGGGA CTCGCCGGCA AGAATGACCG 360
CGGCTTGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
CTGCAAGCC AAGCTCAACC TCACCTCGCG GCGCTCGAC CCGGCAAGTA ATGAGAGTGC 480
75 ATACCGGCC AACCGCTGG AGTGCTACAG CTGTGTGGC CTGAGCCGGG AGGCGTCCCA 540
GGGTACATCG CCGCGGCTCG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
CTTGACGGC AACGTCACTT TGACGGCAGC TAATGTGACT GTGTCCTTGC CTGTCCGGGG 660
CTGTGTCCAG GATGAATTCT GCACCTCGGA TGGAGTAACA GGCCCGAGGT TCACGCTCAG 720

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TGGCTCCTGT TGCACGGGGT CCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
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ATTGGCAGCC CTCTGTTGG CCGTGGCTGC TGGTGTCCCTA CTGTGAGCTT CTCCACCTGG 1140
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ATCGGTCCCC CATATGCTCT CTTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC 1620
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Seq ID NO: 195 Protein Sequence

Protein Accession #: NP_055215

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CTEAVGAVET IHGQFSLAVX GCGSGLPGKN DRGLDLHGLL AFILQLQCCA DRCNAKLNLT 120
SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCFDGNVTLT 180
AANVTVSLPV RGCVDDEPCT RDGVTGPFT LSGSCCQSSR CNSDLRNKTY FSPRIPLPLVR 240
LPPPEPTTVA STTSVTTSTS APVRPTSTTK PMPAPTSQTP RQGVHEEASR DEEPRLTGGA 300
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Seq ID NO: 196 DNA Sequence

Nucleic Acid Accession #: NM_006536

Coding sequence: 109..2940

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AGCATTGCAG GTCTTATTTC CAACCTGAAG TTTGTGACTC TCCTGTTTGC CTTAAGTTCA 180
GAACCTCCAT TCCTGGGAGC TGGAGTACAG CTTCAGACA ATGGGTATAA TGGATTGTCTC 240
ATTGCAATTA ATCTTCAGGT ACCTGAGAAT CAGAACCCTCA TCTCAACCAT TAAGGAAATG 300
ATAACTGAAG CTTCATTTTA CTTATTTAAT GCTACCAAGA GAAGAGTATT TTTTCAAAAI 360
ATAAAGATTT TAATACCTGC CACATGSAAA GCTAATAATA ACACCAAAAT AAAACAAGAA 420
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TACACCTTAC AATACAGAGG GTGTGGAATA GAGGGAAAA ACATTCAATT CACACCTAAT 540
TTCCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT 600
GAATGGGCCC ACCTCCGTTG GGGTGTGTTT GATGAGTATA ACATGACAA ACCTTTCTAC 660
ATAAATGGGC AAAATCAAAAT TAAAGTGACA AGGTGTTTCT CTGACATCAC AGGCATTTTT 720
GTGTGTGAAA AAGGTCTCTG CCCCAGAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
AGTTTATCTT CTGTGGTTGA ATTTTGTAAAT GCAAGTACCC ACRAACCAAG AGCACCAGAA 900
CTACAGAAC AGATGTGCAG CCTCAGAAGT GCATGGGATG TAATCAGACA CTCTGCTGAC 960
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GTACAGCTCG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG 1080
GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAATTTT ATTGTATGCA GATTGTGAA 1140
ATTCTATCCT TCGTGGCAT TGCCAGTTTC GACAGCAAG GAGAGATCAG AGCCAGCTGA 1200
CACCAAAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA 1260
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AAACTGAATG GAAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAAGCG AGATGATAAG 1380
CTTCTTGCCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCCATTGCC 1440
CTGGGTTTCAT CTGCAGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500
TTCTTTGTTT CAGATATATC AAACCTCCAAT AGCATGATTG ATGCTTTCAG TAGAATTTCC 1560
TCTGGAAGTG GAGACATTTT CCAGCAACAT ATTCAAGCTG AAAGTACAGG TGAATAATGTC 1620
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TGGATTCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCTGAACAA TACCCATCAT 1860
TCTCTGCAAG CCTGAAAGT GACAGTGACC TCTGCGCCT CCAACTCAGC TGTGCCCCCA 1920
GCCACTGTGG AAGCCTTTGT GGAAAGAGAG AGCCTCCATT TTCTCATCC TGTGATGATT 1980
TATGCCAATG TGAAACAGGG ATTTTATCCC ATTCCTTAAG CCACTGTCAC TGCCACAGTT 2040
GAGCCAGAGA CTGGAGATCC TGTTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100
GTTATAAAAA ATGATGGAAT TTAAGTCAAG TATTTTCTCT CTTTGTCTGC AAATGGGTAGA 2160
TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCAGC CCACTCTATT 2220
CCAGGGAGTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280
GCTCCAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340
AGCTCAGGAG GCTCCTTTTC AGTGTCTGGG GTTCCAGCTG GCCCCACCC TGATGTGTTT 2400
CCACCATGCA AAATTTATGA CCTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCTATCT 2460
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AGTAAAAGTC TACAGAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA 2580
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ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTTATGTT 2700
GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCCCAGCG 2760
CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820
GGAGTTTTAA CAGCAATGGG TTTGATAGGA ATCATTGGCC TTATTATAGT TGTGACACAT 2880
CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAAACAA ATTATTATAA 2940
ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTCG ACTACAAAAA 3000
CATACTAACA AAGTCAAAAT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTGACA 3060
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CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATTCT TTAAGTAAT GTCTTTAAAG 3180
GCAAGCGGAA GGGTAAAGTC GGACCAAGTG CAAGGAAAGT TTGTTTTATT GAGGTGGAAA 3240
AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACTGTCTG TGTGAAGCAA 3300
TCATTTAGTT ACTTTGATTA ATTTTCTTT TCTCCTTATC TGTGCAGTAC AGGTGTCTTG 3360
TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAAIGCAAAG CTCTTTACCT 3420
CTTGCTATTT TGTATATAT ATTTTATATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540
TTTAGACAAA AGGTCTATTG AATTATTATT TGTGTAAGTT TCTACTCCCA TCAAGCAGC 3600
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TACCTAGGAA A

Seq ID NO: 197 Protein Sequence
Protein Accession #: NP_006527

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1 11 21 31 41 51
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GDDPYTLQYR GCGKEGKYIH FTFNLLNDN LTAGYGSRRG VFVHEWAHLR WGVFDEYNND 180
KPFYINGNQK IKVTRCSSDI TGFVCEKEGP CPQENCIISK LFKGCTFIY NSTQNATASI 240
MFMQSLSSVV EFCNASTHNQ EAPNLQMQMC SLRSAMDVIT DSADEHHSFP MNGTELPPPP 300
TFSLVQAGDK VVCLVLDVSS KMAEADRLQ LQQAEEFYLM QIVEIHTFVG IASPDSKGEI 360
RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKGF EVVEKLNKGA YGSMVLVTS 420
GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRLT GGLKFFVPDI SNSNSMIDAF 480
SRSSSGTDGI FQHQIQLST GENVKPHHL KNTVTVDNTV GNDTMLFVTV QASGPPEIIL 540
FDDPGRKYIT NNFITNLFTR TASLWIPGTA KPGHWTYTLN NTHHSLQALK VVTVSRAANS 600
AVPPATVEAF VERDSLHFFH FVMYANVKQ GFYPILNATV TATVEPETGD PVTLRLLDDG 660
AGADVIKNDG IYSRYFFSFA ANGRYSLKVH VNHSFSPIS TP AHSIPGSHAM YVPGYTANGN 720
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LTLSTWAPGE DFDQGGATSY EIRMSKSLON IQDDFNNAIL VNTSKRNPOQ AGIREIFTFS 840
PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
LILKGVLTAM GLIGIICLI VVTHHTLSRK KRADKKENG T KLL

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Seq ID NO: 198 DNA Sequence
Nucleic Acid Accession #: NM_001944
Coding sequence: 84..3083

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1 11 21 31 41 51
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CCATCTTCGT GGTGGTCATA TTGGTTCATG GAGAAATGCG AATAGAGACT AAAGGTCAAT 180
ATGATGAAGA AGAGATGACT ATGCAACAAG CTAAAAGAAG GCAAAAACGT GAATGGGTGA 240
AATTGGCCAA ACCCTGCAGA GAAGGAGAAG ATAACCTCAA AAGAAACCCA ATTGCCAAGA 300
TTACTTCAGA TTACCAAGCA ACCCAGAAAA TCACCTACCG AATCTCTGGA GTGGGAATCG 360
ATCAGCCGCV TTTTGGAAATC TTTGTTGTTG ACAAAAACAC TGGAGATATT AACATAACAG 420
CTATAGTCGA CCGGAGGAA ACTCCAAGCT TCCTGATCAC ATGTCGGGCT CTAATGCCCC 480
AAGGACTAGA TGTAGAGAAA CCACTTATAC TAACGGTTAA AATTTTGGAT ATTAATGATA 540
ATCCTCCAGT ATTTTCACAA CAAATTTTCA TGGGTGAAAT TGAAGAAAT AGTGCCTCAA 600
ACTCACTGGT GATGATACTA AATGCCACAG ATGCAGATGA ACCAAACCCAC TTGAATTCTA 660
AAATTGCCTT CAAAATTGTC TCTCAGGAAC CAGCAGGCAC ACCCATGTTCT CTTCTAAGCA 720
GAAACACTGG GGAAGTCCGT ACTTTGACCA ATTTCTCTGA CCGAGAGCAA GCTAGCAGCT 780
ATCGTCTGGT TGTGAGTGGT GCAGACAAAG ATGAGAGAAG ACTATCAACT CAATGTGAAT 840
GTAATATTAA AGTGAAAGAT GTCAACGATA ACTTCCCAAT GTTTAGAGAC TCTCAGTATT 900
CAGCAGCTAT TGAAGAAAT ATTTTAAAGT CTGAATTACT TCGATTTCAA GTAACAGATT 960
TGGATGAAGA GTACACAGAT AATTGGCTTG CAGTATATTT CTTTACCTCT GGGAAATGAAG 1020
GAAATGGTT TGAATACAA ACTGATCCTA GAACTAATGA AGGCATCCTG AAATCGGTGA 1080
AGGCTCTAGA TTAATGAACAA CTACAAAGCG TGAAACTTAG TATTGCTGTC AAAAACAAAG 1140
CTGAATTTCA CCAATTCAGT ATCTCTCGAT ACCGAGTTCA GTCAACCCCA GTCACAATT 1200
AGGTATATAA TGTATAGAAA GGAATTGCAT TCCGTCCTGC TTCCAAGACA TTTACTGTGC 1260
AAAAAGGCAT AAGTAGCAAA AATTGGTGG ATTATATCCT GGAACATAT CAAGCCATCG 1320
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ATTCTACTTT CATAGTTAAC AAAACAATCA CAGCTGAGGT TCTGCCCATA GATGAATACA 1500
CGGGTAAAC TTCTACAGC ACGGTATATG TTAGAGTACC CGATTTCAT GACAAATTGTC 1560
CAACAGCTGT CCTCGAAAAA ATGCTGCTTC CGAGTTCTTC ACCTTCCTG GTTCTCTCCG 1620
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TAAAGTTGCC TGCCGTATGG AGTATCACAA CCCTCAATGC TACCTCGGCC CTCCTCAGAG 1740
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ACAATCCGCT TCAGATGCCA CGCAGCTTGA CACTGGAAAGT CTGTCACTGT GACAAACAGG 1860
GCATCTGTGG AACTTCTTAC CCAACCACAA GCCCTGGGAC CAGGTATGGC AGGCCGCACT 1920
CAGGGAGGCT GGGGCTGCC GCCATCGGCC TGCTGCTCCT TGGTCTCCTG CTGCTGCTGT 1980
TGGCCCCCTT TCTGCTGTG ACCTGTGACT GTGGGGCAGG TTCTACTGGG GGAGTGACAG 2040
GTGGTTTTAT CCCAGTTTCT GATGGCTCAG AAGGAACAAT TCATCAGTGG GGAATTGAAG 2100
GAGCCCATCC TGAAGACAAG GAAATCACAA ATATTTGTGT GCCTCCTGTA ACAGCCAATG 2160
GAGCCGATTT CATGGAAAGT TCTGAAGTTT GTACAAATAC GTATGCCAGA GGCACAGCGG 2220
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GTGCTCGRGG CTTTGCAACA GGGACAGTGT CAGGAGCTGC TTCAGGATTC GGAGCAGCCA 2340
CTGGAGTTGG CATCTGTTCC TCAGGGCAGT CTGGAACCAT GAGAACAAGG CATTCCACTG 2400
GAGGAACCAA TAAGGACTAC GCTGATGGGG CGATAAGCAT GAATTTTCTG GACTCCTACT 2460
TTTCTCAGAA AGCATTTGCC TGTGCGGAGG AAGACGATGG CCAGGAAGCA AATGACTGCT 2520
TGTGTATCTA TGATAATGAA GGCAGCATG CCACTGGTTC TCCTGTGGGC TCCGTGGGTT 2580
GTTGCAGTTT TATTGCTGAT GACCTGGATG ACAGCTTCTT GGACTCACTT GGACCCAAAT 2640
TTAAAAAATC TGACAGAGATA AGCCTTGGTG TTGATGGTGA AGGCAAGAA GTTCAGCCAC 2700
CCTCTAAAGA CAGCGGTTAT GGGATTGAAT CCTGTGGCCA TCCCATAGAA GTCCAGCAGA 2760
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CTGGGTCGTG CCAGCCGACT GTTTCCATCC CTGACCTCTG GCAGCATGCT AACTATTTAG 2880
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CACTTCTCAC ACAAAATGTG ATAGTGACAG AAAGGGTGAT CTGTCCCAT TCCAGTGTTC 3000
CTGGCAACCT AGCTGGCCCA ACGCAGCTAC GAGGGTCACA TACTATGCTC TGTACAGAGG 3060
ATCCTTGCTC CCCTCTAATA TGACCAGAAAT GAGCTGAAGT ACCCACTTGA CCAAAATCTG 3120
ATCTTTGGAC TAAAGTATTC AAAATAGCAT AGCAAAGCTC ACTGTATTGG GCTAATATTG 3180
TGGCACTTAT TAGCTTCTCT CATAAACTGA TCACGATTAT AAATTAATG TTTGGGTTCA 3240
TACCCCAAAA GCAATATGTT GTCACTCCTA ATTCCTAAGT ACTATTCAAA TTGTAGTAAA 3300
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Seq ID NO: 199 Protein Sequence
Protein Accession #: NP_001935

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GEDNSRRNPI AKITSDYQAT QKITYRISGV GIDQPPFGIF VVDKNTGDIN ITAIVDREET 120
PSFLITCRAL NAQGLDVEKP LILTVKILDI NDNPPVFSQQ IFMGEIEENS ASNSLVMILN 180
ATDADEPNHL NSKIAFKIVS QEPAGTFMFL LSRNTGEVRT LTNSLDREQA SSYRLVVSQA 240
DKDGEGLSTQ CECNIKVKDV NDNPFMRDYS QYSARIEENI LSSELLRFQV TDLDEEYTDN 300
WLAVYFFTSQ NEGNWFIEQT DPRTNEGILK VVKALDVEQL QSVKLSIAVK NKAEPHQSVI 360
SRYRVQSTPV TIQVINVRG IAFRPASKTF TVQKGISSKK LVDYILGTQY AIDEDTNKAA 420
SNVKYVMGRN DGGVLMIDSK TAEIKFVKNM NRDSTFIVNK TITAEVLAI D EYTGKTSTGT 480
VYVRVPDFND NCPTAVLEKD AVCSSSPSVV VSARTLNNRY TGPYTFALD QPVKLPVWVS 540
ITTLNATSL LRAQEQIPPQ VYHISLVLT D SONNRCEMPR SLTLEVQCQD NRGICGTSYP 600
TTSFPGTRYGR PHSGRIGPAA IGLLLLGLLL LLLAPLLLLT CDCGAGSTGG VTGGFIPVPD 660
GSEGTIHQWG IEGAHPEDEK ITNICVPVPT ANGADFMESS EVCTNTYARG TAVEGTSGME 720
MTTKLGAATE SGGAAGFATG TVSGAASGFG AATGVGICSS QSGTMRTRH STGGTNKDYA 780
DGAISMNPLD SYFSQKAFAC AEEDDGQEAN DCLLIYDNAG ADATGSPVGS VGCCSFIADD 840
LDDSPFLSLG PKFKKLAEIS LGVDGEGKEV QPPSKDSGYG IESCGHPLEV QQTGFVKCQT 900
LSGSQGSASL SASGSVQPAV SIPDPLQHGN YLVTETYSAS GSLVQPSTAG FDPLLTQNV I 960
VTERVICPIS SVPQNLGAPT QLRGSHMLC TEDPCSRLI

Seq ID NO: 200 DNA Sequence
Nucleic Acid Accession #: NM_020411
Coding sequence: 86..526

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ACTGGGCGTC TTCCCATCGG CCCCTTCGCC AGTGTGGGGA ACGCGGCGGA GCTGTGAGCC 180
GGCGACTCGG GTCCTGAGG TCTGGATTCT TTCTCCGCTA CTGAGACACG GCGGACACAC 240
ACAAACACAG AACCACACAG CCAGTCCCAG GAGCCCAGTA ATGGAGAGCC CCAAAAAGAA 300
GAACCAAGCAG CTGAAAGTCG GATCCTTACA CCTGGGCAGC AGACAGAAGA AGATCAGGAT 360
ACAGCTGAGA TCCCATGCGC CGACATGGAA GGTGATCTGC AAGAGCTGCA TCAGTCAAA 420
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ACACTGTAAA ATGCCAGAAG CAGGTGAAGA GCAACCACAA GTTTAAATGA AGACAAGCTG 540
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CAGCTTTCAC CAAAAAATAA AAAAAA

Seq ID NO: 201 Protein Sequence
Protein Accession #: NP_065144.1

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1 11 21 31 41 51
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MLLWCPQQA CSLGVFSPAP SPVWGTRRSC EPATRVPEVW ILSPLLRHGG HTQTQNHAS 60
PRSPVMESPK KKNQQLKVG I LHLGSRQKKI RIQLRSQCAT WKVICKSCIS QTPGINLDLG 120

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SGVKVKIIPK EEHCKMPEAG EEQPQV

Seq ID NO: 202 DNA Sequence

Nucleic Acid Accession #: AA172056

Coding sequence: 121..339

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	ATGTTTTTTA	TACAGAAAGG	AGAATGCAGA	ATGGTCAGAC	TATCATGCAC	TGTTAAATTT	180
	GATTTCAAGA	AATTACAGGA	AAACTTTCCA	AAGITCCATC	TCACAGAANN	TTATTTTNCC	240
	AAGAATTCCA	AGATAAGTTT	AGTTTTATGG	AAGACTTTTA	TGTGGITTTT	ACTCACTCTT	300
15	CATCTCAGAC	ATCGACAGAT	GATTACATCA	CTTATAGTTC	TAGTAAATTT	ATTAATATAA	360
	AACTCAGAGA	CATTCCAATA	TCCACATTGC	TTACACCATT	AGGCATAGAT	TCAGTGTGAG	420
	CTATGACAA	TGAAATGAG	CTGTTTTGTC	ATTTAAAGGT	TTAAATTTCT	CTAACCAAAC	480
	TGCTTGATCC	AGATGCAGGA	CTGCAATGT	TAATATTGT	TCTGGAAGAA	CAATCAAATA	540
	AGACTTAAGA	GGAAGGGGAA	TGGCCACAAT	CCACCTGAAA	TTTTTCTTA	AAAAGTGTGC	600
20	AGCCTACTAA	ATCAGATGA	AAATAGAAAT	ACAGATATAT	AAACAAAATG	CAATCAAAT	660
	TTTCTTAAGC	TTACCTAAAG	TTATTTTCATC	TGAAAATTTT	AAGCAACTTT	GTTCAACATT	720
	AAATTGACAA	TCTAAACTAA	CAAGTCTTTT	GAATTTATGC	ATGGTAGTAA	ACATTCCTCT	780
	TATTAACCTT	ATTACCTAAG	GCTAAACCTA	AAATTTTTAA	GCAAAATTAG	AAAAATAGTC	840
	TTCACTCATC	AAAAAATAAA	GTTTGTGTACA	TTTAGTATTT	TCCCAATAAA	ATTGGTCGTT	900
25	CTTGGTTTTT	TATTGGGAGA	GTCGTGCAA	AATGTCACTA	AAAAATAAAT	AGCACTAGAA	960
	ATTATTTCTA	AATACCAA					

Seq ID NO: 203 DNA Sequence

Nucleic Acid Accession #: NM_005656.1

Coding sequence: 57..1535

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	1	11	21	31	41	51	
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	CGGAAACACC	CTATCCCGCA	CAGCCCACTG	TGGTCCCCAC	TGCTACGAG	GTGCATCCGG	180
	CTCAGTACTA	CCCGTCCCCC	GTGCCCCAGT	ACGCCCCGAG	GCTCCTGACG	CAGGCTTCCA	240
	ACCCCTCGCT	CTGCACGCGA	CCCAAAATCCC	CATCCGGGAC	AGTGTGCACC	TCAAAGACTA	300
	AGAAAGCACT	GTGCATCAC	TTGACCTTCC	GGACCTTCC	CGTGGGAGCT	GCGCTGGCCG	360
40	CTGGCCCTACT	CTGGAAGTTC	ATGGGCAGCA	AGTGCTCCAA	CTCTGGGATA	GAGTGGCACT	420
	CCTCAGGTAC	CTGCATCAAC	CCCTCTAACT	GGTGTGATGG	CGTGTCAAC	TGCCCCGGCG	480
	GGGAGGACGA	GAATCGGTGT	GTTGCGCTCT	ACGGACCAAA	CTTCATCCTT	CAGATGTACT	540
	CATCTCAGAG	CAAGTCTCTG	CACCTGTGT	GCCRAAGCGA	CTGGAACGAG	AACTACGGGC	600
	GGGCGGCTCG	CAGGACATG	GGCTATAAGA	ATAATTTTTA	CTCTAGCCAA	GGAATAGTGG	660
45	ATGACAGCGG	ATCCACCAGC	TTTATGAAAC	TGAACACAAG	TGCCGGCAAT	GTGATATCT	720
	ATAAAAAACT	GTACCAAGT	GATGCCTGTT	CTTCAAAAGC	AGTGGTTTCT	TTACGCTGTT	780
	TAGCCTGCGG	GGTCAACTTG	AACTCAAGCC	GCCAGAGCAG	GATCGTGGGC	GGTGAGAGCG	840
	CGCTCCCGGG	GGCTTGGCCC	TGGCAGGTCA	GCCTGCACGT	CCAGAAGCTC	CACGTGTGCG	900
	GAGGCTCCAT	CATCACCCTC	GAGTGGATCG	TGACAGCCGC	CCACTGCGTG	GAAAAACCTC	960
50	TTAACAAATC	ATGGCATTGG	ACGGCATTTG	CGGGGATTTT	GAGACAATCT	TTCATGTTCT	1020
	ATGGAGCGGG	ATACCAAGTA	CAAAAAGTGA	TTTCTCATCC	AAATTATGAC	TCCAAGACCA	1080
	AGAACAAATG	CATTGCGCTG	ATGAAGCTGC	AGAAGCCTCT	GACTTTCAAC	GACCTAGTGA	1140
	AACCAATGTG	TCTGCCCAAC	CCAGGCATGA	TGCTGCAGCC	AGAACAGCTC	TGCTGGATTT	1200
	CCGGTGGGG	GGCCACCGAG	GAGAAAAGGA	AGACCTCAGA	AGTGTGAAC	GCTGCCAAGG	1260
55	TGCTTCTCAT	TGAGACACAG	AGATGCAACA	GCAGATATGT	CTATGACAAC	CTGATCACAC	1320
	CAGCCATGAT	CTGTGCCGGC	TTCCTGCAGG	GGAACGTCTG	TTCTTGCCAG	GGTGACAGTG	1380
	GAGGGCCTCT	GGTCACTTCC	AACAACAATA	TCTGGTGGCT	GATAGGGGAT	ACAAGCTGGG	1440
	GTCTGGCTG	TGCCAAAGCT	TACAGACCAG	GAGGTGACGG	GAATGTGATG	GTATTACAGG	1500
	ACTGGATTTA	TGACAAAATG	AAGGCAAAAG	GCTAATCCAC	ATGGTCTTCG	TCCTTGACGT	1560
60	CGTTTTTCAA	GAAAACAATG	GGGCTGGTTT	TGCTTCCCG	TGCATGATTT	ACTCTTAGAG	1620
	ATGATTCAGA	GGTCACTTCA	TTTTTATTAA	ACAGTGAAC	TGCTGGCTT	TGGCACTCTC	1680
	TGCCATACCT	TGCAGGCTGC	AGTGGCTCCC	CTGCCAGCC	TGCTCTCCCT	AAACCTTGT	1740
	CCGCAAGGGG	TGATGGCCGG	CTGGTTCTGG	GCACCTGGCG	TCAATTGTGG	AAGGAAGAGG	1800
	GTTGGAGGCT	GGCCCATTTG	AGATCTTCTT	GCTGAGTCTT	TTCCAGGGGC	CAATTTTGGG	1860
65	TGAGCATGGA	GCTGTCACTT	CTCAGCTGCT	GGATGACTTG	AGATGAAAAA	GGAGAGACAT	1920
	GGAAAGGGAG	ACAGCCAGGT	GGCACCTGCA	GCGGCTGCCC	TCTGGGGCCA	CTTGGTAGTG	1980
	TCCCCAGCCT	ACTTCAACAAG	GGGATTTTGC	TGATGGGTTT	TTAGAGCCTT	AGCAGCCCTG	2040
	GATGGTGGCC	AGAAATAAAG	GGACCAAGCC	TTTATGGGTG	GTGACGTGGT	AGTCACTTGT	2100
	AAGGGGAACA	GAAACATTTT	TGTTCTTATG	GGGTGAGAA	ATAGACAGTG	CCCTTGGTGC	2160
70	GAGGGAAGCA	ATTGAAAAGG	AACTTGCCCT	GAGCACTCCT	GGTGCAGGTC	TCCACCTGCA	2220
	CATTGGGTGG	GGCTCTGGGG	AGGGAGACTC	AGCCTTCTCT	CTCATCTCTC	CTGACCTGTC	2280
	TCTTAGCACC	CTGGAGAGTG	AATGCCCTTT	GGTCCCTGGC	AGGGCGCCAA	GTTTGGCACC	2340
	ATGCTGGCCT	CTTCAGGCCT	GATAGTCATT	GGAAATTGAG	GTCCATGGGG	GAAATCAAGG	2400
75	ATGCTCAGTT	TAAGGTACAC	TGTTTCCATG	TTATGTTTCT	ACACATTGAT	GCTGGTGACC	2460
	CTGAGTTCAA	AGCCATCTT					

Seq ID NO: 204 Protein Sequence

Protein Accession #: NP_005647.1

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	SNFVVCTQPK	SPSGTVCTSK	TKKALCITLT	LGTFLVGAAL	AAGLLWKFMG	SKCSNSGIEC	120
	DSSGTCINPS	NWCDGVSHCP	GGEDENRCVR	LYGPNFILQM	YSSQRKSWHP	VQQDWNENY	180
	GRAACRDMGY	KNNFYSSQGI	VDDSGSTFSM	KLNTSAGNVD	IYKKLYHSDA	CSSKAVVSLR	240
	CLACGVNLNS	SRQSRIVGGE	SALEFGAWPWQ	VSLHVQNVHV	CGSSIITPEW	IVTAAHCVEK	300
10	PLNNPWHHTA	FAGILRQSCW	FYGAGYQVQK	VISHENYDSK	TKNNDIALMK	LOKPLTFNDL	360
	VKEPVLCPNG	MMQLPBLQCLW	ISGWGATEEK	GKTSEVLNAA	KVLLIETQRC	NSRYVVDNLI	420
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	TDWIYRQMK	NG					

Seq ID NO: 205 DNA Sequence
Nucleic Acid Accession #: XM_044533
Coding sequence: 238..2751

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	AGGGGCTGAG	TTTGCCAGGG	CCCACTTGAC	CCTGTTTCCC	ACCTCCCGCC	CCCCAGGTCC	120
	GGAGGCGGGG	GCCCCGCGGG	CGACTCGGGG	GCGGACCGCG	GGGCGGAGCT	GCCGCCCGTG	180
	AGTCCGCGCG	AGCCACCTGA	GCCCGAGCCG	CGGGACACCG	TGCTCTCTGC	TCTCCGAATG	240
25	CTGCGCACCG	CGATGGGCCT	GAGGAGCTGG	CTCGCCGCCC	CATGGGGCGC	GCTGCCGCCT	300
	CGGCCACCGC	TGCTGCTGCT	CCTGCTGCTG	CTGCTCTGTC	TGCAGCCGCC	GCCTCCGACC	360
	TGGGGCTCTA	GCCCCCGGAT	CAGCCTGCCT	CTGGGCTCTG	AAGAGCGGCC	ATTCCTCAGA	420
	TTCGAAGCTG	AACACATCTC	CAACTACACA	GCCCTTCTGC	TGAGCAGGGA	TGGCAGGACC	480
	CTGTACGTGG	GTGCTCGAGA	GGCCCTCTTT	GCACTCAGTA	GCAACCTCAG	CTTCCTGCCA	540
30	GGCGGGGAGT	ACCAGGAGCT	GCTTTGGGGT	GCAGACGCAG	AGAAGAAACA	GCAGTGCAGC	600
	TTCAAGGGCA	AGGACCCACA	CGCGCACTGT	CAAAACTACA	TCAAGATCCT	CCTGCCGCTC	660
	AGCGGCAGTC	ACCTGTTCAC	CTGTGGCACA	GCAGCCTTCA	GCCCCATGTG	TACCTACATC	720
	AACATGAGGA	ACTTCAACCT	GGCAAGGGAC	GAGAAGGGGA	ATGTCTCTCT	GGAAGATGGC	780
	AAGGGCCGTT	GTCCCTTCGA	CCCGAATTTT	AAGTCCACTG	CCCTGGTGGT	TGATGCGCAG	840
35	CTCTACACTG	GAAAGCTCAG	CAGCTTCCAA	GGGAATGACC	CGGCCATCTC	GCGGAGCCAA	900
	AGCCTTCGCC	CCACCAAGAC	CGAGAGCTCC	CTCAACTGGC	TGCAGACCCC	AGCTTTTGTG	960
	GCCTCAGCCT	ACATTCTCTA	GAGCCTGGGC	AGCTTGCAAG	GCGATGATGA	CAAGATCTAC	1020
	TTTTTCTTCA	CGGAGACTGG	CCAGGAATTT	GAGTTCTTTG	AGAACACCAT	TGTGTCCC GC	1080
	ATTGCCCGCA	TCTGCAAGGG	CGATGAGGGT	GGAGAGCGGG	TGCTACAGCA	CGCTGGGACC	1140
40	TCTTCTCTCA	AGGCCCGAGT	GCTGTGCTCA	CGGCCCGACG	ATGGCTTCCC	CTTCAACGTG	1200
	CTGCAGGATG	TCTTCAAGCT	GAGCCCCAGC	CCCCAGGACT	GGCGTGACAC	CCTTTTCTAT	1260
	GGGGTCTTCA	CTTCCCAGTG	GCACAGGGGA	ACTACAGAAG	GCTCTGCCGT	CTGTGTCTTC	1320
	ACAAATGAAG	ATGTGCAGAG	AGTCTTCAGC	GGCCTCTACA	AGGAGGTGAA	CCGTGAGACA	1380
	CAGCAGTGCT	ACACCGTGAC	CCACCCGGTG	CCCACACCCC	GGCCTGGAGC	GTGCATCACC	1440
45	AACAGTGCCC	GGGAAAGGAA	GATCAACTCA	TCCCTGCAGC	TCCACAGCCG	CTGTCTGAAC	1500
	TTCTCTCAAG	ACCACITCTC	GATGGACGGG	CAGGTCCGAA	GCCGCATGCT	GCTGTGCAG	1560
	CCCCAGGCTC	GCTACCAGCG	CGTGGCTGTA	CACCGCGTCC	CTGGCCTGCA	CCACACCTAC	1620
	GATGTCTCTC	TCTGTGGCAC	TGTTGACGGC	CGGCTCCACA	AGGCAGTGAG	CGTGGGCCCC	1680
	CGGGTGACCA	TCAATTGAGG	GCTGCAGATC	TTCTCATCGG	GACAGCCCGT	GCAGAACTCT	1740
50	CTCTCTGACA	CCACAGGGG	GCTGCTGTAT	GCGGCCTCAC	ACTCGGGCGT	AGTCCAGGTG	1800
	CCCATGGCCA	ACTGCAGCCT	GTACAGGAGC	TGTGGGAGCT	GCCTCTCTGC	CCGGGACCCC	1860
	TACTGTGCTT	GGAGCGGCTC	CAGCTGCAAG	CACGTGAGCC	TCTACCAGCC	TCAGCTGGCC	1920
	ACCAGGCGGT	GGATCCAGGA	CATCGAGGGA	GCCAGCGCCA	AGGACCTTTG	CAGCGCGTCT	1980
	TCCGTTGTGT	CCCCGTCTTT	TGTACCAACA	GGGGAGAAAG	CATGTGAGCA	AGTCCAGTTC	2040
	CAGCCCAACA	CTGTGAACAC	TTTGGCCTGC	CCGCTCCTCT	CCAACCTGGC	GACCCGACTC	2100
55	TGGCTACGCA	ACGGGGCCCC	CGTCAATGCC	TCGGCCCTCT	GCCACGTGCT	ACCCACTGGG	2160
	GACCTGCTGC	TGTTGGGCAC	CCAACAGCTG	GGGGAGTTCC	AGTGTCTGTC	ACTAGAGGAG	2220
	GGCTTCCAGC	AGCTGTGAGC	CAGCTACTGC	CCAGAGGTGG	TGGAGGAGCG	GGTGGCAGAC	2280
	CAAAACAGAT	AGGGTGGCAG	TGTACCCGTC	ATTATCAGCA	CATCGCGTGT	GAGTGCACCA	2340
60	GCTGGTGCCA	AGGCCAGCTG	GGGTGCAGAC	AGTCTCTACT	GGAAAGAGTT	CCTGGTGATG	2400
	TGCACGCTCT	TTGTGCTGGC	CGTGTGCTC	CCAGTTTTAT	TCTTGCTCTA	CCGGCACCGG	2460
	AACAGCATGA	AAGTCTTCTT	GAAGCAGGGG	GAATGTGCCA	GCGTGACACC	CAAGACCTGC	2520
	CCTGTGCTGC	TGCCCTCTGA	GACCCGCCCA	CTCAACGGCC	TAGGGCCCCC	TAGCACCCCG	2580
	CTCGATCACCC	GAGGGTACCA	GTCCCTGTCA	GACAGCCCCC	CGGGTGCCCG	AGTCTTCACT	2640
65	GAGTCAGAGA	AGAGGCCACT	CAGCATCCAA	GACAGCTTCG	TGGAGGTATC	CCCAGTGTGC	2700
	CCCGGGCCCC	GGGTCCGCCT	TGGCTCGGAG	ATCCGTGACT	CTGTGGTGTG	AGAGCTGACT	2760
	TCCAGAGGAC	GCTGCCCTGC	CTTCAGGGGC	TGTGAATGCT	CGGAGAGGGT	CAACTGGACC	2820
	TCCCTCTCGC	TCTGCTCTTC	GTGGAACACG	ACCGTGGTGC	CCGGCCCTTG	CGAGCCTTGG	2880
	GGCCAGCTGG	CCTGTGCTGC	TCCAGTCAAG	TAGCGAAGCT	CCTACACCCC	AGACACCCAA	2940
70	CAGGCCGTGG	CCCCAGAGGT	CCTGGCCAAA	TATGGGGGCC	TGCTTAGGTT	GGTGAACAG	3000
	TGCTCTCTAT	GTAAACTGAG	CCCTTTGTTT	AAAAAAACAAT	TCCAAATGTG	AAACTAGAAT	3060
	GAGAGGGAG	AGATAGCATG	GCAATGCAGCA	CACACGGCTG	CTCCAGTTCA	TGGCTCCCA	3120
	GGGGTGCTGG	GGATGCATCC	AAAGTGTTTG	TCTGAGACAG	AGTTGGAAC	CCTCACCAAC	3180
	TGGCTCTTTC	ACCTTCCACA	TTATCCCGCT	GCCACCGGCT	GCCCTGTCTC	ACTGCAGATT	3240
75	CAGGACCAAG	TTGGGCTGCG	TGCGTTCTGC	CTTGCCAGTC	AGCCGAGGAT	GTAAGTGTGT	3300
	CTGCCGTGCT	CCGACCACTC	CAGGACCAAG	AGGGCTAGGT	TGGCACTGCG	GCCCTCACCA	3360
	GGTCTCTGGC	TCCGACCCAA	CTCCTGGACC	TTTCCAGCCT	GTATCAGGCT	GTGGCCACAC	3420
	GAGAGGACAG	CGCGAGCTCA	GGACAGATTT	CGTGACAATG	TACGCCITTC	CCTCAGAAAT	3480
	CAGGGAAGAG	ACTGTGCCTT	GCTTCTCTCC	GTTGTTGCGT	GAGAACCCGT	GTGCCCTTTC	3540

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CCACCATATC CACCCCTCGCT CCATCTTTGA ACTCAAACAC GAGGAACTAA CTGCACCCCTG 3600
GTCTCTCTCCC CAGTCCCCCAG TTCACCCCTCC ATCCCTCACC TTCCTCCACT CTAAGGGATA 3660
TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGGTT TTTATACATT TTTTAATAAG 3720
ATGCACCTTA TGTCATTTT TAATAAAGTC TGAAGAATTA CTGTTT

5

Seq ID NO: 206 Protein Sequence
Protein Accession #: XP_044533.6

10 1 11 21 31 41 51
| | | | | |
MLRTAMGLRS WLAAPWGALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60
RFEAEHISNY TALLLSRDGR TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQQC 120
SFKGKDPQRD CQNYIKILLF LSGSHLFTCG TAAFSPMCTY INMENFTLAR DEKGNVLLED 180
15 GKGRCPFDPN FKSTALVVDG ELYTGTVSSF QGNDFPAISRS QSLRPTKTES SLNWLQDPAF 240
VASAYIPBSL CSLQCGDDKI YFFSETCQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
TSFLKAQLLC SRPDDGFPPN VLQDVFTLSP SPQDWRDILF YGVFTSQWHR GTTEGSAVCV 360
FTMKDVQRVF SGLYKEVNRE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
NFLKDHFLMD GQVRSRMLLL QPQARYQRVA VHRVPGLHHT YDVLPLGTGD GRLHKAIVSVG 480
20 PRVHIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540
PYCAWSGSSC KHVSLYQPQL ATRPWIQDIE GASAKDLCAS SSVVSPSFVP TGEKPCEQVQ 600
FQNTVNTLA CPLLSNLATR LWLRNGAPVN ASASCHVLPT GDLLLVTGQQ LGEFQCWSLE 660
EGFQQLVASV CPEVVEDGVA DOTDEGGSPV VIISTSRVSA PAGGKASWGA DRSYWKFLV 720
MCTLFVLAVL LPVLFLLYRH RNSMKVFLLKQ GECASVHPKT CPVVLPPETR PLNGLQPPST 780
25 PLDHRGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV

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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein
5 incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1. A method of detecting a bladder cancer-associated transcript in a cell from a patient,
5 the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.
2. The method of Claim 1, wherein the biological sample comprises isolated nucleic
10 acids.
3. The method of Claim 2:
 - a) wherein the nucleic acids are mRNA; or
 - b) further comprising the step of amplifying nucleic acids before the step of contacting
15 the biological sample with the polynucleotide.
4. The method of Claim 1, wherein the polynucleotide:
 - a) comprises a sequence as shown in Tables 1A-13; or
 - b) is immobilized on a solid surface.
20
5. The method of Claim 1, wherein the patient is:
 - a) undergoing a therapeutic regimen to treat bladder cancer; or
 - b) suspected of having bladder cancer.
- 25 6. An isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-13.
7. The nucleic acid molecule of Claim 6, which is labeled.
- 30 8. An expression vector comprising the nucleic acid of Claim 7.

9. A host cell comprising the expression vector of Claim 8.
10. An isolated polypeptide which is encoded by a nucleic acid molecule having
5 polynucleotide sequence as shown in Tables 1A-13.
11. An antibody that specifically binds a polypeptide of Claim 10.
12. The antibody of Claim 11, further conjugated to an effector component.
- 10 13. The antibody of Claim 12, wherein the effector component is a fluorescent label.
14. The antibody of Claim 12, wherein the effector component is a radioisotope or a
cytotoxic chemical.
- 15 15. The antibody of Claim 11, which is
a) an antibody fragment; or
b) a humanized antibody
- 20 16. A method of detecting a bladder cancer cell in a biological sample from a patient, the
method comprising contacting the biological sample with an antibody of Claim 11.
17. The method of Claim 16, wherein the antibody is further conjugated to an effector
component.
- 25 18. The method of Claim 17, wherein the effector component is a fluorescent label.
19. A method for identifying a compound that modulates a bladder cancer-associated
polypeptide, the method comprising the steps of:

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- a) contacting the compound with a bladder cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13; and
- b) determining the functional effect of the compound upon the polypeptide.

5

20. A drug screening assay comprising the steps of

- a) administering a test compound to a mammal having bladder cancer or a cell isolated therefrom;
 - b) comparing the level of gene expression of a polynucleotide that selectively hybridizes
- 10 to a sequence at least 80% identical to a sequence as shown in Tables 1A-13 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of bladder cancer.